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(54) Title: **NF-KB ACTIVATING GENE**

(57) Abstract: Provided are proteins capable of activating NF-κB, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of NF-κB. Using plasmid pNFκB-Luc, cDNA encoding a protein capable of activating NF-κB has been cloned from a cDNA library constructed from human lung fibroblasts and the like, and the DNA sequence and the deduced amino acid sequence determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting NF-κB activation.



**WO 03/048202 A2**

## DESCRIPTION

### NF- $\kappa$ B ACTIVATING GENE

#### TECHNICAL FIELD

The present invention relates to a protein capable of activating NF- $\kappa$ B, a DNA sequence encoding the protein, a method for obtaining the DNA, a recombinant vector containing the DNA, a transformant containing the recombinant vector, and an antibody which specifically reacts with the protein. The present invention also relates to use of the protein, DNA or antibody of the invention in the diagnosis, treatment or prevention of diseases associated with the excessive activation or inhibition of NF- $\kappa$ B.

The present invention also relates to a method for screening a substance capable of inhibiting or promoting NF- $\kappa$ B activation by using the protein, DNA, recombinant vector and transformant.

#### BACKGROUND ART

The transcription factor NF- $\kappa$ B (nuclear factor kappa B) plays an important role in the transcriptional regulation of various genes involved in inflammation and immunological reactions. NF- $\kappa$ B is a homo- or heterodimer protein which belongs to the Rel family. In unstimulated conditions, NF- $\kappa$ B normally resides in the cytoplasm as an inactive form by forming a complex with an I $\kappa$ B (inhibitory protein of NF- $\kappa$ B) to mask the nuclear transport signal of NF- $\kappa$ B.

When cytokines such as interleukin (IL)-1 and tumor necrosis factor (TNF)- $\alpha$  stimulate cells, I $\kappa$ B is phosphorylated by IKK (I $\kappa$ B kinase) and degraded by the 26S proteasome through ubiquitination. The released NF- $\kappa$ B moves to the nucleus, where it binds to the DNA sequence called the NF- $\kappa$ B binding sequence and induces the transcription of the gene under control of NF- $\kappa$ B. NF- $\kappa$ B is believed to regulate the expression of genes such as those for immunoglobulins, inflammatory cytokines (e.g.,

IL-1 and TNF- $\alpha$ ), interferons and cell adhesion factors. NF- $\kappa$ B is involved in inflammation and immune responses through the expression induction of these genes.

The inhibition of the function or activation of NF- $\kappa$ B may inhibit the expression of many factors (proteins) involved in inflammatory or immunological diseases or other diseases such as tumor proliferation. Thus, NF- $\kappa$ B is a promising target for medicaments against diseases caused or characterized by autoimmunity or inflammation [see e.g., Clinical Chemistry 45, 7-17 (1999); J Clin. Pharmacol. 38, 981-993 (1998); Gut 43, 856-860 (1998); The New England Journal of Medicine 366, 1066-1071 (1997); TiPS 46-50 (1997); The FASEB Journal 9, 899-909 (1995); Nature 395, 225-226 (1998); Science 278, 818-819 (1997); Cell 91, 299-302 (1997)].

Extracellular information is converted into a certain signal, which passes through the cell membrane and goes through the cytoplasm to the nucleus, where it regulates the expression of the target gene and causes cell responses. Therefore the elucidation of the mechanism of intracellular signal transduction from extracellular stimuli to NF- $\kappa$ B activation is of very important significance, because it provides very important means of developing new medicaments or therapies against autoimmune diseases and diseases exhibiting inflammatory symptoms.

It is believed that the signal transduction pathway from certain cell stimulation to NF- $\kappa$ B activation includes many steps mediated by various transmitters such as protein kinases. Therefore it is desirable for more efficient drug discovery to identify the transmitters which play a key role in the pathway, and to focus research on the transmitters to establish a new drug-screening method. Some signaling molecules involved in NF- $\kappa$ B activation have been identified [e.g., IKK, ubiquitination enzymes and the 26S proteasome described above, as well as TNF receptor associated factor 2 (TRAF2) and NF- $\kappa$ B inducing kinase (NIK)]. However, most of the mechanism of NF- $\kappa$ B activation remains unknown, and it has been desired to identify new signaling molecules and further to elucidate NF- $\kappa$ B activation mechanism.

## DISCLOSURE OF THE INVENTION

The object of the present invention is to identify a new gene and protein capable of directly, or indirectly, activating NF- $\kappa$ B, and to provide a method of use of them in medicaments, diagnostics and therapy. That is, an object of the present invention is to provide a new protein capable of activating NF- $\kappa$ B, a DNA sequence encoding the protein, a recombinant vector containing the DNA, a transformant containing the recombinant vector, a process for producing the protein, an antibody directed against the protein or a peptide fragment thereof, and a process for producing the antibody.

Another object of the present invention is to provide a method for screening a substance capable of inhibiting or promoting NF- $\kappa$ B activation using the protein, the DNA, the recombinant vector or the transformant, a kit for the screening, a substance capable of inhibiting or promoting NF- $\kappa$ B activation obtainable by the screening method or the screening kit, a process for producing the substance, a pharmaceutical composition containing a substance capable of inhibiting or promoting NF- $\kappa$ B activation, etc.

The present inventors have intensively studied to solve the above problems. As a result, the present inventors have succeeded in constructing a full-length cDNA library by using the oligo-capping method; establishing a gene function assay system by expression cloning using 293-EBNA cells; and isolating a new DNA (cDNA) encoding a protein having a function of activating NF- $\kappa$ B by using the assay system. This new DNA molecule induced NF- $\kappa$ B activation by its expression in 293-EBNA cells. This result shows that this new DNA is a signal transduction molecule involved in NF- $\kappa$ B activation. Thus, the present invention has been completed.

That is, the present invention provides the followings:

- (1) A purified protein selected from the group consisting of:
  - (a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,



98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF- $\kappa$ B (Nuclear factor kappa B) and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(2) A purified protein that activates NF- $\kappa$ B and comprises an amino acid sequence having at least 95% identity to the protein according to (1) over the entire length thereof.

(3) An isolated polynucleotide which comprises a nucleotide sequence encoding a protein selected from the group consisting of:

(a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168,

170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF- $\kappa$ B and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(4) An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- $\kappa$ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence

complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- $\kappa$ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

(5) An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- $\kappa$ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- $\kappa$ B and consists

of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

(6) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- $\kappa$ B and has at least 95% identity to the polynucleotide sequence according to (3) over the entire length thereof.

(7) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- $\kappa$ B and has at least 95% identity to the polynucleotide sequence according to (4) or (5) over the entire length thereof.

(8) A purified protein encoded by the polynucleotide according to any one of (3) to (7).

(9) A recombinant vector which comprises a polynucleotide according to any one of (3) to (7).

(10) A agent for gene therapy which comprises the recombinant vector according to (9) as an active ingredient.

- (11) A transformed cell which comprises the recombinant vector according to (9).
- (12) A membrane of the cell according to (11), which has the protein according to (1) or (2) which is a membrane protein.
- (13) A process for producing a protein according to (1), (2) or (8) comprising the steps of;
- (a) culturing a transformed cell according to (11) under conditions providing expression of the protein according to (1), (2) or (8); and
  - (b) recovering the protein from the culture product.
- (14) A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of (1), (2) or (8) in a subject comprising the steps of:
- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
  - (b) analyzing the amount of expression of said protein in a sample derived from said subject.
- (15) A method for screening compounds capable of inhibiting or promoting NF- $\kappa$ B activation, which comprises the steps of:
- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- $\kappa$ B into a cell;
  - (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
  - (c) measuring the signal which can detect activation of NF- $\kappa$ B; and
  - (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of

inhibiting or promoting NF- $\kappa$ B activation.

(16) A method for screening compounds capable of inhibiting or promoting NF- $\kappa$ B activation, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to (1), (2) or (8) into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$ B; and
- (d) selecting a candidate compound which can change the activation of NF- $\kappa$ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation.

(17) A compound capable of inhibiting or promoting NF- $\kappa$ B activation, which is selected by the method for screening according to (15) or (16).

(18) A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- $\kappa$ B into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- $\kappa$ B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the

step of (d).

(19) A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to (1), (2) or (8) into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$ B; and
- (d) selecting a candidate compound which can change the activation of NF- $\kappa$ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

(20) A kit for screening a compound capable of inhibiting or promoting NF- $\kappa$ B activation, which comprises:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- $\kappa$ B according to (1), (2) or (8) and a gene encoding a signal which can detect activation of NF- $\kappa$ B; and
- (b) reagents for measuring the signal.

(21) A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to (1), (2) or (8).

(22) The monoclonal or polyclonal antibody or a fragment thereof according to (21), which inhibits the activity of promoting activation of NF- $\kappa$ B by the protein according to (1), (2) or (8).

(23) A process for producing a monoclonal or polyclonal antibody according to (21) or (22), which comprises administering the protein according to (1), (2) or (8) or epitope-bearing fragments thereof to a non-human animal as an antigen.

(24) An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of (3) to (7), which prevents the expression of a protein which promotes NF- $\kappa$ B activation.

(25) A ribozyme or deoxyribozyme capable of inhibiting NF- $\kappa$ B activation, which has an action of cleavage of RNA that encodes the protein according to (1), (2) or (8) or an action of cleavage of RNA that encodes a protein involved in a pathway leading to NF- $\kappa$ B activation.

(26) A method for treating a disease associated with NF- $\kappa$ B activation, which comprises administering to a subject a compound screened by the process according to (15) or (16), and/or a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22), and/or an antisense oligonucleotide according to (24), and/or a ribozyme or deoxyribozyme according to (25) in an effective amount to treat a disease selected from the group consisting of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

(27) A pharmaceutical composition produced by the process according to (18) or (19) for inhibiting or promoting NF- $\kappa$ B activation.

(28) The pharmaceutical composition according to (27) for the treatment of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and/or ischemic disorders.



(29) A method of treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders, which comprises administering a pharmaceutical composition produced by the process according to (18) or (19) to a patient suffering from a disease associated with NF- $\kappa$ B activation.

(30) A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22) as an active ingredient.

(31) A pharmaceutical composition which comprises an antisense oligonucleotide according to (24) as an active ingredient.

(32) A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to (25) as an active ingredient.

(33) The pharmaceutical composition according to any one of (30) to (32) for the treatment and/or prevention of a disease which is selected from the group consisting of inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

(34) A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195,

197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

(35) A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to (34) with data of said other nucleotide sequences and/or amino acid sequences.

(36) An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 are fixed.

(37) An insoluble substrate to which polypeptides comprising all or a part of the

amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed.

The contents of the specifications and/or drawings of Japanese Patent Applications Nos. 2001-368692 and 2002-291302 and U.S. Provisional Applications Nos. 60/335829 and 60/415,769, which from the bases of priority of the instant application, are incorporated herein.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a graph showing NF- $\kappa$ B reporter activity inhibition by the proteasome inhibitor MG-132 in Example 3. The axis of abscissa is MG-132 concentration and the transversal axis is relative luciferase activity.

#### BEST MODE FOR CARRYING OUT THE INVENTION

At first, in order to further clarify the basic feature of the present invention, the present invention is explained by following how the present invention is completed. In order to obtain a new gene having a function of activating NF- $\kappa$ B, the following experiments were carried out as shown in the examples.

First, using the oligo-capping method, a full-length cDNA was produced from mRNA prepared from normal human lung fibroblasts (purchased from Sanko Junyaku Co., Ltd.) and the like, and a full-length cDNA library was constructed in which the cDNA was inserted into the vector pME18S-FL3 (GenBank Accession AB009864).

Next, the cDNA library was introduced into *E. coli* cells, and plasmid preparation was carried out per clone. Then, the pNK  $\kappa$  B-Luc reporter plasmid (STRATAGENE) containing a DNA encoding luciferase and the above full-length cDNA plasmid were cotransfected into 293-EBNA cells (Invitrogen). After 24 or 48 hours of culture, luciferase activity was measured, and the plasmid with significantly increased luciferase activity compared to that of a control experiment (vector pME18S-FL3 is introduced into a cell in place of a full-length cDNA) was selected (the selected plasmid showed a 5-fold or more increase in luciferase activity compared to that of the control experiment), and the entire nucleotide sequence of the cDNA cloned into the plasmid was determined. The protein encoded by the cDNA thus obtained shows that this protein is a signal transduction molecule involved in NF-  $\kappa$  B activation.

The present invention is described in detail below.

In the present invention, activation of NF-  $\kappa$  B refers to activation of NF-  $\kappa$  B (including induction of NF-  $\kappa$  B activation) when a gene is introduced into a suitable cell and the protein encoded by the gene is excessively expressed. Activation of NF-  $\kappa$  B can be measured, for example, by an assay using an NF-  $\kappa$  B dependant reporter gene. Activation of NF-  $\kappa$  B is reflected by increasing the reporter activity compared to control cells (cells into which the vector only was introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 2 or more, and still more preferably by a factor of 5 or more.

Reporter activity can be measured by cloning a polynucleotide (e.g. cDNA) encoding the protein to be expressed into a suitable expression vector, co-transfecting the expression vector and an NF-  $\kappa$  B dependant reporter plasmid into a suitable cell, and after culturing for a certain period, then measuring reporter activity. Suitable expression vectors are well known to those skilled in the art, examples of which include pME18S-FL3, pcDNA3.1 (Invitrogen). The reporter gene can be one which enables a person skilled in the art to easily detect the expression thereof, and examples include a gene encoding luciferase, chloramphenicol acetyl transferase, or  $\beta$ -galactosidase. Use

of a gene encoding luciferase is most preferable, and examples of an NF- $\kappa$ B dependent reporter plasmid include pNF- $\kappa$ B-Luc (STRATAGENE). Suitable cells include cells which exhibit an NF- $\kappa$ B activation response to stimulation by IL-1, TNF- $\alpha$  and the like. Examples include 293-EBNA cells. Cell culture and introduction of genes into cells (transfection) can be performed and optimized by a person skilled in the art by known techniques.

As a preferable method, 293-EBNA cells are inoculated on DMEM medium (Dulbecco's Modified Eagle Medium) containing 5% FBS (Fetal Bovine Serum) in a 96-well cell culture plate to a final cell density of  $1 \times 10^4$  cells/well, and cultured for 24 hours at 37°C in the presence of 5% CO<sub>2</sub>. Then, reporter plasmid pNF- $\kappa$ B-Luc (STRATAGENE) and the expression vector are cotransfected into the cells in a well using FuGENE 6 (Roche). After 24 hours of culture at 37°C, NF- $\kappa$ B activation is then measured by measuring luciferase activity using a long term luciferase assay system, Picagene LT2.0 (Toyo Ink Mfg). For example, luciferase activity can be measured using PerkinElmer's Wallac ARVOTMST 1420 MULTILABEL COUNTER. The method for gene introduction by FuGENE6, and measurement of luciferase activity by Picagene LT2.0 can be performed respectively according to the attached protocols. In a method of gene introduction with a 96-well plate using FuGENE6, the amount of FuGENE6 per 1 well is suitably 0.3 to 0.5  $\mu$ l, preferably 0.3  $\mu$ l; the amount of pNF- $\kappa$ B-Luc plasmid is suitably 50 to 100ng, preferably 50ng; the amount of expression vector is suitably 50-100ng, and preferably 100ng. An ability to activate NF- $\kappa$ B can be confirmed by an ability to increase the reporter activity (luciferase activity) relative to the control experiment (cells into which only a null vector was introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 2 or more, and still more preferably by a factor of 5 or more.

Related to the amino acid sequences of any one of SEQ ID NOS. 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104,

106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, the present invention provides the following proteins:

- (a) a protein which comprises one of the above amino acid sequences;
- (b) a peptide having one of the above amino acid sequences;
- (c) a protein which activates NF- $\kappa$ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in the above amino acid sequences;
- (d) a protein which comprises an amino acid sequence, which has at least 95% identity, preferably at least 97-99% identity, to one of the above amino acid sequences over the entire length thereof.

As known in the art, "identity" used herein is a relationship between two or more protein sequence or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between protein or polynucleotide sequences, as determined by the match between protein or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods. Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. "Identity" can be determined by using the BLAST program (for example, Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschul SF, Madden TL, Schaffer AA, Zhang Z, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997)). Where software such as BLAST is used, it is preferable to use default values. The main initial conditions generally used in a BLAST search are as follows, but are not limited to these.

An amino acid substitution matrix is a matrix numerically representing the degree of analogy of each pairing of each of the 20 types of amino acid, and normally the default matrix of BLOSUM62 is used. The theory of this amino acid substitution matrix is shown in Altschul S.F., J. Mol. Biol. 219: 555-565 (1991), and applicability to DNA sequence comparison is shown on States D. J., Gish W., Altschul S.F., Methods, 3: 66-70 (1991). In this case, optimal gap cost is determined by experience and in the case of BLOSUM62 preferably parameters of Existence 11, Extension 1 are used. The expected value (EXPECT) is the threshold value concerning statistical significance for a match with a database sequence, and the default value is 10.

As one example, a protein having, for example, 95% or more identity to the amino acid sequence of SEQ ID NO: 2 may contain in the amino acid sequence up to 5 amino acid changes per 100 amino acids of the amino acid sequence of SEQ ID NO: 2. In other words, a protein having 95% or more amino acid sequence identity to a subject amino acid sequence, may have amino acids up to 5% of the total number of amino acids within the subject sequence, deleted or substituted by other amino acids, or amino acids up to 5% of the total number of amino acids within the subject sequence may be inserted within the subject sequence. These changes within the subject sequence, may exist at the amino terminus or the carboxy terminus of the subject sequence, or may exist at any position between these termini, or may form one or more groups of changes.

The Examples described below demonstrate that the protein consisting of an amino acid sequence of any one of the above SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, is capable of activating

NF-  $\kappa$  B.

Related to the polynucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or the polynucleotide of a coding region (CDS) of these sequences, the present invention further provides the following isolated polynucleotides:

- (a) a polynucleotide of any one of the above sequences;
- (b) a polynucleotide which encodes a protein that activates NF-  $\kappa$  B, and comprises a nucleotide sequence which has at least 95% identity, preferably at least 97-99% identity to any one of the above sequences; and
- (c) a polynucleotide having a nucleotide sequence which encodes a protein that activates NF-  $\kappa$  B and has an amino acid sequence which has at least 95% identity, preferably, at least 97-99% identity, to the amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

Polynucleotides which are identical or almost identical to nucleotide sequences contained in the above nucleotide sequences may be used as hybridization probes to isolate full-length cDNA and genomic clones encoding the protein of the present



invention, or cDNA or genomic clones of other genes that have a high sequence similarity to the above sequences, or genomic clones, or may be used as primers for nucleic acid amplification reactions. Typically, these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to the above sequences. The probes or primers will generally comprises at least 15 nucleotides, preferably 30 nucleotides and may have 50 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers have between 20 and 25 nucleotides.

The polynucleotide of the present invention may be either in the form of a DNA such as cDNA, a genomic DNA obtained by cloning or synthetically produced, or may be in the form of RNA such as mRNA. The polynucleotide may be single-stranded or double-stranded. The double-stranded polynucleotides may be double-stranded DNA, double-stranded RNA or DNA:RNA hybrid. The single-stranded polynucleotide may be sense strand also known as coding strand or antisense strand also known as non-coding strand.

Those skilled in the art can prepare a protein having the same activity that activates NF- $\kappa$ B as the protein having an amino acid sequence of any one of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, by means of appropriate substitution of an amino acid in the protein using known methods. One such method involves using conventional mutagenesis procedures for the DNA encoding the protein. Another method is, for example, site-directed mutagenesis (e.g., Mutan-Super Express Km Kit from Takara Shuzo Co., Ltd.).

Mutations of amino acids in proteins may also occur in nature. Thus, the present invention also includes a mutated protein which is capable of activating NF- $\kappa$ B and which has at least one amino acid deletion, substitution or addition relative to the protein of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, and the DNA encoding the protein. The number of mutations is preferably 1 to 10, more preferably 1 to 5, most preferably 1 to 3.

The substitutions of amino acids are preferably conservative substitutions, specific examples of which are substitutions within the following groups: (glycine, alanine), (valine, isoleucine, leucine), (aspartic acid, glutamic acid), (asparagine, glutamine), (serine, threonine), (lysine, arginine) and (phenylalanine, tyrosine).

Based on DNA (e.g., SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287) encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140,

142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 or a fragment thereof, those skilled in the art can routinely isolate a DNA with a high sequence similarity to these nucleotide sequences by using hybridization techniques and the like, and obtain proteins having the same activity that activates NF- $\kappa$ B as the protein having of an amino acid sequence of any one of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288. Thus, the present invention also includes a protein that activates NF- $\kappa$ B and comprises an amino acid sequence having a high identity to the amino acid sequence of any one of the above SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288. "High identity" refers to an amino acid sequence having an identity of at least 90%, preferably at least 97 to 99% over the entire length of an amino acid sequence expressed by any one of the above SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,

74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

The proteins of the present invention may be natural proteins derived from any human or animal cells or tissues, chemically synthesized proteins, or proteins obtained by genetic recombination techniques. The protein may or may not be subjected to post-translational modifications such as sugar chain addition or phosphorylation.

Examples of the proteins which are encoded by the genes of the present invention include secretion proteins (growth factors, cytokines, hormones, and the like), protein modification enzymes (protein kinase, protein phosphatase, protease, and the like), signal transduction molecules (protein-protein interaction molecules and the like), nuclear proteins (nuclear receptor, transcription factors and the like), and membrane proteins. The membrane proteins include receptors, cell adhesion molecules, ion channels, and transporters. When the protein is a membrane protein, a compound which is selected by the screening mentioned herein below is more useful as a research tool for a pharmaceutical compound since the compound is expected to easily move into a cell or transmit a signal into a cell.

The present invention also includes a polynucleotide encoding the above protein of the present invention. Examples of nucleotide sequences encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224,

226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 include nucleotide sequences of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287. The DNA includes cDNA, genomic DNA, and chemically synthesized DNA. In accordance with the degeneracy of the genetic code, at least one nucleotide in the nucleotide sequence encoding a protein consisting of an amino acid sequence of any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288 can be substituted with other nucleotides without altering the amino acid sequence of the protein produced from the gene. Therefore, the DNA sequences of the present invention also include nucleotide sequences altered by substitution based on the degeneracy of the genetic code. Such DNA sequences can be synthesized using known methods.

The DNA of the present invention includes a DNA which encodes a protein capable of activating NF- $\kappa$ B and hybridizes under stringent conditions with the DNA sequence of the above nucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11,

13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287, or any complementary sequence thereof. Stringent conditions are apparent to those skilled in the art, and can be easily attained in accordance with various laboratory manuals such as T. Maniatis et al., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory 1982, 1989.

That is, "stringent conditions" refer to overnight incubation at 37°C in a hybridization solution containing 30% formamide, 5 x SSC (0.75 M NaCl, 75mM trisodium citrate), 5 x Denhardt's solution, 0.5% SDS, 100 µg/ml denatured, sheared salmon sperm DNA) followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 37°C (low stringency). Preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 40% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 42°C (moderate stringency). More preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 50% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 50°C (high stringency). The DNA sequence thus obtained must encode a protein capable of activating NF-κB.

The present invention also includes a polynucleotide comprising a nucleotide sequence which encodes a protein capable of activating NF-κB and has a high sequence

similarity to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5). Typically these nucleotide sequence are 95% identical, preferably 97% identical, more preferably 98-99% identical, most preferably at least 99% identical to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5) over the entire length thereof.

The above DNA of the present invention can be used to produce the above protein using recombinant DNA techniques. In general, the DNA and peptide of the present invention can be obtained by:

- (A) cloning the DNA encoding the protein of the present invention;
- (B) inserting the DNA encoding the entire coding region of the protein or a part thereof into an expression vector to construct a recombinant vector;
- (C) transforming host cells with the recombinant vector thus constructed; and
- (D) culturing the obtained cells to express the protein or its analogue, and then purifying it by column chromatography.

General procedures necessary to handle DNA and recombinant host cells (e.g., *E. coli*) in the above steps are well known to those skilled in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. All the enzymes, reagents, etc., used in these procedures are commercially available, and unless otherwise stated, such commercially available products can be used according to the use conditions specified by the manufacturer's instructions to attain completely its objects. The above steps (A) to (D) can be further illustrated in more details as follows.

Techniques for cloning the DNA encoding the protein of the present invention in the above step (A) include, in addition to the methods described in the specification of the present application, PCR amplification using a synthetic DNA having a part of the nucleotide sequence of the present invention (e.g., any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139,

141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287) as a primer, and selection of the DNA inserted into a suitable vector by hybridization with a labeled DNA fragment encoding a partial or full coding region of the protein of the present invention or a labeled synthetic DNA. Another technique involves direct amplification from total RNAs or mRNA fractions prepared from cells or tissues, using the reverse transcriptase polymerase chain reaction (RT-PCR method).

As a DNA inserted into a suitable vector, for example, a commercially available library (e.g., from CLONTECH and STRATAGENE) can be used. Techniques for hybridization are normally used in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. Depending on the intended purpose, the cloned DNA encoding the protein of the present invention can be used as such or if desired after digestion with a restriction enzyme or addition of a linker. The DNA thus obtained may have a nucleotide sequence of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287, or a polynucleotide of above items (3) to (7). The DNA sequence to be inserted into an expression vector in the above step (B) may be a full-length cDNA or a DNA fragment encoding the above full-length protein, or a DNA fragment constructed so that it expresses a part thereof.

Thus, the present invention also provides a recombinant vector, which comprises



the above DNA sequence. The expression vector for the protein of the present invention can be produced, for example, by excising the desired DNA fragment from the DNA encoding the protein of the present invention, and ligating the DNA fragment downstream of a promoter in a suitable expression vector.

Expression vectors for use in the present invention may be any vectors derived from prokaryotes (e.g., *E. coli*), yeast, fungi, insect viruses and vertebrate viruses so long as such vectors are replicable. However, the vectors should be selected to be compatible with microorganisms or cells used as hosts. Suitable combinations of host cell – expression vector systems are selected depending on the desired expression product.

When microorganisms are used as hosts, plasmid vectors compatible with these microorganisms are generally used as replicable expression vectors for recombinant DNA molecules. For example, the plasmids pBR322 and pBR327 can be used to transform *E. coli*. Plasmid vectors normally contain an origin of replication, a promoter, and a marker gene conferring upon a recombinant DNA a phenotype useful for selecting the cells transformed with the recombinant DNA. Example of such promoters include a  $\beta$ -lactamase promoter, lactose promoter and tryptophan promoter. Examples of such marker genes include an ampicillin resistance gene, and a tetracycline resistance gene. Examples of suitable expression vectors include the plasmids pUC18 and pUC19 in addition to pBR322, pBR327.

In order to express the DNA of the present invention in yeast, for example, YEp24 can be used as a replicable vector. The plasmid YEp24 contains the URA3 gene, which can be employed as a marker gene. Examples of promoters in expression vectors for yeast cells include promoters derived from genes for 3-phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase and alcohol dehydrogenase.

Examples of promoters and terminators for use in expression vectors to express the DNA of the present invention in fungal cells include promoters and terminators derived from genes for phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dehydrogenase (GAPD) and actin. Examples of suitable expression vectors include the

plasmids pPGACY2 and pBSFAHY83.

Examples of promoters for use in expression vectors to express the DNA of the present invention in insect cells include a polyhedrin promoter and P10 promoter. Examples of expression vectors which are suitable for insect cells include baculo virus vector.

Recombinant vectors used to express the DNA of the present invention in animal cells normally contain functional sequences to regulate genes, such as an origin of replication, a promoter to be placed upstream of the DNA of the present invention, a ribosome-binding site, a polyadenylation site and a transcription termination sequence. Such functional sequences, which can be used to express the DNA of the present invention in eukaryotic cells, can be obtained from viruses and viral substances.

Examples of such functional sequences include an SR $\alpha$  promoter, SV40 promoter, LTR promoter, CMV (cytomegalovirus) promoter and HSV-TK promoter. Among them, a CMV promoter and SR $\alpha$  promoter can be preferably used. As promoters to be placed inherently upstream of the gene encoding the protein of the present invention, any promoters can be used so long as they are suitable for use in the above host-vector systems. Examples of origins of replication include foreign origins of replication, for example, those derived from viruses such as adenovirus, polyoma virus and SV40 virus. When vectors capable of integration into host chromosomes are used as expression vectors, origins of replication of the host chromosomes may be employed. Examples of suitable expression vectors include the plasmids pSV-dhfr (ATCC 37146), pBPV-1(9-1) (ATCC 37111), pcDNA3.1 (INVITROGEN) and pME18S-FL3.

The present invention also provides a transformed cell, which comprises the above recombinant vector. Microorganisms or cells transformed with the replicable recombinant vector of the present invention can be selected from remaining untransformed parent cells based on at least one phenotype conferred by the recombinant vector as mentioned above. Phenotypes can be conferred by inserting at least one marker gene into the recombinant vector. Marker genes naturally contained in

replicable vectors can be employed. Examples of marker genes include drug resistance genes such as neomycin resistance genes, and genes encoding dihydrofolate reductase.

As hosts for use in the above step (C), any of prokaryotes (e.g., *E. coli*), microorganisms (e.g., yeast and fungi) as well as insect and animal cells can be used so long as such hosts are compatible with the expression vectors used. Examples of such microorganisms include *Escherichia coli* strains such as *E. coli* K12 strain 294 (ATCC 31446), *E. coli* X1776 (ATCC 31537), *E. coli* C600, *E. coli* JM109 and *E. coli* B strain; bacterial strains belonging to the genus *Bacillus* such as *Bacillus subtilis*; intestinal bacteria other than *E. coli*, such as *Salmonella typhimurium* or *Serratia marcescens*; and various strains belonging to the genus *Pseudomonas*. Examples of such yeast include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and *Pichia pastoris*. Examples of such fungi include *Aspergillus nidulans*, and *Acremonium chrysogenum* (ATCC 11550).

As insect cells, for example, *Spodoptera frugiperda* (Sf cells), High Five<sup>TM</sup> cells derived from eggs of *Trichoplusia*, etc., can be used when the virus is AcNPV. Examples of such animal cells include HEK 293 cells, COS-1 cells, COS-7 cells, Hela cells, and Chinese hamster ovary (CHO) cells. Among them, CHO cells and HEK 293 cells are preferred. When cells are used as hosts, combinations of expression vectors and host cells to be used vary with experimental objects. According to such combinations, two types of expression (i.e. transient expression and constitutive expression) can be included.

"Transformation" of microorganisms and cells in the above step (C) refers to introducing DNA into microorganisms or cells by forcible methods or phagocytosis of cells and then transiently or constitutively expressing the trait of the DNA in a plasmid or an intra-chromosome integrated form. Those skilled in the art can carry out transformation by known methods [see e.g., "Idenshi Kougaku Handbook (Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.]. For example, in the case of animal cells, DNA can be

introduced into cells by known methods such as DEAE-dextran method, calcium-phosphate-mediated transfection, electroporation, lipofection, etc. For stable expression of the protein of the present invention using animal cells, there is a method in which selection can be carried out by clonal selection of the animal cells containing the chromosomes into which the introduced expression vectors have been integrated. For example, transformants can be selected using the above selectable marker as an indication of successful transformation. In addition, the animal cells thus obtained using the selectable marker can be subjected to repeated clonal selection to obtain stable animal cell strains highly capable of expressing the protein of the present invention. When a dihydrofolate reductase (DHFR) gene is used as a selectable marker, one can culture animal cells while gradually increasing the concentration of methotrexate (MTX) and select the resistant strains, thereby amplifying the DNA encoding the protein of the present invention together with the DHFR gene in the cell to obtain animal cell strains having higher levels of expression.

The above transformed cells can be cultured under conditions which permit the expression of the DNA encoding the protein of the present invention to produce and accumulate the protein of the present invention. In this manner, the protein of the present invention can be produced. Thus, the present invention also provides a process for producing a protein, which comprises culturing a transformed cell comprising the isolated polynucleotide according to above item (3) to (7) under conditions providing expression of the encoded protein, and recovering the protein from the culture (that is, cells or culture medium).

The above transformed cells can be cultured by methods known to those skilled in the art (see e.g., "Bio Manual Series 4", YODOSHA CO., LTD.). For example, animal cells can be cultured by various known animal cell culture methods including attachment culture such as Petri dish culture, multitray type culture and module culture, attachment culture in which cells are attached to cell culture carriers (microcarriers), suspension culture in which productive cells themselves are suspended. Examples of

media for use in the culture include media commonly used for animal cell culture, such as D-MEM and RPMI 1640.

In order to separate and purify the protein of the present invention from the above culture, suitable combinations of per se known separation and purification methods can be used. Examples such methods include methods based on solubility, such as salting-out and solvent precipitation; methods based on the difference in charges, such as ion-exchange chromatography; methods mainly based on the difference in molecular weights, such as dialysis, ultrafiltration, gel filtration and SDS-polyacrylamide gel electrophoresis; methods based on specific affinity, such as affinity chromatography; methods based on the difference in hydrophobicity, such as reverse phase high performance liquid chromatography; and methods based on the difference in isoelectric points, such as isoelectric focusing. For example, a protein of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation or purification.

The protein of the present invention can also be produced as a fusion protein with another protein. These fusion proteins are also included within the present invention. For the expression of such fusion proteins, any vectors can be used so long as the DNA encoding the protein can be inserted into the vectors and the vectors can express the fusion protein. Examples of proteins to which a polypeptide of the present invention can be fused include glutathione S-transferase (GST) and a hexa-histidine sequence (6 x His). The fusion protein of the protein of the present invention with another protein can be advantageously purified by affinity chromatography using a substance with an affinity

for the fusion partner protein. For example, fusion proteins with GST can be purified by affinity chromatography using glutathione as a ligand.

When the protein of the present invention is a membrane protein, a transformed cell into which DNA encoding the protein of the present invention has been introduced can express the protein on its membrane. The membrane which is prepared from such transformed cells and contains the protein of the present invention is also included within the present invention. As used herein, "membrane of a cell" includes cell membrane, and membrane of cell organelle. The membrane of a cell can be prepared by a method known to those skilled in the art. For example, cells are collected from the culture where transformed cells are cultured, and suspended in a suitable buffer. Then, the cells are lysed by a homogenizer or by vortex after addition of glassbeads. The obtained solution is centrifuged to remove uncrushed cells and the like, and the supernatant is ultracentrifuged under a suitable condition, and the obtained precipitate is suspended in a buffer to prepare a membrane fraction. The condition for ultracentrifugation can be suitably selected depending on the type of membrane and the like.

The present invention also includes a protein capable of inhibiting the activity of the protein of the present invention. Examples of such proteins include antibodies, or other proteins that bind to active sites of the protein of the present invention, thereby inhibiting the expression of their activity.

The present invention also relates to an antibody that reacts with the protein of the present invention or a fragment thereof, and to production of such an antibody. More preferably, the present invention relates to an antibody that specifically react with the protein of the present invention or a fragment thereof, and to production of such an antibody. As used herein, "specifically" means that cross-reactivity is low, more preferably cross-reactivity is not present.

The antibody of the present invention is not specifically limited so long as it can recognize the protein of the present invention. Examples of such antibodies include polyclonal antibodies, monoclonal antibodies and their fragments, single chain antibodies

and humanized antibodies. Antibody fragments can be produced by known techniques. Examples of such antibody fragments include, but not limited to,  $F(ab')_2$  fragments, Fab' fragments, Fab fragments and Fv fragments. For example, a monoclonal or polyclonal antibody can be produced by administering the protein according to above item (1) or (2) as an antigen or epitope-bearing fragments to a non-human animal. The antibody against the protein of the present invention can be produced by using the protein of the present invention or a peptide thereof as an immunogen according to per se known process for producing antibodies or antisera. Such methods are described, for example, in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition, an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

In the case of polyclonal antibodies, for example, the protein of the present invention or a peptide thereof can be injected to animals such as rabbits to produce antibodies directed against the protein or peptide, and then their blood can be collected. The polyclonal antibodies can be purified from the blood, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

In the case of monoclonal antibodies, for example, animals such as mice are immunized with the protein of the present invention, their spleen is removed and homogenized to obtain spleen cells, which are then fused with mouse myeloma cells by using a reagent such as polyethylene glycol. From the resulting hybrid cells (i.e. hybridoma cells), the clone producing the antibody directed against the protein of the present invention can be selected. Then, the resulting clonal hybridoma cells can be implanted intraperitoneally into mice, the ascitic fluid recovered from the mice. The resulting monoclonal antibody can be purified, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

When the resulting antibody is used to administer it to humans, it is preferably

used as a humanized antibody or human antibody in order to reduce its immunogenicity. The humanized antibody can be produced using transgenic mice or other mammals. For a general review of these humanized antibodies and human antibodies, see, for example, Morrison, S.L. et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984); Jones, P.T. et al., Nature 321:522-525 (1986); Hiroshi Noguchi, Igaku no Ayumi (J. Clin. Exp. Med.) 167:457-462 (1993); Takashi Matsumoto, Kagaku to Seibutsu (Chemistry and Biology) 36:448-456 (1998). Humanized chimeric antibodies can be produced by linking a V region of a mouse antibody to a C region of a human antibody. Humanized antibodies can be produced by substituting a sequence derived from a human antibody for a region other than a complementarity-determining region (CDR) from a mouse monoclonal antibody.

In addition, human antibodies can be directly produced in the same manner as the production of conventional monoclonal antibodies by immunizing the mice whose immune systems have been replaced with human immune systems. These antibodies can be used to isolate or to identify clones expressing the protein.

Also, these antibodies can be used to purify the protein of the present invention from a cell extract or transformed cells producing the protein of the present invention. These proteins can also be used to construct ELISA, RIA (radioimmunoassay) and western blotting systems. These assay systems can be used for diagnostic purposes for detecting an amount of the protein of the present invention present in a body sample in a tissue or a fluid in the blood of an animal, preferably human. For example, they can be used for diagnosis of a disease characterized by undesirable activation of HF- $\kappa$  B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

In order to provide a basis for diagnosis of a disease, a standard value (that is, a normal value for the expression of the protein of the present invention) must be established. However, this is a well-known technique to those skilled in the art. For



example, a method of calculating the standard value comprises binding a body fluid or a cell extract of normal individual of a human or an animal to an antibody against the protein of the present invention under a suitable condition for the complex formation, detecting the amount of the antibody-protein complex by chemical or physical means and then calculating the standard value for the normal sample using a standard curve prepared from a standard solution containing a known amount of an antigen (the protein of the present invention). The presence of a disease can be confirmed by deviation from the standard value obtained by comparison of the standard value with the value obtained from a sample of an individual latently suffering from a disease associated with the protein of the present invention. These antibodies can also be used as reagents for studying functions of the protein of the present invention.

The antibody of the present invention can be used as a medicament as mentioned below. When the antibody of the present invention is used as a medicament, it is preferred to use an antibody capable of inhibiting the activity of activating NF- $\kappa$ B of the protein of the present invention (that is, neutralizing antibody).

The antibodies of the present invention can be purified and then administered to patients of a disease characterized by undesirable activation of NF- $\kappa$ B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus in another aspect, the present invention is a pharmaceutical composition which comprises the above antibody as an active ingredient, and a method for therapy and/or prevention using the antibody of the present invention. In such pharmaceutical compositions, the active ingredient may be combined with other therapeutically or preventively active ingredients or inactive ingredients (e.g., conventional pharmaceutically acceptable carriers or diluents such as immunogenic adjuvants) and physiologically non-toxic stabilizers and excipients. The resulting combinations can be sterilized by filtration, and formulated into vials after lyophilization or into various dosage forms in stabilized and preservable aqueous

preparations.

Administration to a patient can be intra-arterial administration, intravenous administration and subcutaneous administration, which are well known to those skilled in the art. The dosage range depends upon the weight and age of the patient, route of administration and the like. Suitable dosages can be determined by those skilled in the art. These antibodies exhibit therapeutic activity by inhibiting the NF- $\kappa$ B activation mediated by the protein of the present invention. More specifically, the antibody of the present invention is useful as a medicament for treating or preventing a disease associated with abnormality of NF- $\kappa$ B activity such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

The DNA of the present invention can also be used to isolate, identify and clone other proteins involved in intracellular signal transduction processes. For example, the DNA sequence encoding the protein of the present invention can be used as a "bait" in yeast two-hybrid systems (see e.g., Nature 340:245-246 (1989)) to isolate and clone the sequence encoding a protein ("prey") which can associate with the protein of the present invention. In a similar manner, it can be determined whether the protein of the present invention can associate with other cellular proteins (e.g., NIK and TRAF2). In another method, proteins which can associate with the protein of the present invention can be isolated from cell extracts by immunoprecipitation [see e.g., "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] using antibodies directed against the protein of the present invention. In still another method, the protein of the present invention can be expressed as a fusion protein with another protein as described above, and immunoprecipitated with an antibody directed against the fusion protein in order to isolate a protein which can associate with the protein of the present invention.

The present invention provides a process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of present

invention in a subject comprising the steps of:

- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
- (b) analyzing the amount of expression of said protein in a sample derived from said subject.

The diagnostic assays offer a process for diagnosing diseases or determining a susceptibility to the diseases through detection of mutation in a gene for the protein of the present invention which has a function of activating NF- $\kappa$ B, by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of protein or mRNA.

The determination of the presence or absence of a mutation in the nucleotide sequence of a the gene encoding the protein of the present invention which has a function of activating NF- $\kappa$ B, may involve RT-PCR using a part of the nucleotide sequences of genes encoding these proteins as a primer, followed by conventional DNA sequencing to detect the presence or absence of the mutation. PCR-SSCP [Genomics 5:874-879 (1989); "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] can also be used to determine the presence or absence of the mutation.

Decreased or increased expression of a gene in a sample can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, for example, nucleic acid amplification methods such as RT-PCR, and methods such as RNase protection assay, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein in a sample derived from a host are well-known to those skilled in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assays. When an expression level is determined at a protein level, the antibody of the present invention mentioned above can be used.

The degree of abnormality of expression level of gene in a sample is not particularly limited. For example, when the level of the expressed protein is 2 or more times, or 1/2 or less, as compared with normal case, the subject may be diagnosed to be a disease. In another example, when the level of the expressed protein is 3 or more times, or 1/3 or less, as compared with normal case, the subject may be diagnosed to be a disease.

The DNA of the present invention can be used to detect abnormality in the DNA or mRNA encoding the protein of the present invention or a peptide fragment thereof. Therefore, the DNA is useful for gene diagnosis such as detection of damage, mutation, decreased, increased or excessively increased expression of said DNA or mRNA.

When the nucleotide sequence encoding the protein of the present invention in a genome of an individual contains a mutation, the mutation may cause a disease associated with the expression and/or activity of NF- $\kappa$ B.

When the amount of the expression of the protein in a sample from an individual is different from the normal value, the abnormal expression of the novel protein of the present invention which acts to activate NF- $\kappa$ B may be responsible for diseases associated with the expression and/or activity of NF- $\kappa$ B.

The present invention also relates to a method for screening compounds which inhibit or promote NF- $\kappa$ B activation using the proteins of the invention.

A compound which inhibits NF- $\kappa$ B activation has an activity as an inhibitor of NF- $\kappa$ B in vivo or in vitro as a result of this function, while a compound which promotes NF- $\kappa$ B activation has an activity as an activator of NF- $\kappa$ B in vivo or in vitro as a result of this function. Therefore, an activity as an inhibitor or activator of NF- $\kappa$ B is screened in the method for screening of the present invention. The above compounds have an activity as an inhibitor or activator of NF- $\kappa$ B.

The method for screening comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to the present invention and a gene encoding a signal

which can detect activation of NF- $\kappa$ B into a cell;

(b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring the signal which can detect activation of NF- $\kappa$ B; and

(d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation.

Further, it is preferable to isolate or identify as an activator compound, a compound that increases said detectable signal 2-fold or higher than normal, and to isolate or identify as an inhibitor compound, a compound that decreases said detectable signal half or less than normal.

Examples of genes encoding a signal which can detect activation of NF- $\kappa$ B include reporter genes. Reporter genes are used instead of directly detecting the activation of transcription factors of interest. The transcriptional activity of a promoter of a gene is analyzed by linking the promoter to a reporter gene and measuring the activity of the product of the reporter gene ("Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Any peptide or protein can be used so long as those skilled in the art can measure the activity or amount of the expression product (including the amount of the produced mRNA) of the reporter genes. For example, enzymatic activity of chloramphenicol acetyltransferase,  $\beta$ -galactosidase, luciferase, etc., can be measured. Any reporter plasmids can be used to evaluate NF- $\kappa$ B activation so long as the reporter plasmids have an NF- $\kappa$ B recognition sequence inserted upstream of the reporter gene. For example, pNF- $\kappa$ B-Luc (STRATAGEGE) can be used. Other examples include NF- $\kappa$ B dependent reporter plasmids described in Tanaka S. et al., J. Vet. Med. Sci. Vol.59 (7); Rothe M. et al., Science Vol.269, p.1424-1427 (1995).

Any host cells may be used so long as NF- $\kappa$ B activation can be detected in the host cells. Preferred host cells are mammalian cells such as 293-EBNA cells.

Transformation and culture of the cells can be carried out as described above.

In a specific embodiment, the method for screening a compound which inhibits or promotes NF- $\kappa$ B activation comprises culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. The reporter activity can be measured by methods known in the art (see e.g., "Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Examples of test compounds include, but not limited to, low molecular weight compounds, high molecular compounds, and peptides. Test compounds may be artificially synthesized compounds or naturally occurring compounds. Test compounds may be a single compound or mixtures. Usable examples include a library of low molecular weight compounds, a compound library which was synthesized by combinatorial chemistry, a naturally occurring product containing cells, plants, animals or a part thereof, or an extracted product of such naturally occurring product. When a mixture containing several compounds is used as a test substance for screening, the test substance which shows an activity of inhibiting or promoting NF- $\kappa$ B activation can be further screened to isolate a single substance having the activity. Isolation and purification of a desired compound from a mixture can be carried out by using any known method such as filtration, extraction, washing, drying, concentration, crystallization or various chromatography in combination.

The method for screening according to the present invention can be carried out by the following steps:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to the present invention into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$ B; and

(d) selecting a candidate compound which can change the activation of NF- $\kappa$ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation.

Methods for measuring the activation of NF- $\kappa$ B in the above method include a method of analyzing the binding of NF- $\kappa$ B to its binding sequence using cell extraction solution by gel shift (for example, Hayashi T. et al. J.Biol.Chem.268, p.26790-26795 (1993), Nauman M. et al. EMBO J. 13, p4597-4607 (1994)). Alternatively, the amount of mRNA or proteins for genes whose expression is known to be induced by NF- $\kappa$ B activation (e.g., genes for IL-1 and TNF- $\alpha$ ), can be measured. The amount of mRNA can be measured, for example, by northern hybridization, RT-PCR, etc. The amount of proteins can be measured, for example, by using antibodies. The antibodies may be produced by known methods. Commercially available antibodies (from, e.g., Wako Pure Chemical Industries, Ltd.) can also be used.

The present invention further provided a method of producing a pharmaceutical composition, which comprises the following steps (a) to (f):

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to the present invention and a gene encoding a signal which can detect activation of NF- $\kappa$ B into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- $\kappa$ B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the present invention, a pharmaceutical composition can be produced by the following steps:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to the present invention into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$ B; and
- (d) selecting a candidate compound which can change the activation of NF- $\kappa$ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the step (d) of the method of producing a pharmaceutical composition, it is preferable to isolate or identify as an activator compound, a compound that increases said detectable signal 2-fold or higher than normal, and to isolate or identify as an inhibitor compound, a compound that decreases said detectable signal half or less than normal.

The protein of the present invention may also be used in a method for the structure-based design of an agonist, antagonist or inhibitor of the protein, by:

- (a) determining in the first instance the three-dimensional structure of the protein;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
- (c) synthesising candidate compounds that are predicted to bind to or react with the deduced binding or reactive site; and
- (d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitor.

The present invention also provides a compound which is selected by the above screening method. This compound has a function of inhibiting or promoting NF- $\kappa$ B activation. More specifically, this compound has a function of inhibiting or promoting NF- $\kappa$ B activation by the protein of the present invention.

The compounds obtained by the above screening methods have a function of inhibiting or promoting NF- $\kappa$ B activation, they are useful as therapeutic or preventive



pharmaceuticals for the treatment of diseases resulting from unfavorable activation or inactivation of NF- $\kappa$ B.

When obtainment of a salt of the compounds is desired, a compound which is obtained in the form of a salt can be purified as it is. A compound which is obtained in the free form can be converted into a salt by isolating and purifying a salt obtained by dispersing or dissolving the compound into a suitable solvent and then adding a desired acid or base. Examples of a step to optimize the compounds or salts thereof obtained by the method of the present invention as a pharmaceutical composition, include methods of formulating according to ordinary processes such as the following. The above compounds or their pharmaceutically acceptable salts in an amount effective as an active ingredient, and pharmaceutically acceptable carriers can be mixed. A form of formulation suitable for the mode of administration is selected. A composition suitable for oral administration includes a solid form such as tablet, granule, capsule, pill and powder, and solution form such as solution, syrup, elixir and dispersion. A form useful for parenteral administration includes sterile solution, dispersion, emulsion and suspension. The above carriers include, for example, sugars such as gelatin, lactose and glucose, starches such as corn, wheat, rice and maize, fatty acids such as stearic acid, salts of fatty acids such as calcium stearate, magnesium stearate, talc, vegetable oil, alcohol such as stearyl alcohol and benzyl alcohol, gum, and polyalkylene glycol. Examples of such liquid carriers include generally water, saline, sugar solution of dextrose and the like, glycols such as ethylene glycol, propylene glycol and polyethylene glycol.

The present invention also provides a kit for screening compounds which inhibit or promote NF- $\kappa$ B activation. The kit comprises reagents and the like necessary for screening compounds which inhibit or promote NF- $\kappa$ B activation, including:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- $\kappa$ B according to the present invention and a gene encoding a signal which can detect activation of NF- $\kappa$ B; and
- (b) reagents for measuring the signal.

In another aspect, the present invention relates to a diagnostic kit which comprises:

(a) a polynucleotide of the present invention having a nucleotide sequence expressed by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide having a nucleotide sequence complementary to that of (a);

(c) a protein of the present invention having an amino acid sequence expressed by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, or a fragment thereof; or

(d) an antibody to the protein of the present invention of (c).

A kit comprising at least one of (a) to (d) is useful for diagnosing a disease or susceptibility to a disease such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

Because NF- $\kappa$ B is involved in a wide variety of pathological conditions such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders, it is an attractive target for drug

design and therapeutic intervention. Many experiments show that NF- $\kappa$ B activity may have significant physiological effects [see e.g., *Ann. Rheum. Dis.* 57:738-741 (1998); *American Journal of Pathology* 152:793-803 (1998); *ARTHRITIS & RHEUMATISM* 40:226-236 (1997); *Am. J. Respir. Crit. Care Med.* 158:1585-1592 (1998); *J. Exp. Med.* 188:1739-1750 (1998); *Gut* 42:477-484 (1998); *The Journal of Immunology* 161:4572-4582 (1998); *Nature Medicine* 3:894-899 (1997)].

The finding of the new protein described herein capable of activating NF- $\kappa$ B has provided a new medicament and method for controlling an abnormal NF- $\kappa$ B function. Thus, the present invention also relates to a method of use of a compound which inhibits the function of the protein capable of activating NF- $\kappa$ B described above, for inhibiting NF- $\kappa$ B activation. Further, the present invention relates to a method of using a compound which activates the function of the protein capable of activating NF- $\kappa$ B described above, for promoting NF- $\kappa$ B activation. The compound obtained by the above screening method, which inhibits NF- $\kappa$ B activation, is useful as a medicament to treat or prevent diseases characterized by undesirable activation of NF- $\kappa$ B, such as inflammation, autoimmune diseases (such as rheumatoid arthritis, systemic lupus erythematosus, asthma, etc), infectious diseases, bone diseases, and graft rejection. Recently, it has also become apparent that NF- $\kappa$ B activation controls apoptosis of cells. The compound obtained by the above screening method, which inhibits NF- $\kappa$ B activation, may be capable of stimulating apoptosis. Diseases which may be treated by the induction of apoptosis include tumors.

Further, examples of diseases related to abnormality in NF- $\kappa$ B activation include AIDS (acquired immunodeficiency syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, etc.), ischemic disorders (i.e. those caused by cardiac infarction, reperfusion injury, etc), myelogenesis incompetency syndrome (aplastic anemia, etc), skin diseases (Toxic epidermal necrolysis, etc), proliferative nephritis (IgA nephritis, purpuric nephritis, lupus nephritis, etc) and fulminant hepatitis. Thus, a compound obtained by the above screening method, which

inhibits or promotes NF- $\kappa$ B activation, is useful as a medicament to treat or prevent these diseases.

In addition, the gene encoding the protein of the present invention is useful for gene therapy to treat various diseases such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. "Gene therapy" refers to administering into the human body a gene or a cell into which a gene has been introduced for the purpose of therapy of diseases. The protein of the present invention and the DNA encoding the protein can also be used for diagnostic purposes. Thus, the present invention provides a agent for gene therapy which comprises a gene encoding the protein of the present invention.

The form of the agent for gene therapy is not particularly limited, but includes a pharmaceutical composition which comprises a expression vector containing a gene of the present invention in a pharmaceutical carrier of physiological buffer. The pharmaceutical carrier may contain suitable stabilizer (for example, nuclease inhibitor), chelate agent (for example, EDTA), and/or other auxiliary agent. Alternatively, the agent for gene therapy of the present invention may be provided as a complex of an expression vector containing a gene of the present invention and a liposome. The agent for gene therapy may be applied using a catheter. For example, the agent for gene therapy of the present invention can be directly injected into a blood vessel of patient and the like.

The dosage of the agent for gene therapy of the present invention should be selected depending on the conditions such as age, sex, body weight and symptom of patient, and administration route, and is generally about 1  $\mu$ g/kg to about 1000 mg/kg, more preferably about 10  $\mu$ g/kg to about 100 mg/kg, as an amount of DNA (which is an effective ingredient) per one administration for adult. The number of administration is not particularly limited.

The compound obtained by the screening method of the present invention or a salt thereof can be formulated into the above pharmaceutical compositions (e.g., tablets,

capsules, elixirs, microcapsules, sterile solutions and suspensions) according to conventional procedures. The formulations thus obtained are safe and of low toxicity, and can be administered, for example, to humans and mammals (e.g., rats, rabbits, sheep, pigs, cattle, cats, dogs and monkeys). Administration to patients can be carried out by methods known in the art, such as intra-arterial injection, intravenous injection and subcutaneous injection. The dosage and administration mode may vary with the weight and age of the patient, but those skilled in the art can appropriately select suitable administration mode and can appropriately select suitable dosage depending on the administration mode. When the compound can be encoded by DNA, the DNA can be inserted into a vector for gene therapy, and gene therapy can be carried out. Thus, the present invention relates to a medicament which comprises a compound capable of inhibiting or promoting NF- $\kappa$ B activation as an active ingredient.

In addition, the above compound is useful as a medicament to treat or prevent diseases characterized by abnormal NF- $\kappa$ B activity, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus, the present invention also relates to a medicament to treat or prevent inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, ischemic disorders and the like, which comprises a compound capable of inhibiting or promoting NF- $\kappa$ B activation. Specifically, the compound is useful as a therapeutic and/or prophylactic drug against, for example, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, diabetes, sepsis, asthma, allergic rhinitis, ischemic heart diseases, inflammatory intestinal diseases, subarachnoid hemorrhage, viral hepatitis, AIDS, atherosclerosis, atopic dermatitis, viral infections, Crohn's disease, gout, hepatitis, multiple sclerosis, cardiac infarction, nephritis, osteoporosis, Alzheimer's, Parkinson's disease, Huntington's chorea, psoriasis, amyotrophic lateral sclerosis, or aplastic anemia.

The present invention also relates to the use of the above compound for manufacturing a medicament for the therapy and/or prevention of inflammation,

autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, ischemic disorders and the like.

The present invention also provides an antisense oligonucleotide against the polynucleotide of any one of above items (3) to (7). An antisense oligonucleotide refers to an oligonucleotide complementary to the target gene sequence. The antisense oligonucleotide can inhibit the expression of the target gene by inhibiting RNA functions such as translation to proteins, transport to the cytoplasm and other activity necessary for overall biological functions. In this case, the antisense oligonucleotide may be RNA or DNA. The DNA sequence of the present invention can be used to produce an antisense oligonucleotide capable of hybridizing with the mRNA transcribed from the gene encoding the protein of the present invention. It is known that an antisense oligonucleotide generally has an inhibitory effect on the expression of the corresponding gene (see e.g., Saibou Kougaku Vol.13, No.4 (1994)). The oligonucleotide containing an antisense coding sequence against a gene encoding the protein of the present invention can be introduced into a cell by standard methods. The oligonucleotide effectively blocks the translation of mRNA of the gene encoding the protein of the present invention, thereby blocking its expression and inhibiting undesirable activity.

The antisense oligonucleotide of the present invention may be a naturally occurring oligonucleotide or its modified form [see e.g., Murakami & Makino, Saibou Kougaku Vol.13, No.4, p.259-266 (1994); Akira Murakami, Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol.40, No.10, p.1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14, No. 4 p85-95(1996)]. Thus, the oligonucleotide may have modified sugar moieties or inter-sugar moieties. Examples of such modified forms include phosphothioates and other sulfur-containing species used in the art. According to several preferred embodiments of the present invention, at least one phosphodiester bond in the oligonucleotide is substituted with the structure which can enhance the ability of the composition to permeate cellular regions where RNA with the activity to be regulated is

located.

Such substitution preferably involves a phosphorothioate bond, a phosphoramidate bond, methylphosphonate bond, or a short-chain alkyl or cycloalkyl structure. The antisense oligonucleotide may also contain at least some modified base forms. Thus, it may contain purine and pyrimidine derivatives other than naturally occurring purine and pyrimidine. Similarly, the furanosyl moieties of the nucleotide subunits can be modified so long as the essential purpose of the present invention is attained. Examples of such modifications include 2'-O-alkyl and 2'-halogen substituted nucleotides. Examples of modifications in sugar moieties at their 2-position include OH, SH, SCH<sub>3</sub>, OCH<sub>3</sub>, OCN or O(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>, wherein n is 1 to about 10, and other substituents having similar properties. All the analogues are included in the scope of the present invention so long as they can hybridize with the mRNA of the gene of the present invention to inhibit functions of the mRNA.

The antisense oligonucleotide of the present invention contains about 3 to about 50 nucleotides, preferably about 8 to about 30 nucleotides, more preferably about 12 to about 25 nucleotides. The oligonucleotide of the present invention can be produced by the well-known solid phase synthesis technique. Devices for such synthesis are commercially available from some manufactures including Applied Biosystems. Other oligonucleotides such as phosphothioates can also be produced by methods known in the art.

The antisense oligonucleotide of the present invention is designed to hybridize with the mRNA transcribed from the gene of the present invention. Those skilled in the art can easily design an antisense oligonucleotides based on a given gene sequence (For example, Murakami and Makino: Saibou Kougaku Vol. 13 No.4 p259-266 (1994), Akira Murakami: Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol. 40 No.10 p1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14 No. 4 p85-95 (1996)). Recent sutudy suggests that antisense oligonucleotides which are designed in a region containing 5' region of

mRNA, preferably, the translation initiation site, are most effective for the inhibition of the expression of a gene. The length of the antisense oligonucleotides is preferably 15 to 30 nucleotides and more preferably 20 to 25 nucleotides. It is important to confirm no interaction with other mRNA and no formation of secondary structure in the oligonucleotide sequence by homology search. The evaluation of whether the designed antisense oligonucleotide is functional or not can be determined by introducing the antisense oligonucleotide into a suitable cell and measuring the amount of the target mRNA, for example by northern blotting or RT-PCR, or the amount of the target protein, for example by western blotting or fluorescent antibody technique, to confirm the effect of expression inhibition.

Another method includes the triple helix technique. This technique involves forming a triple helix on the targeted intra-nuclear DNA sequence, thereby regulating its gene expression, mainly at the transcription stage. The oligonucleotide is designed mainly in the gene region involved in the transcription and inhibits the transcription and the production of the protein of the present invention. Such RNA, DNA and oligonucleotide can be produced using known synthesizers.

The antisense oligonucleotide may be introduced into the cells containing the target nucleic acid sequence by any of DNA transfection methods such as calcium phosphate method, electroporation, lipofection, microinjection, or gene transfer methods including the use of gene transfer vectors such as viruses. An antisense oligonucleotide expression vector can be prepared using a suitable retrovirus vector, then the expression vector can be introduced into the cells containing the target nucleic acid sequence by contacting the vector with the cells in vivo or ex vivo.

The DNA of the present invention can be used in the antisense RNA/DNA technique or the triple helix technique to inhibit NF- $\kappa$ B activation mediated by the protein of the present invention.

The antisense oligonucleotide against the gene encoding the protein of the present invention is useful as a medicament to treat or prevent diseases characterized by



undesirable activation of NF- $\kappa$ B, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders. Thus, the present invention also provides a medicament which comprises the above antisense oligonucleotide as an active ingredient. The antisense oligonucleotide can also be used to detect such diseases using northern hybridization or PCR.

The present invention also provides a ribozyme or deoxyribozyme which inhibits NF- $\kappa$ B activation. A ribozyme and deoxyribozyme is an RNA capable of recognizing a nucleotide sequence of a nucleic acid and cleaving the nucleic acid (see e.g., Hiroshi Yanagawa, "Jikken Igaku (Experimental Medicine) Bioscience 12: New Age of RNA). The ribozyme or deoxyribozyme can be produced so that it cleaves the selected target RNA (e.g., mRNA encoding the protein of the present invention). Based on the nucleotide sequence of the DNA encoding the protein of the present invention, the ribozyme or deoxyribozyme specifically cleaving the mRNA of the protein of the present invention can be designed. Such ribozyme has a complementary sequence to the mRNA for the protein of the present invention, complementarily associates with the mRNA and then cleaves the mRNA, which results in reduction or entire loss of the expression of the protein of the present invention. The level of the reduction of the expression is dependent on the level of the ribozyme or deoxyribozyme expression in the target cells.

There are two types of ribozyme or deoxyribozyme commonly used: a hammerhead ribozyme and a hairpin ribozyme. In particular, hammerhead ribozymes or deoxyribozymes have been well studied regarding their primary and secondary structure necessary for their cleavage activity, and those skilled in the art can easily design the ribozymes nucleotided solely on the nucleotide sequence information for the DNA encoding the protein of the present invention [see e.g., Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994)]. It is known that the hammerhead ribozymes or deoxyribozymes have a structure consisting of two recognition sites (recognition site I and recognition site II forming a chain complementary to target RNA) and an active site,

and cleave the target RNA at the 3'end of its sequence NUX (wherein N is A or G or C or U, and X is A or C or U) after the formation of a complementary pair with the target RNA in the recognition sites. In particular, the sequence GUC (or GUA) has been found to have the highest activity [see e.g., Koizumi, M. et al., Nucl. Acids Res. 17:7059-7071 (1989); Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994); Kawasaki & Taira, Jikken Igaku (Experimental Medicine) Vol.18, No.3, p.381-386 (2000)].

Therefore the sequence GTC (or GTA) is searched out, and a ribozyme is designed to form several, up to 10 to 20 complementary base pairs around that sequence. The suitability of the designed ribozyme can be evaluated by checking whether the prepared ribozyme can cleave the target mRNA in vitro according to the method described for example in Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994). The ribozyme can be prepared by methods known in the art to synthesize RNA molecules.

Alternatively, the sequence of the ribozyme can be synthesized on a DNA synthesizer and inserted into various vectors containing a suitable RNA polymerase promoter (e.g., T7 or SP6) to enzymatically synthesize an RNA molecule in vitro. Such ribozymes can be introduced into cells by gene transfer methods such as microinjection. Another method involves inserting a ribozyme DNA into a suitable expression vector and introducing the vector into cell strains, cells or tissues. Suitable vectors can be used to introduce the ribozyme into a selected cell. Examples of vectors commonly used for such purpose include plasmid vectors and animal virus vectors (e.g., retrovirus, adenovirus, herpes or vaccinia virus vectors). Such ribozymes are capable of inhibiting the NF- $\kappa$ B activation mediated by the protein of the present invention.

The present invention further provides a process for obtaining a new gene having a function, which comprises using the oligo-capping method to construct a full-length cDNA library, and detecting the presence of a protein having the function by using a signal factor. An example of such signal factor is a reporter gene.

Methods using a cDNA library containing a lot of non-full-length cDNAs are inefficient in obtaining many genes (cDNAs) having functions. Therefore libraries with a high ratio of the number of the full-length cDNA clones to the total number of the clones are necessary. "Full-length cDNA" refers to a complete DNA copy of mRNA from a gene. The cDNA libraries produced using the oligo-capping method contain full-length cDNA clones in a ratio of 50 to 80%, namely, a 5 to 10-fold increase in full-length cDNA clones compared to the cDNA libraries produced by prior art methods (Sumio Sugano, the monthly magazine BIO INDUSTRY Vol.16, No.11, p.19-26). Full-length cDNA clones are essential for protein expression in functional analyses of genes, and full-length cDNA clones themselves are very important materials for activity measurement. Thus, cloning of full-length cDNA is necessary for functional analyses of genes. Sequencing of the cDNA not only provides important information for establishing the primary sequence of the protein encoded by the cDNA, but also reveals the entire exon sequence. Thus, the full-length cDNA provides valuable information for identifying a gene, such as information for determining the primary sequence of a protein, exon-intron structure, the transcription initiation site of mRNA, the location of a promoter, etc.

The construction of full-length cDNA libraries by the oligo-capping method can be carried out, for example, according to the method described in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD. The oligo-capping method used herein involves substituting a cap structure with a synthetic oligo sequence by using BAP, TAP and an RNA ligase, as described in Suzuki & Sugano, "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

The reporter gene which can be used as a signal factor which indicates the presence of a protein having a function contains one or more suitable expression regulation sequence portion to which a protein factor such as a transcriptional factor can

bind, and a structural gene portion which allows the measurement of the activation of the proteins factor. The structural gene portion may encode any peptide or protein so long as those skilled in the art can measure the activity or amount of its expression product (including the amount of the mRNA produced). For example, chloramphenicol acetyltransferase,  $\beta$ -galactosidase, luciferase, etc., can be used and their enzymatic activity measured.

Examples of reporter genes which indicate the presence of a protein having a function include reporter genes containing a CREB (cAMP responsive element binding protein) binding sequence or AP-1 (activator protein-1) binding sequence at the expression regulation sequence region of the reporter genes, in addition to the NF- $\kappa$ B reporter genes described herein.

For example, if a gene capable of activating CREB is to be obtained, a CREB-dependent reporter plasmid and an expression vector comprising full-length cDNA produced by the oligo-capping method can be cotransfected into cells, and an expression vector having increased reporter activity can be selected from the cells to attain the purpose. If a gene capable of inhibiting CREB is to be obtained, a CREB-dependent reporter plasmid and an expression vector comprising full-length cDNA produced by the oligo-capping method can be cotransfected into cells, and an expression vector having decreased reporter activity can be selected from the cells to attain the purpose. These procedures may be carried out in the presence of a certain stimulus to the cells. The cDNA clone (expression vector) to be transfected into the cells may be a single clone or multiple clones which may be transfected simultaneously. One embodiment of the process of the present invention is detailed in Examples herein. Alternatively, a screening system for obtaining a gene capable of inhibiting NF- $\kappa$ B activation can also be constructed by cotransfecting an expression vector comprising full-length cDNA and a reporter gene into cells, stimulating the cells with IL-1 or TNF- $\alpha$  and the like, and selecting a clone having subnormally increased reporter activity. By preparing a reporter gene suitably, a gene encoding a protein capable of activating various

factors (for example, MAP kinase, transcription factor) can be obtained in addition to a gene encoding the protein capable of activating NF- $\kappa$ B.

The process of the present invention uses an in vitro system or a cell-based system, preferably a cell-based system. Examples of such cells include cells of prokaryotes such as E. coli, microorganisms such as yeast and fungi, as well as insects and animals. Preferred examples include animal cells, in particular, 293-EBNA cells and NIH3T3 cells.

Because the cDNA of the present invention is full-length, its 5' end sequence is the transcription initiation site of the corresponding mRNA. Therefore the cDNA sequence can be used to identify the promoter region of the gene by comparing the cDNA with the genomic nucleotide sequence. Genomic nucleotide sequences are available from various databases when the sequences have been deposited in the databases. Alternatively, the cDNA can also be used to clone the desired sequence from a genomic library, for example, by hybridization, and determine its nucleotide sequence. Thus, by comparing the nucleotide sequence of the cDNA of the present invention with a genomic sequence, the promoter region of the gene located upstream the cDNA can be identified. In addition, the promoter fragment thus identified can be used to construct a reporter plasmid for evaluating the expression of the gene. In general, the DNA fragment spanning 2kb (preferably 1kb) upstream from the transcription initiation site can be inserted upstream of the reporter gene to produce the reporter plasmid. The reporter plasmid can be used to screen for a compound which enhances or reduces the expression of the gene. For example, such screening can be carried out by transforming a suitable cell with the reporter plasmid, culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. These methods are also included in the scope of the present invention.

The present invention also relates to a computer-readable medium on which a

sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

In another aspect, the present invention relates to a method for calculating a homology, which comprises comparing data on the above medium with data of other nucleotide sequences. Thus, the gene and amino acid sequence of the present invention provide valuable information for determining their secondary and tertiary structure, e.g., information for identifying other sequence having a similar function and high homology. These sequences are stored on the computer-readable medium, then a database is searched using data stored in a known macromolecule structure program and a known search tool such as GCG. In this manner, a sequence in a database having a certain homology can be easily found.

The computer-readable medium may be any composition of materials used to

store information or data. Examples of such media include commercially available floppy disks, tapes, chips, hard drives, compact disks and video disks. The data on the medium allows a method for calculating a homology by comparing the data with other nucleotide sequence data. This method comprises the steps of providing a first polynucleotide sequence containing the polynucleotide sequence of the present invention for the computer-readable medium, and then comparing the first polynucleotide sequence with at least one-second polynucleotide or polypeptide sequence to identify the homology.

The present invention also relates to an insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 are fixed. A plurality of the various polynucleotides which are DNA probes are fixed on a specifically processed solid substrate such as slide glass to form a DNA microarray and then a labeled target polynucleotide is hybridized with the fixed polynucleotides to detect a signal from each of the probes. The data obtained is analyzed and the gene expression is determined.

The present invention further relates to an insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160,

162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed. By mixing organism-derived cell extract with the insoluble substrate on which these proteins are fixed, it is possible to isolate or identify cell-derived components such as proteins captured on the insoluble substrate that can be expected to be useful in diagnosis or drug development.

## EXAMPLES

The following examples further illustrate, but do not limit the present invention.

Example 1: Construction of a full-length cDNA library using the oligo-capping method

### (1) Preparation of RNA from human lung fibroblasts (Cryo NHLF)

Human lung fibroblasts (Cryo NHLF: purchased from Sanko Junyaku Co., Ltd.) were cultured according to the manufacture's protocol. After repeating subculturing the cells to obtain fifty 10cm dishes containing the resulting culture, the cells were recovered with a cell scraper. Then, total RNA was obtained from the recovered cells by using the RNA extraction reagent ISOGEN (purchased from NIPPON GENE) according to the manufacturer's protocol. Then, poly A<sup>+</sup> RNA was obtained from the total RNA by using an oligo-dT cellulose column according to Maniatis et al., supra.

### (2) Preparation of RNA from mouse ATDC5 cells

ATDC5, a cell strain cloned from mouse EC (embryonal carcinoma) (Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116)(1990) was repeatedly subcultured to obtain fifty 10cm dishes containing the resultant culture. Thereafter, poly A<sup>+</sup> RNA was obtained by a method similar to that of (1) above. Culture of ATDC5 cells was performed according to the method described in Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116 (1990).

### (3) Preparation of RNA from Jurkat cells

From Jurkat cells, a human T cell strain (purchased from DAINIPPON PHARMACEUTICAL CO.,LTD), poly A<sup>+</sup> RNA was obtained in the same way as in the



above (1). Jurkat cells were cultured in PRMI 1640 medium (GIBCO) containing 10%FBS (Fetal Bovine Serum: GIBCO) and 10mM HEPES (GIBCO) in the presence of 5% CO<sub>2</sub> at 37°C.

(4) Preparation of RNA from RAW264.7 cells

RAW264.7 cells, a mouse macrophage-like cell strain (ATCC Number TIB-71), were cultured to obtain poly A<sup>+</sup> RNA in the same way as in the above (1).

(5) Construction of a full-length cDNA library by the oligo-capping method

A full-length cDNA library was constructed from poly A<sup>+</sup> RNA of the above human lung fibroblasts, ATDC5 cells, Jurkat cells and RAW264.7 cells by the oligo-capping method according to the method of Sugano S. et al. [e.g., Maruyama, K. & Sugano, S., *Gene*, 138:171-174 (1994); Suzuki, Y. et al., *Gene*, 200:149-156 (1997); Suzuki, Y. & Sugano, S. "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.].

(6) Preparation of plasmid DNA

The full-length cDNA library constructed as above was transformed into *E. coli* strain TOP 10 by electroporation, then spread on LB agar medium containing 100 µg/ml of ampicillin, and incubated overnight at 37°C. Then, using QIAwell 96 Ultra Plasmid Kit (QIAGEN) according to the manufacturer's protocol, the plasmids were recovered from the colonies grown on ampicillin-containing LB agar medium.

Example 2: Cloning of DNA capable of activating NF- κ B

(1) Screening of the cDNA encoding the protein capable of activating NF- κ B

293-EBNA cells (purchased from Invitrogen) were seeded on DMEM medium containing 5% FBS in a 96 well cell culture plate to a final cell density of 1 x 10<sup>4</sup> cells/100 µl/well, and cultured for 24 hours at 37°C in the presence of 5% CO<sub>2</sub>. Then, 50ng of pNF κ B-Luc (purchased from STRATAGENE) and 2 µl of the full-length cDNA expression vector prepared in above Example 1.(6) were cotransfected into the cells in a

well using FuGENE 6 (purchased from Roche) according to the manufacturer's protocol. After 24 hours of culture at 37°C, the reporter activity of NF- $\kappa$ B (luciferase activity) was measured using long-term luciferase assay system, PIKKA GENE LT2.0 (TOYO INK) according to the attached manufacturer's instructions. The luciferase activity was measured using Wallac ARVO<sup>TM</sup> ST 1420 MULTILABEL COUNTER (Perkin Elmer).

## (2) DNA sequencing

The above screening was carried out, and plasmids showing a 5-fold or more increase in luciferase activity compared to that of the control experiment (luciferase activity of the cell into which vacant vector pME18S-FL3 is introduced instead of full-length cDNA expression vector) were selected. One pass sequencing was carried out from the 5' end of the cloned cDNA (sequencing primer: 5'-CTTCTGCTCTAAAAGCTGCG-3' (SEQ ID NO: 289)) and from the 3' end (sequencing primer: 5'-CGACCTGCAGCTCGAGCACA-3' (SEQ ID NO: 290)) so that as long sequence as possible is determined. The sequencing was carried out using the reagent Thermo Sequenase II Dye Terminator Cycle Sequencing Kit (Amersham Pharmacia Biotech) or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit (Applied Biosystems) and the device ABI PRISM 377 sequencer or ABI PRISM 3100 sequencer according to the manufacturer's instructions.

## (3) Full-length sequencing

The full-length DNA sequences for the 144 new clones which were obtained by the above screening, were determined (SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287). The

amino acid sequences of the protein coding regions (open reading frames) were deduced (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288).

The results of measurement of NF- $\kappa$ B reporter activity (luciferase activity) of 41 clones among the above obtained clones are shown in Table 1 below. The value of activity shown in Table 1 is a relative value to the value of control experiment (luciferase activity of a cell into which pME183-FL3 vector containing no insert has been introduced in place of full length cDNA).

Table 1

Clone	activity (-fold)
SEQ ID NO:7	9
SEQ ID NO:9	12
SEQ ID NO:19	6
SEQ ID NO:23	5
SEQ ID NO:29	92
SEQ ID NO:35	54
SEQ ID NO:37	33
SEQ ID NO:39	22
SEQ ID NO:43	31
SEQ ID NO:47	63
SEQ ID NO:51	12

SEQ ID NO:75	9
SEQ ID NO:77	13
SEQ ID NO:85	13
SEQ ID NO:91	7
SEQ ID NO:103	7
SEQ ID NO:111	70
SEQ ID NO:115	11
SEQ ID NO:119	9
SEQ ID NO:123	10
SEQ ID NO:143	6
SEQ ID NO:151	10
SEQ ID NO:157	29
SEQ ID NO:165	145
SEQ ID NO:171	134
SEQ ID NO:175	19
SEQ ID NO:181	22
SEQ ID NO:185	33
SEQ ID NO:195	6
SEQ ID NO:197	5
SEQ ID NO:199	14
SEQ ID NO:201	31
SEQ ID NO:205	32
SEQ ID NO:211	16
SEQ ID NO:229	13
SEQ ID NO:237	7
SEQ ID NO:239	23
SEQ ID NO:247	15
SEQ ID NO:257	5

SEQ ID NO:261 17

SEQ ID NO:287 66

**Example 3: Screening compounds inhibiting NF- $\kappa$ B activation**

293-EBNA cells were seeded on DMEM medium containing 5% FBS in a 96-well cell culture plate to a final cell density of  $1 \times 10^4$  cells/100  $\mu$ l/well, and cultured for 24 hours at 37°C in the presence of 5% CO<sub>2</sub>. Then, 50ng of the plasmid comprising the gene encoding NF- $\kappa$ B activating protein of SEQ ID NO: 12 which was obtained in Example 2 above, and 50ng of the reporter plasmid pNF  $\kappa$ B-Luc were cotransfected into the cells in a well using FuGENE 6. After 1 hour, the proteasome inhibitor MG-132 (purchased from CALBIOCHEM) (Uehara T. et al., J. Biol. Chem. 274, p.15875-15882 (1999); Wang X. C. et al., Invest. Ophthalmol. Vis. Sci. 40, p.477-486) was added to the culture to final concentrations of 1.0  $\mu$ M. After 24 hours of culture at 37°C, the reporter activity was measured using PIKKA GENE LT2.0. The results showed that MG132 inhibited the expression of the reporter gene (Fig. 1).

**INDUSTRIAL APPLICABILITY**

As described above, the present invention provides industrially highly useful proteins capable of activating NF- $\kappa$ B and genes encoding the proteins. The proteins of the present invention and the genes encoding the proteins allow not only screening for compounds useful for treating and preventing diseases associated with the excessive activation or inhibition of NF- $\kappa$ B, but also production of diagnostics for such diseases. The genes of the present invention are also useful as a gene source used for gene therapy.

All publications, patents and patent applications cited herein are incorporated herein in their entirety.

## CLAIMS

1. A purified protein selected from the group consisting of:
  - (a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and
  - (b) a protein that activates NF- $\kappa$ B (Nuclear factor kappa B) and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.
2. A purified protein that activates NF- $\kappa$ B and comprises an amino acid sequence having at least 95% identity to the protein according to claim 1 over the entire length thereof.
3. An isolated polynucleotide which comprises a nucleotide sequence encoding a

protein selected from the group consisting of:

(a) a protein which comprises an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288; and

(b) a protein that activates NF-  $\kappa$  B and comprises an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

4. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,

179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- $\kappa$ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- $\kappa$ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

5. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243,



245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287;

(b) a polynucleotide sequence encoding a protein that activates NF- $\kappa$ B and hybridizing under stringent conditions with a polynucleotide having a polynucleotide sequence complementary to the polynucleotide sequence of (a); and

(c) a polynucleotide sequence which encodes a protein that activates NF- $\kappa$ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287.

6. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- $\kappa$ B and has at least 95% identity to the polynucleotide sequence according to claim 3 over the entire length thereof.

7. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- $\kappa$ B and has at least 95% identity to the polynucleotide sequence according to claim 4 or 5 over the entire length thereof.

8. A purified protein encoded by the polynucleotide according to any one of claims 3 to 7.

9. A recombinant vector which comprises a polynucleotide according to any one of claims 3 to 7.
10. A agent for gene therapy which comprises the recombinant vector according to claim 9 as an active ingredient.
11. A transformed cell which comprises the recombinant vector according to claim 9.
12. A membrane of the cell according to claim 11, which has the protein according to claim 1 or 2 which is a membrane protein.
13. A process for producing a protein according to claim 1, 2 or 8 comprising the steps of;
- (a) culturing a transformed cell according to claim 11 under conditions providing expression of the protein according to claim 1, 2 or 8; and
  - (b) recovering the protein from the culture product.
14. A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of claim 1, 2 or 8 in a subject comprising the steps of:
- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
  - (b) analyzing the amount of expression of said protein in a sample derived from said subject.
15. A method for screening compounds capable of inhibiting or promoting NF- $\kappa$ B activation, which comprises the steps of:
- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes

activation of NF- $\kappa$ B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- $\kappa$ B into a cell;

- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- $\kappa$ B; and
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation.

16. A method for screening compounds capable of inhibiting or promoting NF- $\kappa$ B activation, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to claim 1, 2 or 8 into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$ B; and
- (d) selecting a candidate compound which can change the activation of NF- $\kappa$ B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$ B activation.

17. A compound capable of inhibiting or promoting NF- $\kappa$ B activation, which is selected by the method for screening according to claim 15 or 16.

18. A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$ B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- $\kappa$ B into a cell;

- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect activation of NF- $\kappa$  B;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$  B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

19. A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformed cell by introducing a gene encoding a protein that promotes activation of NF- $\kappa$  B according to claim 1, 2 or 8 into a cell;
- (b) culturing the transformed cell under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the activation of NF- $\kappa$  B; and
- (d) selecting a candidate compound which can change the activation of NF- $\kappa$  B as compared with the case of the absence of candidate compounds, as a compound capable of inhibiting or promoting NF- $\kappa$  B activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

20. A kit for screening a compound capable of inhibiting or promoting NF- $\kappa$  B activation, which comprises:

- (a) a transformed cell comprising a gene encoding a protein that promotes activation of NF- $\kappa$  B according to claim 1, 2 or 8 and a gene encoding a signal which can detect activation of NF- $\kappa$  B; and
- (b) reagents for measuring the signal.

21. A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to claim 1, 2 or 8.
22. The monoclonal or polyclonal antibody or a fragment thereof according to claim 21, which inhibits the activity of promoting activation of NF- $\kappa$ B by the protein according to claim 1, 2 or 8.
23. A process for producing a monoclonal or polyclonal antibody according to claim 21 or 22, which comprises administering the protein according to claim 1, 2 or 8 or epitope-bearing fragments thereof to a non-human animal as an antigen.
24. An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of claims 3 to 7, which prevents the expression of a protein which promotes NF- $\kappa$ B activation.
25. A ribozyme or deoxyribozyme capable of inhibiting NF- $\kappa$ B activation, which has an action of cleavage of RNA that encodes the protein according to claim 1, 2 or 8 or an action of cleavage of RNA that encodes a protein involved in a pathway leading to NF- $\kappa$ B activation.
26. A method for treating a disease associated with NF- $\kappa$ B activation, which comprises administering to a subject a compound screened by the process according to claim 15 or 16, and/or a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22, and/or an antisense oligonucleotide according to claim 24, and/or a ribozyme or deoxyribozyme according to claim 25 in an effective amount to treat a disease selected from the group consisting of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and

ischemic disorders.

27. A pharmaceutical composition produced by the process according to claim 18 or 19 for inhibiting or promoting NF-  $\kappa$  B activation.

28. The pharmaceutical composition according to claim 27 for the treatment of inflammation, autoimmune diseases, cancers, infectious disease, bone diseases, AIDS, neurodegenerative diseases and/or ischemic disorders.

29. A method of treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders, which comprises administering a pharmaceutical composition produced by the process according to claim 18 or 19 to a patient suffering from a disease associated with NF-  $\kappa$  B activation.

30. A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22 as an active ingredient.

31. A pharmaceutical composition which comprises an antisense oligonucleotide according to claim 24 as an active ingredient.

32. A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to claim 25 as an active ingredient.

33. The pharmaceutical composition according to any one of claims 30 to 32 for the treatment and/or prevention of a disease which is selected from the group consisting of inflammation, autoimmune diseases, infectious diseases, cancers, bone diseases, AIDS, neurodegenerative diseases and ischemic disorders.

34. A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 or a coding region thereof, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288.

35. A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to claim 34 with data of said other nucleotide sequences and/or amino acid sequences.

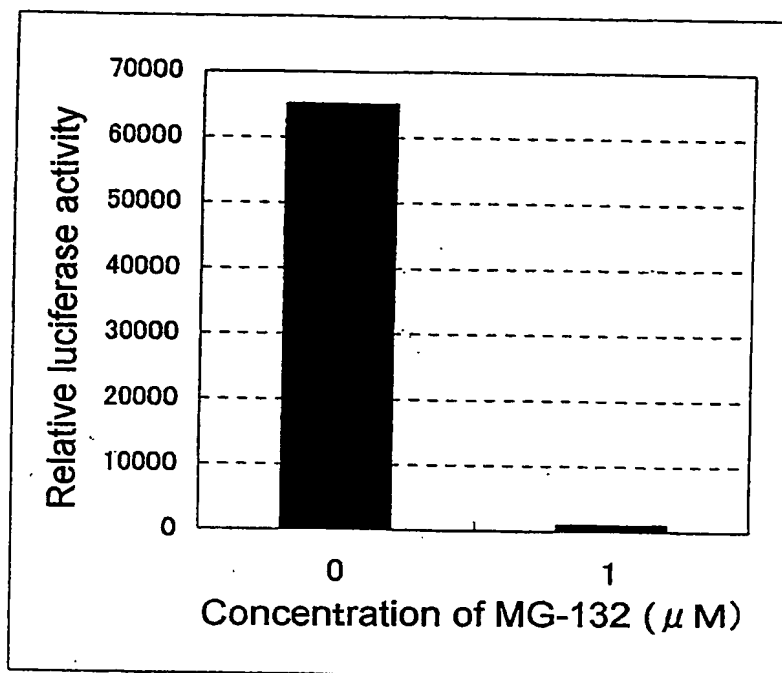
36. An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,

107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285 and 287 are fixed.

37. An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286 and 288, are fixed.



Fig. 1



BEST AVAILABLE COPY

## SEQUENCE LISTING

&lt;110&gt; Asahi Kasei Kabushiki Kaisha

<120> NF- $\kappa$ B activating gene

&lt;130&gt; A21698A

&lt;160&gt; 290

&lt;210&gt; 1

&lt;211&gt; 2860

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (56)..(2545)

&lt;400&gt; 1

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2/861

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&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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 Phe Gln Val Leu Asn Glu Lys Lys Gln Ile Asn Ala Ile Lys Tyr Val  
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 Val Gly Thr Val Asn Tyr Met Ala Pro Glu Ala Ile Arg Asp Met Ser  
 660 665 670  
 Ser Ser Arg Glu Asn Ser Lys Ile Arg Thr Lys Val Ser Pro Arg Ser

675	680	685
Asp Val Trp Ser Leu Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly Arg		
690	695	700
Thr Pro Phe Gln His Ile Ile Asn Gln Val Ser Lys Leu His Ala Ile		
705	710	715
Ile Asn Pro Ala His Glu Ile Glu Phe Pro Glu Ile Ser Glu Lys Asp		
725	730	735
Leu Arg Asp Val Leu Lys Cys Cys Leu Val Arg Asn Pro Lys Glu Arg		
740	745	750
Ile Ser Ile Pro Glu Leu Leu Thr His Pro Tyr Val Gln Ile Gln Pro		
755	760	765
His Pro Gly Ser Gln Met Ala Arg Gly Ala Thr Asp Glu Met Lys Tyr		
770	775	780
Val Leu Gly Gln Leu Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys		
785	790	795
Thr Ala Lys Thr Leu Tyr Glu Arg Tyr Asn Cys Gly Glu Gly Gln Asp		
805	810	815
Ser Ser Ser Ser Lys Thr Phe Asp Lys Lys Arg Glu Arg Lys		
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&lt;210&gt; 3

&lt;211&gt; 2975

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (84).. (2654)

&lt;400&gt; 3

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 Met Glu Ser Glu Asp Leu Ser Gly Arg Glu  
 1 5 10  
 ttg aca att gat tcc ata atg aac aaa gtg aga gac att aaa aat aag 161  
 Leu Thr Ile Asp Ser Ile Met Asn Lys Val Arg Asp Ile Lys Asn Lys  
 15 20 25  
 ttt aaa aat gaa gac ctt act gat gaa cta agc ttg aat aaa att tct 209  
 Phe Lys Asn Glu Asp Leu Thr Asp Glu Leu Ser Leu Asn Lys Ile Ser  
 30 35 40  
 gct gat act aca gat aac tcg gga act gtt aac caa att atg atg atg 257  
 Ala Asp Thr Thr Asp Asn Ser Gly Thr Val Asn Gln Ile Met Met Met  
 45 50 55  
 gca aac aac cca gag gac tgg ttg agt ttg ttg ctc aaa cta gag aaa 305  
 Ala Asn Asn Pro Glu Asp Trp Leu Ser Leu Leu Leu Lys Leu Glu Lys  
 60 65 70  
 aac agt gtt ccg cta agt gat gct ctt tta aat aaa ttg att ggt cgt 353  
 Asn Ser Val Pro Leu Ser Asp Ala Leu Leu Asn Lys Leu Ile Gly Arg  
 75 80 85 90  
 tac agt caa gca att gaa gcg ctt ccc cca gat aaa tat ggc caa aat 401  
 Tyr Ser Gln Ala Ile Glu Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn  
 95 100 105  
 gag agt ttt gct aga att caa gtg aga ttt gct gaa tta aaa gct att 449  
 Glu Ser Phe Ala Arg Ile Gln Val Arg Phe Ala Glu Leu Lys Ala Ile  
 110 115 120  
 caa gag cca gat gat gca cgt gac tac ttt caa atg gcc aga gca aac 497

Gln Glu Pro Asp Asp Ala Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn  
 125 130 135  
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 Cys Lys Lys Phe Ala Phe Val His Ile Ser Phe Ala Gln Phe Glu Leu  
 140 145 150  
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 Ser Gln Gly Asn Val Lys Lys Ser Lys Gln Leu Leu Gln Lys Ala Val  
 155 160 165 170  
 gaa cgt gga gca gta cca cta gaa atg ctg gaa att gcc ctg cgg aat 641  
 Glu Arg Gly Ala Val Pro Leu Glu Met Leu Glu Ile Ala Leu Arg Asn  
 175 180 185  
 tta aac ctc caa aaa aag cag ctg ctt tca gag gag gaa aag aag aat 689  
 Leu Asn Leu Gln Lys Lys Gln Leu Leu Ser Glu Glu Glu Lys Lys Asn  
 190 195 200  
 tta tca gca tct acg gta tta act gcc caa gaa tca ttt tcc ggt tca 737  
 Leu Ser Ala Ser Thr Val Leu Thr Ala Gln Glu Ser Phe Ser Gly Ser  
 205 210 215  
 ctt ggg cat tta cag aat agg aac aac agt tgt gat tcc aga gga cag 785  
 Leu Gly His Leu Gln Asn Arg Asn Asn Ser Cys Asp Ser Arg Gly Gln  
 220 225 230  
 act act aaa gcc agg ttt tta tat gga gag aac atg cca cca caa gat 833  
 Thr Thr Lys Ala Arg Phe Leu Tyr Gly Glu Asn Met Pro Pro Gln Asp  
 235 240 245 250  
 gca gaa ata ggt tac cgg aat tca ttg aga caa act aac aaa act aaa 881  
 Ala Glu Ile Gly Tyr Arg Asn Ser Leu Arg Gln Thr Asn Lys Thr Lys  
 255 260 265  
 cag tca tgc cca ttt gga aga gtc cca gtt aac ctt cta aat agc cca 929

Gln Ser Cys Pro Phe Gly Arg Val Pro Val Asn Leu Leu Asn Ser Pro	
270 275 280	
gat tgt gat gtg aag aca gat gat tca gtt gta cct tgt ttt atg aaa	977
Asp Cys Asp Val Lys Thr Asp Asp Ser Val Val Pro Cys Phe Met Lys	
285 290 295	
aga caa acc tct aga tca gaa tgc cga gat ttg gtt gtg cct gga tct	1025
Arg Gln Thr Ser Arg Ser Glu Cys Arg Asp Leu Val Val Pro Gly Ser	
300 305 310	
aaa cca agt gga aat gat tcc tgt gaa tta aga aat tta aag tct gtt	1073
Lys Pro Ser Gly Asn Asp Ser Cys Glu Leu Arg Asn Leu Lys Ser Val	
315 320 325 330	
caa aat agt cat ttc aag gaa cct ctg gtg tca gat gaa aag agt tct	1121
Gln Asn Ser His Phe Lys Glu Pro Leu Val Ser Asp Glu Lys Ser Ser	
335 340 345	
gaa ctt att att act gat tca ata acc ctg aag aat aaa acg gaa tca	1169
Glu Leu Ile Ile Thr Asp Ser Ile Thr Leu Lys Asn Lys Thr Glu Ser	
350 355 360	
agt ctt cta gct aaa tta gaa gaa act aaa gag tat caa gaa cca gag	1217
Ser Leu Leu Ala Lys Leu Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu	
365 370 375	
gtt cca gag agt aac cag aaa cag tgg caa tct aag aga aag tca gag	1265
Val Pro Glu Ser Asn Gln Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu	
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tgt att aac cag aat cct gct gca tct tca aat cac tgg cag att ccg	1313
Cys Ile Asn Gln Asn Pro Ala Ala Ser Ser Asn His Trp Gln Ile Pro	
395 400 405 410	
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Glu Leu Ala Arg Lys Val Asn Thr Glu Gln Lys His Thr Thr Phe Glu  
 415 420 425  
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 Gln Pro Val Phe Ser Val Ser Lys Gln Ser Pro Pro Ile Ser Thr Ser  
 430 435 440  
 aaa tgg ttt gac cca aaa tct att tgt aag aca cca agc agc aat acc 1457  
 Lys Trp Phe Asp Pro Lys Ser Ile Cys Lys Thr Pro Ser Ser Asn Thr  
 445 450 455  
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 Leu Asp Asp Tyr Met Ser Cys Phe Arg Thr Pro Val Val Lys Asn Asp  
 460 465 470  
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 Phe Gln Gln Gln Gln His Gln Ile Leu Ala Thr Pro Leu Gln Asn Leu  
 495 500 505  
 cag gtt tta gca tct tct tca gca aat gaa tgc att tcg gtt aaa gga 1649  
 Gln Val Leu Ala Ser Ser Ser Ala Asn Glu Cys Ile Ser Val Lys Gly  
 510 515 520  
 aga att tat tcc att tta aag cag ata gga agt gga ggt tca agc aag 1697  
 Arg Ile Tyr Ser Ile Leu Lys Gln Ile Gly Ser Gly Gly Ser Ser Lys  
 525 530 535  
 gta ttt cag gtg tta aat gaa aag aaa cag ata tat gct ata aaa tat 1745  
 Val Phe Gln Val Leu Asn Glu Lys Lys Gln Ile Tyr Ala Ile Lys Tyr  
 540 545 550  
 gtg aac tta gaa gaa gca gat aac caa act ctt gat agt tac cgg aac 1793



Val Asn Leu Glu Glu Ala Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn  
 555 560 565 570  
 gaa ata gct tat ttg aat aaa cta caa caa cac agt gat aag atc atc 1841  
 Glu Ile Ala Tyr Leu Asn Lys Leu Gln Gln His Ser Asp Lys Ile Ile  
 575 580 585  
 cga ctt tat gat tat gaa atc acg gac cag tac atc tac atg gta atg 1889  
 Arg Leu Tyr Asp Tyr Glu Ile Thr Asp Gln Tyr Ile Tyr Met Val Met  
 590 595 600  
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 Glu Cys Gly Asn Ile Asp Leu Asn Ser Trp Leu Lys Lys Lys Lys Ser  
 605 610 615  
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 Ile Asp Pro Trp Glu Arg Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala  
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 gtt cac aca atc cat caa cat ggc att gtt cac agt gat ctt aaa cca 2033  
 Val His Thr Ile His Gln His Gly Ile Val His Ser Asp Leu Lys Pro  
 635 640 645 650  
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 Ala Asn Phe Leu Ile Val Asp Gly Met Leu Lys Leu Ile Asp Phe Gly  
 655 660 665  
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 Ile Ala Asn Gln Met Gln Pro Asp Thr Thr Ser Val Val Lys Asp Ser  
 670 675 680  
 cag gtt ggc aca gtt aat tat atg cca cca gaa gca atc aaa gat atg 2177  
 Gln Val Gly Thr Val Asn Tyr Met Pro Pro Glu Ala Ile Lys Asp Met  
 685 690 695  
 tct tcc tcc aga gag aat ggg aaa tct aag tca aag ata agc ccc aaa 2225

Ser Ser Ser Arg Glu Asn Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys  
 700 705 710  
 agt gat gtt tgg tcc tta gga tgt att ttg tac tat atg act tac ggg 2273  
 Ser Asp Val Trp Ser Leu Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly  
 715 720 725 730  
 aaa aca cca ttt cag cag ata att aat cag att tct aaa tta cat gcc 2321  
 Lys Thr Pro Phe Gln Gln Ile Ile Asn Gln Ile Ser Lys Leu His Ala  
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 Asp Leu Gln Asp Val Leu Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln  
 765 770 775  
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 Arg Ile Ser Ile Pro Glu Leu Leu Ala His Pro Tyr Val Gln Ile Gln  
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 Thr His Pro Val Asn Gln Met Ala Lys Gly Thr Thr Glu Glu Met Lys  
 795 800 805 810  
 tat gtt ctg ggc caa ctt gtt ggt ctg aat tct cct aac tcc att ttg 2561  
 Tyr Val Leu Gly Gln Leu Val Gly Leu Asn Ser Pro Asn Ser Ile Leu  
 815 820 825  
 aaa gct gct aaa act tta tat gaa cac tat agt ggt ggt gaa agt cat 2609  
 Lys Ala Ala Lys Thr Leu Tyr Glu His Tyr Ser Gly Gly Glu Ser His  
 830 835 840  
 aat tct tca tcc tcc aag act ttt gaa aaa aaa agg gga aaa aaa 2654

Asn Ser Ser Ser Ser Lys Thr Phe Glu Lys Lys Arg Gly Lys Lys

845

850

855

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 aaaaaattca gtagattatc tttaaaagaa aactgtaaaa atagcaacca cttatggtac 2834  
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&lt;210&gt; 4

&lt;211&gt; 857

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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1

5

10

15

Met Asn Lys Val Arg Asp Ile Lys Asn Lys Phe Lys Asn Glu Asp Leu

20

25

30

Thr Asp Glu Leu Ser Leu Asn Lys Ile Ser Ala Asp Thr Thr Asp Asn

35

40

45

Ser Gly Thr Val Asn Gln Ile Met Met Met Ala Asn Asn Pro Glu Asp

50

55

60

Trp Leu Ser Leu Leu Leu Lys Leu Glu Lys Asn Ser Val Pro Leu Ser

65

70

75

80

Asp Ala Leu Leu Asn Lys Leu Ile Gly Arg Tyr Ser Gln Ala Ile Glu

85

90

95

Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser Phe Ala Arg Ile

100	105	110	
Gln Val Arg Phe Ala Glu Leu Lys Ala Ile Gln Glu Pro Asp Asp Ala			
115	120	125	
Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys Lys Phe Ala Phe			
130	135	140	
Val His Ile Ser Phe Ala Gln Phe Glu Leu Ser Gln Gly Asn Val Lys			
145	150	155	160
Lys Ser Lys Gln Leu Leu Gln Lys Ala Val Glu Arg Gly Ala Val Pro			
165	170	175	
Leu Glu Met Leu Glu Ile Ala Leu Arg Asn Leu Asn Leu Gln Lys Lys			
180	185	190	
Gln Leu Leu Ser Glu Glu Glu Lys Lys Asn Leu Ser Ala Ser Thr Val			
195	200	205	
Leu Thr Ala Gln Glu Ser Phe Ser Gly Ser Leu Gly His Leu Gln Asn			
210	215	220	
Arg Asn Asn Ser Cys Asp Ser Arg Gly Gln Thr Thr Lys Ala Arg Phe			
225	230	235	240
Leu Tyr Gly Glu Asn Met Pro Pro Gln Asp Ala Glu Ile Gly Tyr Arg			
245	250	255	
Asn Ser Leu Arg Gln Thr Asn Lys Thr Lys Gln Ser Cys Pro Phe Gly			
260	265	270	
Arg Val Pro Val Asn Leu Leu Asn Ser Pro Asp Cys Asp Val Lys Thr			
275	280	285	
Asp Asp Ser Val Val Pro Cys Phe Met Lys Arg Gln Thr Ser Arg Ser			
290	295	300	
Glu Cys Arg Asp Leu Val Val Pro Gly Ser Lys Pro Ser Gly Asn Asp			
305	310	315	320

Ser Cys Glu Leu Arg Asn Leu Lys Ser Val Gln Asn Ser His Phe Lys  
325 330 335  
Glu Pro Leu Val Ser Asp Glu Lys Ser Ser Glu Leu Ile Ile Thr Asp  
340 345 350  
Ser Ile Thr Leu Lys Asn Lys Thr Glu Ser Ser Leu Leu Ala Lys Leu  
355 360 365  
Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu Val Pro Glu Ser Asn Gln  
370 375 380  
Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu Cys Ile Asn Gln Asn Pro  
385 390 395 400  
Ala Ala Ser Ser Asn His Trp Gln Ile Pro Glu Leu Ala Arg Lys Val  
405 410 415  
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420 425 430  
Ser Lys Gln Ser Pro Pro Ile Ser Thr Ser Lys Trp Phe Asp Pro Lys  
435 440 445  
Ser Ile Cys Lys Thr Pro Ser Ser Asn Thr Leu Asp Asp Tyr Met Ser  
450 455 460  
Cys Phe Arg Thr Pro Val Val Lys Asn Asp Phe Pro Pro Ala Cys Gln  
465 470 475 480  
Leu Ser Thr Pro Tyr Gly Gln Pro Ala Cys Phe Gln Gln Gln Gln His  
485 490 495  
Gln Ile Leu Ala Thr Pro Leu Gln Asn Leu Gln Val Leu Ala Ser Ser  
500 505 510  
Ser Ala Asn Glu Cys Ile Ser Val Lys Gly Arg Ile Tyr Ser Ile Leu  
515 520 525  
Lys Gln Ile Gly Ser Gly Gly Ser Ser Lys Val Phe Gln Val Leu Asn

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Glu Lys Lys Gln Ile Tyr Ala Ile Lys Tyr Val Asn Leu Glu Glu Ala  
545                      550                      555                      560  
Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn Glu Ile Ala Tyr Leu Asn  
565                      570                      575  
Lys Leu Gln Gln His Ser Asp Lys Ile Ile Arg Leu Tyr Asp Tyr Glu  
580                      585                      590  
Ile Thr Asp Gln Tyr Ile Tyr Met Val Met Glu Cys Gly Asn Ile Asp  
595                      600                      605  
Leu Asn Ser Trp Leu Lys Lys Lys Lys Ser Ile Asp Pro Trp Glu Arg  
610                      615                      620  
Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala Val His Thr Ile His Gln  
625                      630                      635                      640  
His Gly Ile Val His Ser Asp Leu Lys Pro Ala Asn Phe Leu Ile Val  
645                      650                      655  
Asp Gly Met Leu Lys Leu Ile Asp Phe Gly Ile Ala Asn Gln Met Gln  
660                      665                      670  
Pro Asp Thr Thr Ser Val Val Lys Asp Ser Gln Val Gly Thr Val Asn  
675                      680                      685  
Tyr Met Pro Pro Glu Ala Ile Lys Asp Met Ser Ser Ser Arg Glu Asn  
690                      695                      700  
Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys Ser Asp Val Trp Ser Leu  
705                      710                      715                      720  
Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly Lys Thr Pro Phe Gln Gln  
725                      730                      735  
Ile Ile Asn Gln Ile Ser Lys Leu His Ala Ile Ile Asp Pro Asn His  
740                      745                      750

Glu Ile Glu Phe Pro Asp Ile Pro Glu Lys Asp Leu Gln Asp Val Leu

755

760

765

Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile Ser Ile Pro Glu

770

775

780

Leu Leu Ala His Pro Tyr Val Gln Ile Gln Thr His Pro Val Asn Gln

785

790

795

800

Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val Leu Gly Gln Leu

805

810

815

Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys Ala Ala Lys Thr Leu

820

825

830

Tyr Glu His Tyr Ser Gly Gly Glu Ser His Asn Ser Ser Ser Ser Lys

835

840

845

Thr Phe Glu Lys Lys Arg Gly Lys Lys

850

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<400> 5

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Met Ala Ala Ala Ala Thr Met Ala Ala Ala

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10

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gag ggc ccg ctg ggg ggg ggt tct gga ctc caa gaa ccc cta caa ctt	149
Glu Gly Pro Leu Gly Gly Gly Ser Gly Leu Gln Glu Pro Leu Gln Leu	
30 35 40	
gga gag ttg gac atc acc tct gat gaa ttc atc ttg gat gaa gtg gat	197
Gly Glu Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp	
45 50 55	
gtt cac atc cag gca aac ctg gag gat gag tta gtg aag gaa gct ctc	245
Val His Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu	
60 65 70	
aaa acg ggt gtg gat ctt cga cac tat tca aag cag gtg gag ctg gag	293
Lys Thr Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu	
75 80 85 90	
ctg cag cag att gag cag aag tca atc cgg gac tat atc caa gag agt	341
Leu Gln Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser	
95 100 105	
gaa aac ata gcg tct ctg cac aat cag atc acg gcc tgt gac gcc gtc	389
Glu Asn Ile Ala Ser Leu His Asn Gln Ile Thr Ala Cys Asp Ala Val	
110 115 120	
ctg gag cgc atg gaa cag atg ctg gga gct ttt cag agc gat ctc agc	437
Leu Glu Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser	
125 130 135	
tcc atc agc tct gag atc cga acc ctg cag gag cag tcg ggg gcc atg	485
Ser Ile Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met	
140 145 150	
aac atc cga ctt cgt aac cga cag gca gtt cgg ggg aaa ctt ggg gaa	533



24/861

Tyr Tyr Arg Ser Tyr Val Gly Arg Leu Met Lys Val Gln Tyr Glu Glu  
 300 305 310  
 gtt gct gag aaa gac gac cta atg ggt gtt gaa gac aca gca aag aaa 1013  
 Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu Asp Thr Ala Lys Lys  
 315 320 325 330  
 ggc ttc ttc tcg aag ccg tcc ctc cga agc agg aac acc atc ttt acc 1061  
 Gly Phe Phe Ser Lys Pro Ser Leu Arg Ser Arg Asn Thr Ile Phe Thr  
 335 340 345  
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 Leu Gly Thr Arg Gly Thr Val Ile Ser Pro Ala Glu Leu Glu Ala Pro  
 350 355 360  
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 Ile Leu Val Pro His Thr Ala Gln Arg Gly Glu Gln Arg Tyr Pro Phe  
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 Glu Ala Leu Phe Arg Ser Gln His Tyr Ala Leu Leu Asp Asn Ser Cys  
 380 385 390  
 cgt gaa tat ctt ttc atc tgt gaa ttt ttc atc gtg tct ggc ccg gct 1253  
 Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe Ile Val Ser Gly Pro Ala  
 395 400 405 410  
 gca cat gac ctg ttc cac gcc gtc atg ggc cgc acg ctc tcc atg acg 1301  
 Ala His Asp Leu Phe His Ala Val Met Gly Arg Thr Leu Ser Met Thr  
 415 420 425  
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 Leu Lys His Leu Glu Ser Tyr Leu Ala Asp Cys Tyr Asp Ala Ile Ala  
 430 435 440  
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Val Phe Leu Cys Ile His Ile Val Leu Arg Phe Arg Asn Ile Ala Ala	
445	450
455	
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Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr Trp Glu Gln Val Leu Ala	
460	465
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ttg ctg tgg cct cgg ttt gag ctg atc ctg gag atg aat gtc cag agt	1493
Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu Met Asn Val Gln Ser	
475	480
485	490
gtc cgc agc act gac ccc cag cgc ctt ggg gga ctg gac act cgg ccc	1541
Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro	
495	500
505	
cac tat atc aca cgc cgc tat gct gag ttc tcc tct gca ctt gtc agc	1589
His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser Ala Leu Val Ser	
510	515
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Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Leu Gln Leu Leu Gly Gln	
525	530
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ctc cag gtg gag gtg gag aat ttt gtc ctc cga gtg gct gca gag ttc	1685
Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg Val Ala Ala Glu Phe	
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550	
tcc tcc agg aag gag cag ctt gtg ttt ctg atc aac aac tat gac atg	1733
Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn Asn Tyr Asp Met	
555	560
565	570
atg ctc ggg gtg ctg atg gag cgg gct gct gat gac agc aaa gag gtg	1781
Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp Asp Ser Lys Glu Val	
575	580
585	

gaa agt ttc cag cag ctg ctc aat gct cgg aca cag gag ttc att gag 1829  
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 gaa gcc cga gtc act cag ctg atc cgt ggc ttt ggt agt tcc tgg aag 1973  
 Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe Gly Ser Ser Trp Lys  
 635 640 645 650  
 gca tca gtg gag tcc ctg agt cag gat gta atg cga agt ttt acc aac 2021  
 Ala Ser Val Glu Ser Leu Ser Gln Asp Val Met Arg Ser Phe Thr Asn  
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 ttc cga aat gga acc agc atc atc cag ggg gcg ctg acc cag ctg atc 2069  
 Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly Ala Leu Thr Gln Leu Ile  
 670 675 680  
 cag ctc tac cat cgc ttc cac cgg gtg ctg tct cag ccc cag ctc cgc 2117  
 Gln Leu Tyr His Arg Phe His Arg Val Leu Ser Gln Pro Gln Leu Arg  
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 gca ctc ccg gcc agg gcc gag ctc atc aac atc cat cac ctc atg gtg 2165  
 Ala Leu Pro Ala Arg Ala Glu Leu Ile Asn Ile His His Leu Met Val  
 700 705 710  
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 Glu Leu Lys Lys His Lys Pro Asn Phe  
 715 720

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 gactggccct cagctcttag ggcagagcac tgcaggccac cctgtagctg atctgtgggc 2512  
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 aacagtg 2579

<210> 6

<211> 723

<212> PRT

<213> Mus musculus

<400> 6

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 Ser Asp Glu Phe Ile Leu Asp Glu Val Asp Val His Ile Gln Ala Asn  
 50 55 60  
 Leu Glu Asp Glu Leu Val Lys Glu Ala Leu Lys Thr Gly Val Asp Leu  
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 Arg His Tyr Ser Lys Gln Val Glu Leu Glu Leu Gln Gln Ile Glu Gln  
 85 90 95  
 Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser Glu Asn Ile Ala Ser Leu  
 100 105 110

His Asn Gln Ile Thr Ala Cys Asp Ala Val Leu Glu Arg Met Glu Gln  
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 Val Pro Ser Ala Leu Val Thr Ala Ile Leu Glu Ala Pro Val Thr Glu  
 180 185 190  
 Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu Asp Ala Lys Ala Ala Ala  
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 Val Arg Glu Gln Glu Ala Met Gly Thr Ala Ala Cys Ala Asp Val Arg  
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 Leu Leu Gly Asn Glu Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr  
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 Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Val  
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Ser	Leu	Arg	Ser	Arg	Asn	Thr	Ile	Phe	Thr	Leu	Gly	Thr	Arg	Gly	Thr
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Val	Ile	Ser	Pro	Ala	Glu	Leu	Glu	Ala	Pro	Ile	Leu	Val	Pro	His	Thr
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Cys	Glu	Phe	Phe	Ile	Val	Ser	Gly	Pro	Ala	Ala	His	Asp	Leu	Phe	His
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Ala	Val	Met	Gly	Arg	Thr	Leu	Ser	Met	Thr	Leu	Lys	His	Leu	Glu	Ser
	420		425		430										
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Ile	Val	Leu	Arg	Phe	Arg	Asn	Ile	Ala	Ala	Lys	Arg	Asp	Val	Pro	Ala
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	485		490		495										
Gln	Arg	Leu	Gly	Gly	Leu	Asp	Thr	Arg	Pro	His	Tyr	Ile	Thr	Arg	Arg
	500		505		510										
Tyr	Ala	Glu	Phe	Ser	Ser	Ala	Leu	Val	Ser	Ile	Asn	Gln	Thr	Ile	Pro
	515		520		525										
Asn	Glu	Arg	Thr	Leu	Gln	Leu	Leu	Gly	Gln	Leu	Gln	Val	Glu	Val	Glu
	530		535		540										

Asn Phe Val Leu Arg Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln  
 545                                      550                                      555                                      560  
 Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met  
    565                                      570                                      575  
 Glu Arg Ala Ala Asp Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu  
    580                                      585                                      590  
 Leu Asn Ala Arg Thr Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro  
    595                                      600                                      605  
 Phe Gly Gly Leu Val Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu  
    610                                      615                                      620  
 Arg Gly Gln Ala Glu Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln  
 625                                      630                                      635                                      640  
 Leu Ile Arg Gly Phe Gly Ser Ser Trp Lys Ala Ser Val Glu Ser Leu  
    645                                      650                                      655  
 Ser Gln Asp Val Met Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser  
    660                                      665                                      670  
 Ile Ile Gln Gly Ala Leu Thr Gln Leu Ile Gln Leu Tyr His Arg Phe  
    675                                      680                                      685  
 His Arg Val Leu Ser Gln Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala  
    690                                      695                                      700  
 Glu Leu Ile Asn Ile His His Leu Met Val Glu Leu Lys Lys His Lys  
 705                                      710                                      715                                      720  
 Pro Asn Phe

<210> 7

<211> 2867

<212> DNA



&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (135).. (2303)

&lt;400&gt; 7

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tgaggctgcg ggga atg gcc gcc gct gcg acc atg gcg gct gcg gcc cgg 170
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gaa ctg gtg ttg cgg gct ggg acc tca gat atg gag gag gaa gag ggc 218
Glu Leu Val Leu Arg Ala Gly Thr Ser Asp Met Glu Glu Glu Glu Gly
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ccg ctg gcg ggt ggt cct ggg ctc cag gaa cca ctg caa ctt ggg gag 266
Pro Leu Ala Gly Gly Pro Gly Leu Gln Glu Pro Leu Gln Leu Gly Glu
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ttg gat atc act tct gat gaa ttc atc ctg gat gaa gtg gat gtt cac 314
Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp Val His
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att cag gca aat ctg gag gat gag tta gta aag gaa gct ctt aaa acg 362
Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu Lys Thr
              65              70              75
ggg gta gat ctc cgt cac tat tca aag caa gtt gag ctg gag cta cag 410
Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu Leu Gln
              80              85              90
cag att gaa cag aaa tcc att cgg gat tat att caa gag agt gag aat 458
Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser Glu Asn

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Ile Ala Ser Leu His Asn Gln Ile Thr Ala Cys Asp Ala Val Leu Glu			
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cga atg gag cag atg ttg gga gct ttt cag agt gac ctc agc tcc atc			554
Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser Ser Ile			
125	130	135	140
agc tct gag atc cgg aca ctg cag gaa cag tca gga gcc atg aac att			602
Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met Asn Ile			
	145	150	155
cga ctt cga aat cgc cag gca gtt cgg ggg aaa ctt ggg gag ctt gtt			650
Arg Leu Arg Asn Arg Gln Ala Val Arg Gly Lys Leu Gly Glu Leu Val			
	160	165	170
gat ggt ctg gtg gtg cct tct gct ctg gtc acg gca att ctg gag gct			698
Asp Gly Leu Val Val Pro Ser Ala Leu Val Thr Ala Ile Leu Glu Ala			
	175	180	185
cca gtg aca gag ccc agg ttc ttg gag cag cta cag gag ctg gat gcc			746
Pro Val Thr Glu Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu Asp Ala			
	190	195	200
aag gca gcc gca gtc aga gag cag gaa gct aga ggc aca gca gcc tgc			794
Lys Ala Ala Ala Val Arg Glu Gln Glu Ala Arg Gly Thr Ala Ala Cys			
205	210	215	220
gca gat gtc aga ggc gtg ctc gat cgg ctc cgg gtc aag gca gtg acg			842
Ala Asp Val Arg Gly Val Leu Asp Arg Leu Arg Val Lys Ala Val Thr			
	225	230	235
aag atc cga gag ttt atc ctc cag aag att tat tcc ttc agg aaa ccc			890
Lys Ile Arg Glu Phe Ile Leu Gln Lys Ile Tyr Ser Phe Arg Lys Pro			

240	245	250	
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Met Thr Asn Tyr Gln Ile Pro Gln Thr Ala Leu Leu Lys Tyr Arg Phe			
255	260	265	
ttc tat cag ttt ctg ctg ggc aat gaa cga gca aca gca aag gag atc			986
Phe Tyr Gln Phe Leu Leu Gly Asn Glu Arg Ala Thr Ala Lys Glu Ile			
270	275	280	
agg gat gaa tat gtg gag acg ctg agc aag att tac ctg tct tac tac			1034
Arg Asp Glu Tyr Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser Tyr Tyr			
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cgc tct tac ctg ggg cgg ctc atg aag gtg cag tat gag gaa gtc gct			1082
Arg Ser Tyr Leu Gly Arg Leu Met Lys Val Gln Tyr Glu Glu Val Ala			
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gag aaa gat gat cta atg ggt gtg gaa gat aca gca aag aaa gga ttc			1130
Glu Lys Asp Asp Leu Met Gly Val Glu Asp Thr Ala Lys Lys Gly Phe			
320	325	330	
ttc tca aag cca tcg ctc cgc agc agg aac acc att ttc acc cta gga			1178
Phe Ser Lys Pro Ser Leu Arg Ser Arg Asn Thr Ile Phe Thr Leu Gly			
335	340	345	
acc cgc ggc tct gtc atc tcc ccc act gaa ctt gag gcc ccc atc ctg			1226
Thr Arg Gly Ser Val Ile Ser Pro Thr Glu Leu Glu Ala Pro Ile Leu			
350	355	360	
gtg cct cac aca gcg cag cgc gga gag cag agg tat cca ttt gag gcc			1274
Val Pro His Thr Ala Gln Arg Gly Glu Gln Arg Tyr Pro Phe Glu Ala			
365	370	375	380
ctc ttc cgc agc cag cac tac gcc ctc cta gac aat tcc tgc cgc gaa			1322
Leu Phe Arg Ser Gln His Tyr Ala Leu Leu Asp Asn Ser Cys Arg Glu			

385	390	395	
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Tyr Leu Phe Ile Cys Glu Phe Phe Val Val Ser Gly Pro Ala Ala His			
400	405	410	
gac ctg ttc cat gct gtc atg ggc cgt aca ctc agc atg acc ctg aaa			1418
Asp Leu Phe His Ala Val Met Gly Arg Thr Leu Ser Met Thr Leu Lys			
415	420	425	
cac ctg gat tct tat cta gct gac tgc tac gat gcc att gct gtt ttt			1466
His Leu Asp Ser Tyr Leu Ala Asp Cys Tyr Asp Ala Ile Ala Val Phe			
430	435	440	
ctc tgt atc cac att gtt ctc cgg ttc cgt aac att gca gca aag agg			1514
Leu Cys Ile His Ile Val Leu Arg Phe Arg Asn Ile Ala Ala Lys Arg			
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Asp Val Pro Ala Leu Asp Arg Tyr Trp Glu Gln Val Leu Ala Leu Leu			
465	470	475	
tgg cca cgg ttt gaa ctg atc ctg gag atg aat gtt cag agc gtc cga			1610
Trp Pro Arg Phe Glu Leu Ile Leu Glu Met Asn Val Gln Ser Val Arg			
480	485	490	
agc act gac ccc cag cgc cta ggg ggg ttg gat act cgg ccc cac tat			1658
Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro His Tyr			
495	500	505	
atc aca cgc cgc tat gca gag ttc tcc tcc gct ctt gtc agt atc aac			1706
Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser Ala Leu Val Ser Ile Asn			
510	515	520	
cag aca att cct aat gaa cgg acc atg caa ttg ctg gga cag ctg cag			1754
Gln Thr Ile Pro Asn Glu Arg Thr Met Gln Leu Leu Gly Gln Leu Gln			

525	530	535	540	
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Val Glu Val Glu Asn Phe Val Leu Arg Val Ala Ala Glu Phe Ser Ser				
545	550	555		
agg aag gag cag ctt gtg ttt ctg atc aac aac tat gac atg atg ctg	1850			
Arg Lys Glu Gln Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met Leu				
560	565	570		
ggt gtg ctg atg gag cgg gct gca gat gac agc aaa gag gtt gag agc	1898			
Gly Val Leu Met Glu Arg Ala Ala Asp Asp Ser Lys Glu Val Glu Ser				
575	580	585		
ttc cag cag ctg ctc aat gct cgg aca cag gaa ttc att gaa gag ttg	1946			
Phe Gln Gln Leu Leu Asn Ala Arg Thr Gln Glu Phe Ile Glu Glu Leu				
590	595	600		
ctg tct ccc cct ttt ggg ggt tta gtg gca ttt gtg aag gag gct gag	1994			
Leu Ser Pro Pro Phe Gly Gly Leu Val Ala Phe Val Lys Glu Ala Glu				
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Ala Leu Ile Glu Arg Gly Gln Ala Glu Arg Leu Arg Gly Glu Glu Ala				
625	630	635		
cgg gta act cag ctg atc cgt ggc ttt ggt agt tcc tgg aaa tca tca	2090			
Arg Val Thr Gln Leu Ile Arg Gly Phe Gly Ser Ser Trp Lys Ser Ser				
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Val Glu Ser Leu Ser Gln Asp Val Met Arg Ser Phe Thr Asn Phe Arg				
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aat ggc acc agt atc att cag gga gcg ctg acc cag ctg atc cag ctc	2186			
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670	675	680	
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Tyr His Arg Phe His Arg Val Leu Ser Gln Pro Gln Leu Arg Ala Leu			
685	690	695	700
cct gcc cgg gct gag ctc atc aac att cac cac ctt atg gtg gag ctc	2282		
Pro Ala Arg Ala Glu Leu Ile Asn Ile His His Leu Met Val Glu Leu			
	705	710	715
aag aag cat aag ccc aac ttc tgatgtgcc aacaccgcc tgagatctgc	2333		
Lys Lys His Lys Pro Asn Phe			
720			
cggtcatctc catggacttc tgcaccccat tccataccct tcttcacctg gggtagccct	2393		
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&lt;210&gt; 8

&lt;211&gt; 723

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

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 Ser Asp Glu Phe Ile Leu Asp Glu Val Asp Val His Ile Gln Ala Asn  
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 Leu Glu Asp Glu Leu Val Lys Glu Ala Leu Lys Thr Gly Val Asp Leu  
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 Arg His Tyr Ser Lys Gln Val Glu Leu Glu Leu Gln Gln Ile Glu Gln  
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 Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser Glu Asn Ile Ala Ser Leu  
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 His Asn Gln Ile Thr Ala Cys Asp Ala Val Leu Glu Arg Met Glu Gln  
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 Met Leu Gly Ala Phe Gln Ser Asp Leu Ser Ser Ile Ser Ser Glu Ile  
                     130                    135                    140  
 Arg Thr Leu Gln Glu Gln Ser Gly Ala Met Asn Ile Arg Leu Arg Asn  
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 Arg Gln Ala Val Arg Gly Lys Leu Gly Glu Leu Val Asp Gly Leu Val  
                     165                    170                    175  
 Val Pro Ser Ala Leu Val Thr Ala Ile Leu Glu Ala Pro Val Thr Glu  
                     180                    185                    190  
 Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu Asp Ala Lys Ala Ala Ala  
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 Val Arg Glu Gln Glu Ala Arg Gly Thr Ala Ala Cys Ala Asp Val Arg  
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Gly Val Leu Asp Arg Leu Arg Val Lys Ala Val Thr Lys Ile Arg Glu  
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Gln Ile Pro Gln Thr Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe  
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305 310 315 320  
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370 375 380  
Gln His Tyr Ala Leu Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile  
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Cys Glu Phe Phe Val Val Ser Gly Pro Ala Ala His Asp Leu Phe His  
405 410 415  
Ala Val Met Gly Arg Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser  
420 425 430  
Tyr Leu Ala Asp Cys Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His



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Glu Leu Ile Leu Glu Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro			
485	490	495	
Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg			
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Tyr Ala Glu Phe Ser Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro			
515	520	525	
Asn Glu Arg Thr Met Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu			
530	535	540	
Asn Phe Val Leu Arg Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln			
545	550	555	560
Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met			
565	570	575	
Glu Arg Ala Ala Asp Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu			
580	585	590	
Leu Asn Ala Arg Thr Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro			
595	600	605	
Phe Gly Gly Leu Val Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu			
610	615	620	
Arg Gly Gln Ala Glu Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln			
625	630	635	640
Leu Ile Arg Gly Phe Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu			
645	650	655	

Ser Gln Asp Val Met Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser

660

665

670

Ile Ile Gln Gly Ala Leu Thr Gln Leu Ile Gln Leu Tyr His Arg Phe

675

680

685

His Arg Val Leu Ser Gln Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala

690

695

700

Glu Leu Ile Asn Ile His His Leu Met Val Glu Leu Lys Lys His Lys

705

710

715

720

Pro Asn Phe

<210> 9

<211> 3352

<212> DNA

<213> Homo sapiens

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<222> (97).. (2037)

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Met Asn Asp Leu Val Ala

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5

ctc cag atg aac cga cgt cac cgg atg cct gga tat gag acc atg aag 162

Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys

10

15

20

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Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
      40              45              50
ggg gcc agt gag aaa aag aaa ttt ttg agt gac gtc aga atc aag ttc 306
Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
      55              60              65              70
gag cac aac ggg gag agg cga att ata gcg ttc agc cgg cct gtg aaa 354
Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
              75              80              85
tat gaa gat gtg gag cac aag gtg aca aca gta ttt gga caa cct ctt 402
Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
              90              95              100
gat cta cat tac atg aac aat gag ctc tcc atc ctg ctg aaa aac caa 450
Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
              105              110              115
gat gat ctt gat aaa gca att gac att tta gat aga agc tca agc atg 498
Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
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Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
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Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg  
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 Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro  
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 Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly  
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 Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser  
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 Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser  
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Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser	
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Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr	
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Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly	
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Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly	
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Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys	
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Ser	Asn	Met	Ile	Val	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	Arg		
			505					510						515			
gac	tct	gct	ggg	aat	gta	aag	ctg	ggg	gac	ttt	ggg	gcc	agc	aaa	cgc	1698	
Asp	Ser	Ala	Gly	Asn	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ala	Ser	Lys	Arg		
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ctg	cag	acg	atc	tgt	atg	tcg	ggg	acg	ggc	atg	cgc	tcc	gtc	act	ggc	1746	
Leu	Gln	Thr	Ile	Cys	Met	Ser	Gly	Thr	Gly	Met	Arg	Ser	Val	Thr	Gly		
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Thr	Pro	Tyr	Trp	Met	Ser	Pro	Glu	Val	Ile	Ser	Gly	Glu	Gly	Tyr	Gly		
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Arg	Lys	Ala	Asp	Val	Trp	Ser	Leu	Gly	Cys	Thr	Val	Val	Glu	Met	Leu		
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Lys	Lys	His	Asn	Ser	Ser	Ser	Ser	Ala	Leu	Leu	Asn	Ser	Pro	Thr	Val
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 Asp Ser Pro Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe  
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 Lys Gly Val Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val  
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 His His Lys Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg  
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 Arg His Gln Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu  
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Ser Thr Asn Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro  
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Arg Gly Arg Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln  
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Glu Arg Asn Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg  
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Arg Gly Lys Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys  
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Tyr Asp Val Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe  
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Asp Pro Asp Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys  
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Glu Ile Gln Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr  
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Tyr Gly Cys Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met  
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Glu Tyr Met Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly  
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Ala Leu Thr Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu  
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Gly Met Ser Tyr Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys  
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Gly Ala Asn Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp  
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Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly  
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Met Arg Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile

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 Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys  
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 Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln  
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 Leu Pro Ser His Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile  
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Cys	Ala	Gly	Ala	Ser	Glu	Lys	Lys	Lys	Phe	Leu	Ser	Asp	Val	Arg	Ile				
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Pro	Leu	Asp	Leu	His	Tyr	Met	Asn	Asn	Glu	Leu	Ser	Ile	Leu	Leu	Lys				
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Ser	Met	Lys	Ser	Leu	Arg	Ile	Leu	Leu	Leu	Ser	Gln	Asp	Arg	Asn	His				
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Asn Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys  
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 Pro Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser  
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Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp  
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Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu  
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 Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr  
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 Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile  
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 Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu  
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Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala  
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taaactggag actgtgtgtg ccctctgggc tctgagtacc cctgctttgg gcttgggcct 2857



aggctgcatt gaaaagagct gaaggttggtg gcctttgctc tcctggccca gcctttgttc 2917  
 cccactggag cagaagggga gatggacgac acggtcgga catctggcct ggccagtgcc 2977  
 ctgatcccag agagcccgag gaggtgtctc aggctgcctg agtcgtgacc tgctaggcca 3037  
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<211> 657

<212> PRT

<213> Homo sapiens

<400> 12

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Leu	Gln	Met	Asn	Arg	Arg	His	Arg	Met	Pro	Gly	Tyr	Glu	Thr	Met	Lys
				20					25					30	
Asn	Lys	Asp	Thr	Gly	His	Ser	Asn	Arg	Gln	Lys	Lys	His	Asn	Ser	Ser
				35					40					45	
Ser	Ser	Ala	Leu	Leu	Asn	Ser	Pro	Thr	Val	Thr	Thr	Ser	Ser	Cys	Ala
				50					55					60	
Gly	Ala	Ser	Glu	Lys	Lys	Lys	Phe	Leu	Ser	Asp	Val	Arg	Ile	Lys	Phe
				65					70					75	
Glu	His	Asn	Gly	Glu	Arg	Arg	Ile	Ile	Ala	Phe	Ser	Arg	Pro	Val	Lys
									85					90	
															95

Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu  
 100 105 110  
 Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln  
 115 120 125  
 Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met  
 130 135 140  
 Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser  
 145 150 155 160  
 Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser  
 165 170 175  
 Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg  
 180 185 190  
 Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro  
 195 200 205  
 Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly  
 210 215 220  
 Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser  
 225 230 235 240  
 Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser  
 245 250 255  
 Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg  
 260 265 270  
 Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu  
 275 280 285  
 Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly  
 290 295 300  
 Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser

305	310	315	320
Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu			
	325	330	335
Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn			
	340	345	350
Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser			
	355	360	365
Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr			
	370	375	380
Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly			
385	390	395	400
Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly			
	405	410	415
Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu			
	420	425	430
Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys			
	435	440	445
Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp			
	450	455	460
Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly			
465	470	475	480
Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val			
	485	490	495
Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His			
	500	505	510
Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg			
	515	520	525

Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg  
530 535 540  
Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly  
545 550 555 560  
Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly  
565 570 575  
Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu  
580 585 590  
Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe  
595 600 605  
Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser  
610 615 620  
Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln  
625 630 635 640  
Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met  
645 650 655  
Tyr

&lt;210&gt; 13

&lt;211&gt; 2447

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (9).. (1802)

&lt;400&gt; 13

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Met Leu Ala Lys Pro Arg Leu Asp Thr Glu Gln Leu Ala Pro

1 5 10

cgg gga gct ggc ctc tgc ttc act ttc gtc tct gct caa caa aac agt 98

Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser Ala Gln Gln Asn Ser

15 20 25 30

cct tct tct acg ggt tct ggc aat aca gaa cat tct tgc agc tcc caa 146

Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln

35 40 45

aaa cag atc tcc atc cag cac aga cag acc cag tct gac ctc aca ata 194

Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile

50 55 60

gaa aaa ata tct gca cta gaa aac agt aag aac tct gac tta gag aag 242

Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys

65 70 75

aag gaa gga aga ata gat gat tta tta aga gcc aac tgt gat ttg aga 290

Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg

80 85 90

cga cag ata gat gaa cag caa aag atg cta gag aaa tac aag gaa cga 338

Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg

95 100 105 110

tta aat aga tgt gtc acc atg agc aag aag ctc ctt ata gaa aag tca 386

Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser

115 120 125

aaa caa gag aag atg gcg tgc aga gat aag agc atg cag gac cgg ttg 434

Lys Gln Glu Lys Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu

130 135 140

cga tta ggc cac ttt act act gtc cgg cat gga gcc tcg ttt act gag 482

Arg Leu Gly His Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu  
 145 150 155  
 cag tgg aca gat ggt tat gct ttc caa aac ctc atc aag caa cag gaa 530  
 Gln Trp Thr Asp Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu  
 160 165 170  
 agg ata aat tca cag aga gaa gag ata gaa agg caa cgg aaa atg tta 578  
 Arg Ile Asn Ser Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu  
 175 180 185 190  
 gca aaa cgg aaa cct cct gcc atg ggt cag gcc cct cct gca acc aat 626  
 Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn  
 195 200 205  
 gag cag aaa caa cgg aaa agc aag act aat gga gct gaa aat gaa acg 674  
 Glu Gln Lys Gln Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr  
 210 215 220  
 tta acg tta gcc gag tac cat gaa caa gag gaa atc ttc aaa ctt aga 722  
 Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg  
 225 230 235  
 tta ggt cat ctt aag aaa gag gaa gca gaa atc cag gca gag ctg gaa 770  
 Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu  
 240 245 250  
 agg ctg gaa agg gtt agg aat cta cac atc agg gaa tta aaa agg ata 818  
 Arg Leu Glu Arg Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile  
 255 260 265 270  
 cat aat gaa gac aat tcg cag ttt aaa gac cat cca aca cta aat gac 866  
 His Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp  
 275 280 285  
 aga tat ttg ttg tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt 914

Arg Tyr Leu Leu Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val  
 290 295 300  
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 Tyr Lys Ala Phe Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile  
 305 310 315  
 cac cag tta aat aaa aac tgg aga gat gag aaa aag gag aat tac cac 1010  
 His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His  
 320 325 330  
 aag cat gcg tgt agg gaa tac cgg att cac aag gag ctg gac cac ccc 1058  
 Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro  
 335 340 345 350  
 agg ata gtg aag ctg tat gat tac ttt tca ctg gac act gac tcg ttt 1106  
 Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe  
 355 360 365  
 tgt aca gta tta gaa tac tgt gaa ggg aat gac ctg gac ttc tac cta 1154  
 Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu  
 370 375 380  
 aaa cag cac aaa tta atg tcg gag aaa gaa gcc cga tcc att att atg 1202  
 Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met  
 385 390 395  
 cag att gtg aat gct tta aag tac tta aat gaa ata aaa cct ccc atc 1250  
 Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile  
 400 405 410  
 ata cac tat gac ctc aaa cca ggt aat atc ctt tta gta aat ggt aca 1298  
 Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr  
 415 420 425 430  
 gca tgt gga gag ata aaa att aca gat ttt ggt ctt tcc aag atc atg 1346

Ala Cys Gly Glu Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met	
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gat gat gat agc tac aat tca gtg gat ggc atg gag ctg acg tca caa	1394
Asp Asp Asp Ser Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln	
450	455
gga gct ggt act tat tgg tat tta cca cca gag tgt ttt gtg gtt ggg	1442
Gly Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly	
465	470
aaa gag cca cca aag atc tca aat aaa gtc gat gtt tgg tca gtg ggt	1490
Lys Glu Pro Pro Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly	
480	485
gtg atc ttc tac cag tgt ctt tat ggg agg aag cct ttt ggc cat aac	1538
Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn	
495	500
cag tcc cag caa gat att cta caa gag aat act att ctt aag gct act	1586
Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr	
515	520
gaa gta cag ttc ccg cca aag cca gta gta aca cct gaa gca aag gca	1634
Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala	
530	535
ttt atc agg aga tgt ctg gcc tat cga aag gaa gat cgc att gat gtg	1682
Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val	
545	550
cag cag ctg gcc tgt gac ccc tac ttg ttg cct cac atc cga aag tca	1730
Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser	
560	565
gtc tcc aca agt agc cct gca gga gct gct att gca tca acc tct ggg	1778





35	40	45
Ile Ser Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys		
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Ile Ser Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu		
65	70	75
Gly Arg Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln		
85	90	95
Ile Asp Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn		
100	105	110
Arg Cys Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln		
115	120	125
Glu Lys Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu		
130	135	140
Gly His Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp		
145	150	155
Thr Asp Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile		
165	170	175
Asn Ser Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys		
180	185	190
Arg Lys Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln		
195	200	205
Lys Gln Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr		
210	215	220
Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg Leu Gly		
225	230	235
His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu		
245	250	255

Glu Arg Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile His Asn  
260 265 270

Glu Asp Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr  
275 280 285

Leu Leu Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys  
290 295 300

Ala Phe Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln  
305 310 315 320

Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His  
325 330 335

Ala Cys Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro Arg Ile  
340 345 350

Val Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr  
355 360 365

Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln  
370 375 380

His Lys Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile  
385 390 395 400

Val Asn Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His  
405 410 415

Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys  
420 425 430

Gly Glu Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp  
435 440 445

Asp Ser Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala  
450 455 460

Gly Thr Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu

465                                      470                                      475                                      480  
Pro Pro Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile  
   485                                      490                                      495  
Phe Tyr Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser  
   500                                      505                                      510  
Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val  
   515                                      520                                      525  
Gln Phe Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile  
   530                                      535                                      540  
Arg Arg Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln  
545                                      550                                      555                                      560  
Leu Ala Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser  
   565                                      570                                      575  
Thr Ser Ser Pro Ala Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser  
   580                                      585                                      590  
Asn Asn Ser Ser Ser Asn  
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (2393)

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 cggcggcggc ggcggcagca gaaatg atg gaa gaa ttg cat agc ctg gac cca 173  
 Met Glu Glu Leu His Ser Leu Asp Pro  
 1 5  
 cga cgg cag gaa tta ttg gag gcc agg ttt act gga gta ggt gtt agt 221  
 Arg Arg Gln Glu Leu Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser  
 10 15 20 25  
 aag gga cca ctt aat agt gag tct tcc aac cag agc ttg tgc agc gtc 269  
 Lys Gly Pro Leu Asn Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val  
 30 35 40  
 gga tcc ttg agt gat aaa gaa gta gag act ccc gag aaa aag cag aat 317  
 Gly Ser Leu Ser Asp Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn  
 45 50 55  
 gac cag cga aat cgg aaa aga aaa gct gaa cca tat gaa act agc caa 365  
 Asp Gln Arg Asn Arg Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln  
 60 65 70  
 ggg aaa ggc act cct agg gga cat aaa att agt gat tac ttt gag ttt 413  
 Gly Lys Gly Thr Pro Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Phe  
 75 80 85  
 gct ggg gga agc gcg cca gga acc agc cct ggc aga agt gtt cca cca 461  
 Ala Gly Gly Ser Ala Pro Gly Thr Ser Pro Gly Arg Ser Val Pro Pro  
 90 95 100 105  
 gtt gca cga tcc tca ccg caa cat tcc tta tcc aat ccc tta ccg cga 509  
 Val Ala Arg Ser Ser Pro Gln His Ser Leu Ser Asn Pro Leu Pro Arg  
 110 115 120  
 cga gta gaa cag ccc ctc tat ggt tta gat ggc agt gct gca aag gag 557  
 Arg Val Glu Gln Pro Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu

125	130	135	
gca acg gag gag cag tct gct ctg cca acc ctc atg tca gtg atg cta			605
Ala Thr Glu Glu Gln Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu			
140	145	150	
gca aaa cct cgg ctt gac aca gag cag ctg gcg caa agg gga gct ggc			653
Ala Lys Pro Arg Leu Asp Thr Glu Gln Leu Ala Gln Arg Gly Ala Gly			
155	160	165	
ctc tgc ttc act ttt gtt tca gct cag caa aac agt ccc tca tct acg			701
Leu Cys Phe Thr Phe Val Ser Ala Gln Gln Asn Ser Pro Ser Ser Thr			
170	175	180	185
gga tct ggc aac aca gag cat tcc tgc agc tcc caa aaa cag atc tcc			749
Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser			
190	195	200	
atc cag cac aga cag acc cag tcc gac ctc aca ata gaa aaa ata tct			797
Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser			
205	210	215	
gca cta gaa aac agt aag aat tct gac tta gag aag aag gag gga aga			845
Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg			
220	225	230	
ata gat gat tta tta aga gcc aac tgt gat ttg aga cgg cag att gat			893
Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp			
235	240	245	
gaa cag caa aag atg cta gag aaa tac aag gaa cga tta aat aga tgt			941
Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn Arg Cys			
250	255	260	265
gtg aca atg agc aag aaa ctc ctt ata gaa aag tca aaa caa gag aag			989
Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys			

270	275	280	
atg gcg tgt aga gat aag agc atg caa gac cgc ttg aga ctg ggc cac			1037
Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His			
285	290	295	
ttt act act gtc cga cac gga gcc tca ttt act gaa cag tgg aca gat			1085
Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp			
300	305	310	
ggt tat gct ttt cag aat ctt atc aag caa cag gaa agg ata aat tca			1133
Gly Tyr Ala Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile Asn Ser			
315	320	325	
cag agg gaa gag ata gaa aga caa cgg aaa atg tta gca aag cgg aaa			1181
Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys			
330	335	340	345
cct cct gcc atg ggt cag gcc cct cct gca acc aat gag cag aaa cag			1229
Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln			
350	355	360	
cgg aaa agc aag acc aat gga gct gaa aat gaa acg tta acg tta gca			1277
Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala			
365	370	375	
gaa tac cat gaa caa gaa gaa atc ttc aaa ctc aga tta ggt cat ctt			1325
Glu Tyr His Glu Gln Glu Glu Ile Phe Lys Leu Arg Leu Gly His Leu			
380	385	390	
aaa aag gag gaa gca gag atc cag gca gag ctg gag aga cta gaa agg			1373
Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg			
395	400	405	
gtt aga aat cta cat atc agg gaa cta aaa agg ata cat aat gaa gat			1421
Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile His Asn Glu Asp			

410	415	420	425	
aat tca caa ttt aaa gat cat cca acg cta aat gac aga tat ttg ttg				1469
Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu				
	430	435	440	
tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt tac aag gca ttt				1517
Leu His Leu Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys Ala Phe				
	445	450	455	
gat cta aca gag caa aga tac gta gct gtg aaa att cac cag tta aat				1565
Asp Leu Thr Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln Leu Asn				
	460	465	470	
aaa aac tgg aga gat gag aaa aag gag aat tac cac aag cat gca tgt				1613
Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His Ala Cys				
	475	480	485	
agg gaa tac cgg att cat aaa gag ctg gat cat ccc aga ata gtt aag				1661
Arg Glu Tyr Arg Ile His Lys Glu Leu Asp His Pro Arg Ile Val Lys				
490	495	500	505	
ctg tat gat tac ttt tca ctg gat act gac tcg ttt tgt aca gta tta				1709
Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr Val Leu				
	510	515	520	
gaa tac tgt gag gga aat gat ctg gac ttc tac ctg aaa cag cac aaa				1757
Glu Tyr Cys Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln His Lys				
	525	530	535	
tta atg tcg gag aaa gag gcc cgg tcc att atc atg cag att gtg aat				1805
Leu Met Ser Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile Val Asn				
	540	545	550	
gct tta aag tac tta aat gaa ata aaa cct ccc atc ata cac tat gac				1853
Ala Leu Lys Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His Tyr Asp				



555	560	565	
ctc aaa cca ggt aat att ctt tta gta aat ggt aca gcg tgt gga gag			1901
Leu Lys Pro Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys Gly Glu			
570	575	580	585
ata aaa att aca gat ttt ggt ctt tcg aag atc atg gat gat gat agc			1949
Ile Lys Ile Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp Asp Ser			
	590	595	600
tac aat tca gtg gat ggc atg gag cta aca tca caa ggt gct ggt act			1997
Tyr Asn Ser Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala Gly Thr			
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tat tgg tat tta cca cca gag tgt ttt gtg gtt ggg aaa gaa cca cca			2045
Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro			
	620	625	630
aag atc tca aat aaa gtt gat gtg tgg tcg gtg ggt gtg atc ttc tat			2093
Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr			
	635	640	645
cag tgt ctt tat gga agg aag cct ttt ggc cat aac cag tct cag caa			2141
Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln			
650	655	660	665
gac atc cta caa gag aat acg att ctt aaa gct act gaa gtg cag ttc			2189
Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val Gln Phe			
	670	675	680
ccg cca aag cca gta gta aca cct gaa gca aag gcg ttt att cga cga			2237
Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg			
	685	690	695
tgc ttg gcc tac cga aag gag gac cgc att gat gtc cag cag ctg gcc			2285
Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala			

700	705	710	
tgt gat ccc tac ttg ttg cct cac atc cga aag tca gtc tct aca agt	2333		
Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser			
715	720	725	
agc cct gct gga gct gct att gca tca acc tct ggg gcg tcc aat aac	2381		
Ser Pro Ala Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser Asn Asn			
730	735	740	745
agt tct tct aat tgagactgac tccaaggcca caaactgttc aacacacaca	2433		
Ser Ser Ser Asn			
aagtggacaa atggcggttca gcagcgggtt tggaacatag cgaatccgaa tggatctgat	2493		
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&lt;210&gt; 16

&lt;211&gt; 749

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Ser Ser Asn Gln Ser Leu Cys Ser Val Gly Ser Leu Ser Asp Lys Glu  
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Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg Asn Arg Lys Arg  
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Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly Thr Pro Arg Gly  
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His Lys Ile Ser Asp Tyr Phe Glu Phe Ala Gly Gly Ser Ala Pro Gly  
85 90 95  
Thr Ser Pro Gly Arg Ser Val Pro Pro Val Ala Arg Ser Ser Pro Gln  
100 105 110  
His Ser Leu Ser Asn Pro Leu Pro Arg Arg Val Glu Gln Pro Leu Tyr  
115 120 125  
Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu Glu Gln Ser Ala  
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Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro Arg Leu Asp Thr  
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Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser  
165 170 175  
Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His  
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Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln  
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 Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn  
 210 215 220  
 Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala  
 225 230 235 240  
 Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu  
 245 250 255  
 Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu  
 260 265 270  
 Leu Ile Glu Lys Ser Lys Gln Glu Lys Met Ala Cys Arg Asp Lys Ser  
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 Met Gln Asp Arg Leu Arg Leu Gly His Phe Thr Thr Val Arg His Gly  
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 Ala Ser Phe Thr Glu Gln Trp Thr Asp Gly Tyr Ala Phe Gln Asn Leu  
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 Ile Lys Gln Gln Glu Arg Ile Asn Ser Gln Arg Glu Glu Ile Glu Arg  
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 Pro Pro Ala Thr Asn Glu Gln Lys Gln Arg Lys Ser Lys Thr Asn Gly  
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 Ala Glu Asn Glu Thr Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu  
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 Ile Phe Lys Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile  
 385 390 395 400  
 Gln Ala Glu Leu Glu Arg Leu Glu Arg Val Arg Asn Leu His Ile Arg

405	410	415
Glu Leu Lys Arg Ile His Asn Glu Asp Asn Ser Gln Phe Lys Asp His		
420	425	430
Pro Thr Leu Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Gly Arg Gly		
435	440	445
Gly Phe Ser Glu Val Tyr Lys Ala Phe Asp Leu Thr Glu Gln Arg Tyr		
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Val Ala Val Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys		
465	470	475
480		
Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys		
485	490	495
Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu		
500	505	510
Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp		
515	520	525
Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala		
530	535	540
Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu		
545	550	555
560		
Ile Lys Pro Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu		
565	570	575
Leu Val Asn Gly Thr Ala Cys Gly Glu Ile Lys Ile Thr Asp Phe Gly		
580	585	590
Leu Ser Lys Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Asp Gly Met		
595	600	605
Glu Leu Thr Ser Gln Gly Ala Gly Thr Tyr Trp Tyr Leu Pro Pro Glu		
610	615	620

Cys Phe Val Val Gly Lys Glu Pro Pro Lys Ile Ser Asn Lys Val Asp  
625                      630                      635                      640  
Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys  
                        645                      650                      655  
Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr  
                        660                      665                      670  
Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr  
                        675                      680                      685  
Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu  
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Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro  
705                      710                      715                      720  
His Ile Arg Lys Ser Val Ser Thr Ser Ser Pro Ala Gly Ala Ala Ile  
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<211> 3224

<212> DNA

<213> Homo sapiens

<220>

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<222> (147)..(2297)

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cggcggcggc ggccggcagca gaaatg atg gaa gaa ttg cat agc ctg gac cca 173  
 Met Glu Glu Leu His Ser Leu Asp Pro  
 1 5  
 cga cgg cag gaa tta ttg gag gcc agg ttt act gga gta ggt gtt agt 221  
 Arg Arg Gln Glu Leu Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser  
 10 15 20 25  
 aag gga cca ctt aat agt gag tct tcc aac cag agc ttg tgc agc gtc 269  
 Lys Gly Pro Leu Asn Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val  
 30 35 40  
 gga tcc ttg agt gat aaa gaa gta gag act ccc gag aaa aag cag aat 317  
 Gly Ser Leu Ser Asp Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn  
 45 50 55  
 gac cag cga aat cgg aaa aga aaa gct gaa cca tat gaa act agc caa 365  
 Asp Gln Arg Asn Arg Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln  
 60 65 70  
 ggg aaa ggc act cct agg gga cat aaa att agt gat tac ttt gag cga 413  
 Gly Lys Gly Thr Pro Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Arg  
 75 80 85  
 cga gta gaa cag ccc ctc tat ggt tta gat ggc agt gct gca aag gag 461  
 Arg Val Glu Gln Pro Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu  
 90 95 100 105  
 gca acg gag gag cag tct gct ctg cca acc ctc atg tca gtg atg cta 509  
 Ala Thr Glu Glu Gln Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu  
 110 115 120  
 gca aaa cct cgg ctt gac aca gag cag ctg gcg caa agg gga gct ggc 557  
 Ala Lys Pro Arg Leu Asp Thr Glu Gln Leu Ala Gln Arg Gly Ala Gly  
 125 130 135

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ctc tgc ttc act ttt gtt tca gct cag caa aac agt ccc tca tct acg      605
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gga tct ggc aac aca gag cat tcc tgc agc tcc caa aaa cag atc tcc      653
Gly Ser Gly Asn Thr Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser
      155              160              165
atc cag cac aga cag acc cag tcc gac ctc aca ata gaa aaa ata tct      701
Ile Gln His Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser
      170              175              180              185
gca cta gaa aac agt aag aat tct gac tta gag aag aag gag gga aga      749
Ala Leu Glu Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg
      190              195              200
ata gat gat tta tta aga gcc aac tgt gat ttg aga cgg cag att gat      797
Ile Asp Asp Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp
      205              210              215
gaa cag caa aag atg cta gag aaa tac aag gaa cga tta aat aga tgt      845
Glu Gln Gln Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn Arg Cys
      220              225              230
gtg aca atg agc aag aaa ctc ctt ata gaa aag tca aaa caa gag aag      893
Val Thr Met Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys
      235              240              245
atg gcg tgt aga gat aag agc atg caa gac cgc ttg aga ctg ggc cac      941
Met Ala Cys Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His
      250              255              260              265
ttt act act gtc cga cac gga gcc tca ttt act gaa cag tgg aca gat      989
Phe Thr Thr Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp
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 cag agg gaa gag ata gaa aga caa cgg aaa atg tta gca aag cgg aaa 1085  
 Gln Arg Glu Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys  
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 cct cct gcc atg ggt cag gcc cct cct gca acc aat gag cag aaa cag 1133  
 Pro Pro Ala Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln  
 315 320 325  
 cgg aaa agc aag acc aat gga gct gaa aat gaa acg tta acg tta gca 1181  
 Arg Lys Ser Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala  
 330 335 340 345  
 gaa tac cat gaa caa gaa gaa atc ttc aaa ctc aga tta ggt cat ctt 1229  
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 Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg  
 365 370 375  
 gtt aga aat cta cat atc agg gaa cta aaa agg ata cat aat gaa gat 1325  
 Val Arg Asn Leu His Ile Arg Glu Leu Lys Arg Ile His Asn Glu Asp  
 380 385 390  
 aat tca caa ttt aaa gat cat cca acg cta aat gac aga tat ttg ttg 1373  
 Asn Ser Gln Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu  
 395 400 405  
 tta cat ctt ttg ggt aga gga ggt ttc agt gaa gtt tac aag gca ttt 1421  
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 410 415 420 425

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Tyr Trp Tyr Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro	
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Lys Ile Ser Asn Lys Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr	
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Gln Cys Leu Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln	
620 625 630	
gac atc cta caa gag aat acg att ctt aaa gct act gaa gtg cag ttc	2093
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Pro Pro Lys Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg	
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Cys Leu Ala Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala	
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tgt gat ccc tac ttg ttg cct cac atc cga aag tca gtc tct aca agt	2237
Cys Asp Pro Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser	
685 690 695	
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700

705

710

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Ser Ser Ser Asn

715

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<212> PRT

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 Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg Asn Arg Lys Arg  
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 Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly Thr Pro Arg Gly  
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 His Lys Ile Ser Asp Tyr Phe Glu Arg Arg Val Glu Gln Pro Leu Tyr  
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 Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu Glu Gln Ser Ala  
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 Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro Arg Leu Asp Thr  
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 Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe Thr Phe Val Ser  
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 Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly Asn Thr Glu His  
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 Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His Arg Gln Thr Gln  
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 Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu Asn Ser Lys Asn  
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 Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp Leu Leu Arg Ala  
                     195                    200                    205  
 Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln Lys Met Leu Glu  
                     210                    215                    220  
 Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met Ser Lys Lys Leu

85/861

Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr Arg Ile His Lys  
450 455 460  
Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp Tyr Phe Ser Leu  
465 470 475 480  
Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp  
485 490 495  
Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Met Ser Glu Lys Glu Ala  
500 505 510  
Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys Tyr Leu Asn Glu  
515 520 525  
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530 535 540  
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595 600 605  
Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu Tyr Gly Arg Lys  
610 615 620  
Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr  
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Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys Pro Val Val Thr  
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Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala Tyr Arg Lys Glu

660	665	670
Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro Tyr Leu Leu Pro		
675	680	685
His Ile Arg Lys Ser Val Ser Thr Ser Ser Pro Ala Gly Ala Ala Ile		
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705	710	715

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&lt;211&gt; 841

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (220).. (627)

&lt;400&gt; 19

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                                     1           5
cgg gag ctg gtg cag tgg ctg agc ttc gcc acc ttt gag ata ttc gtg    282
Arg Glu Leu Val Gln Trp Leu Ser Phe Ala Thr Phe Glu Ile Phe Val
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His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu Ala Leu Arg Val

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ttc gcc gcc gac ggg ctc agt acc tac ttc acc acc atc gtt tcc gtt			426
Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr Ile Val Ser Val			
55	60	65	
cga ctc ttc caa gat ggg gag aag cga ctg gct gtg ctg cgc ctc ttc			474
Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val Leu Arg Leu Phe			
70	75	80	85
tgg gtt ctc acc gtc ctt agc ctc aag ttt gtc ttt gag atg ttg ctg			522
Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val Phe Glu Met Leu Leu			
90	95	100	
tgc cag aag cta gtg gag cag act cga gag ctc tgg ttc ggc ctg atc			570
Cys Gln Lys Leu Val Glu Gln Thr Arg Glu Leu Trp Phe Gly Leu Ile			
105	110	115	
acg tct ccg gtc ttc att ctc ctg cag ctg ctc atg atc cgg gct tgt			618
Thr Ser Pro Val Phe Ile Leu Leu Gln Leu Leu Met Ile Arg Ala Cys			
120	125	130	
cgc gtc aac tagcctcttg cagtggctgg aaatggagca ctgcgcagct			667
Arg Val Asn			
135			
ggagtctctgg acctcccggt cctgacccaa cttagtgcca cactggtgga gctctggtca			727
gaaatcagtg tttgcttggtg ccagttttac tgtccagttt tctttatata taagatcggt			787
tcctcgagca aagcttaaaa gtgaagtctt gtttattaaa acttatttcc agtt			841

&lt;210&gt; 20

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 20

Met Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Ser Phe Ala Thr

1 5 10 15

Phe Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu

20 25 30

Leu Ala Leu Arg Val Asp Gly Leu Thr Pro Gly Leu Ser Trp Trp Asn

35 40 45

Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr

50 55 60

Thr Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala

65 70 75 80

Val Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val

85 90 95

Phe Glu Met Leu Leu Cys Gln Lys Leu Val Glu Gln Thr Arg Glu Leu

100 105 110

Trp Phe Gly Leu Ile Thr Ser Pro Val Phe Ile Leu Leu Gln Leu Leu

115 120 125

Met Ile Arg Ala Cys Arg Val Asn

130 135

&lt;210&gt; 21

&lt;211&gt; 1563

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (234).. (641)

&lt;400&gt; 21

ggcacgaggg gcgtccgata gaggcgggacg ttcacgggacg gccagggttg agtcccgggt 60  
 cggggccggg ggattgccgg cgcatacagg cagagggttg gggctggcgg ggccgctcgc 120  
 tgcctctcgc tcgcagcagc ggccggcagg gcgggagagg gccacgggga gaggagacgc 180  
 agccccgcgg gtggcacgct cggccggggc ccggcccgcg ctcaacgggc gcg atg 236

Met

1

ctc ttc tcg ctc cgg gag ctg gtg cag tgg cta ggc ttc gcc acc ttc 284  
 Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr Phe

5

10

15

gag atc ttc gtg cac ctg ctg gcc ctg ttg gtg ttc tct gtg ctg ctg 332  
 Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu Leu

20

25

30

gca ctg cgt gtg gat ggc ctg gtc ccg ggc ctc tcc tgg tgg aac gtg 380  
 Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn Val

35

40

45

ttc gtg cct ttc ttc gcc gct gac ggg ctc agc acc tac ttc acc acc 428  
 Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr Thr

50

55

60

65

atc gtg tcc gtg cgc ctc ttc cag gat gga gag aag cgg ctg gcg gtg 476  
 Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala Val

70

75

80

ctc cgc ctt ttc tgg gta ctt acg gtc ctg agt ctc aag ttc gtc ttc 524  
 Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val Phe

85	90	95	
gag atg ctg ttg tgc cag aag ctg gcg gag cag act cgg gag ctc tgg			572
Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu Trp			
100	105	110	
ttc ggc ctc att acg tcc ccg ctc ttc att ctc ctg cag ctg ctc atg			620
Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu Met			
115	120	125	
atc cgc gcc tgt cgg gtc aac tagcctcacc gaggtgccgg agagggagcg			671
Ile Arg Ala Cys Arg Val Asn			
130	135		
ctggacaact agaatgttga cctcgagccg aggccctact tgcagcgcac cggaggagag			731
gctctctagt ctgaaggcac cgccggcttg cgccgagctg agtgccgggt ttccctattc			791
caatcctgtt tgaaatggtt tcttcagcag ggcttaaaag agcagccttc atcctgaaaa			851
tgtatttcct tttgtttaat gctttgagta gataatcctg aattgaggtc atgaggaggc			911
ccccaggcc agacagtcct gaacccctct gacacttgga aactgaatat aagtaaaatg			971
tccaggtgga ctctgagtat ttctgtgga tcctgggaaa gtactgttgc acaaaggctg			1031
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tgtatctcct tccctgtgcc acgagagaga ttggcttttt attccagtct aggcagagac			1211
agaagaatgt tgaataagag cagcattaga gtctgtctg gttatctgtt gccaagaaa			1271
agaactctgc tgtccaggca ctgcttggt tactatccca gcaaagactg cagttttgtg			1331
gacttttgac caccttgggc tggcactctt agcacacctg agacagattt aagcctccct			1391
aagagactga agagaggaac aggtgtcaga tactcatagg cactgagatc tacaaatggg			1451
aagcttgtga gtggcccatc tttgttggtc tacgaacttt ggtttgatgc cagtcaggtg			1511
ccacatgaga acctttgctg agatgcaa atagtaagag aatgttttcc tg			1563

&lt;210&gt; 22

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

Met Leu Phe Ser Leu Arg Glu Leu Val Gln Trp Leu Gly Phe Ala Thr

1 5 10 15

Phe Glu Ile Phe Val His Leu Leu Ala Leu Leu Val Phe Ser Val Leu

20 25 30

Leu Ala Leu Arg Val Asp Gly Leu Val Pro Gly Leu Ser Trp Trp Asn

35 40 45

Val Phe Val Pro Phe Phe Ala Ala Asp Gly Leu Ser Thr Tyr Phe Thr

50 55 60

Thr Ile Val Ser Val Arg Leu Phe Gln Asp Gly Glu Lys Arg Leu Ala

65 70 75 80

Val Leu Arg Leu Phe Trp Val Leu Thr Val Leu Ser Leu Lys Phe Val

85 90 95

Phe Glu Met Leu Leu Cys Gln Lys Leu Ala Glu Gln Thr Arg Glu Leu

100 105 110

Trp Phe Gly Leu Ile Thr Ser Pro Leu Phe Ile Leu Leu Gln Leu Leu

115 120 125

Met Ile Arg Ala Cys Arg Val Asn

130 135

&lt;210&gt; 23

&lt;211&gt; 2950

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (9)..(659)

&lt;400&gt; 23

gggcagtg atg gcg gcg ggt gat ggg gac gta aag cta agc acc ctg ggg 50

Met Ala Ala Gly Asp Gly Asp Val Lys Leu Ser Thr Leu Gly

1

5

10

agc ggc ggg gag agt ggc ggc gac ggg agc ccg ggt ggc gcc gga gcg 98

Ser Gly Gly Glu Ser Gly Gly Asp Gly Ser Pro Gly Gly Ala Gly Ala

15

20

25

30

acg gcg gtg agg agc agt tgg gtg gcg gcg ctg ctg gcg acg ggc ggg 146

Thr Ala Val Arg Ser Ser Trp Val Ala Ala Leu Leu Ala Thr Gly Gly

35

40

45

gag atg ctg ctg aac gtg gcg ctg gtg gcg ctg gtg ctg ctg ggg gcc 194

Glu Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala

50

55

60

tac cgg ctg tgg gtg cgc tgg ggg cgg cgt ggt ctg tgc tgc gga ccc 242

Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Cys Ser Gly Pro

65

70

75

ggg gcg ggc gag gag agc ccg gcc gcc acg ctg ccg cgc atg aag aag 290

Gly Ala Gly Glu Glu Ser Pro Ala Ala Thr Leu Pro Arg Met Lys Lys

80

85

90

cgg gac ttc agc ctg gag cag ctg cgc cag tac gac ggg gcg cgc acg 338

Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ala Arg Thr

95

100

105

110

ccg cgc atc ctg ctc gcg gtc aat ggg aaa gtc ttc gac gtg acc aaa 386

Pro Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys

115

120

125

ggc agc aag ttc tac ggc ccc gcg ggt cca tat ggc atc ttt gct ggc 434

Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly

130

135

140

agg gac gcc tcc agg ggg ctg gcg aca ttc tgc ctg gat aag gat gca 482

Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala

145

150

155

ctt aga gat gga tat gac gac ctc tca gat ttg aac gca gtg caa atg 530

Leu Arg Asp Gly Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met

160

165

170

gag agt gtt cga gaa tgg gaa atg cag ttt aaa gaa aaa tat gat tat 578

Glu Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr

175

180

185

190

gta ggc aga ctc cta aag cca ggg gag gag cca tca gag tac aca gat 626

Val Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp

195

200

205

gag gag gac acc aag gat cac agt aaa cag gac tgaactttgt gagcaaccaa 679

Glu Glu Asp Thr Lys Asp His Ser Lys Gln Asp

210

215

agccaggggc cttcagaact gcagctcgta cccctttcag agaatgtcca gtctttgggt 739

gtgatgctcc tgctgtgaga aacacctcac cagcgtgaac aagataatct gcctgactga 799

agatctgagg atgaggcgtt gggtgtgtg ccaggtgaat ttgttgccgt tgggtgtaat 859

gtctggtggg cttcatcatc ctaaacagga gacaggacct tcttaacagc aagaaagtca 919

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tcctttcttt cccccacccc tcccatgtct ctcttaaaac aaaaaagtat caaagacaac 1039

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ggacagtgtc ctcaggcctc gctgccactc agtgtgtctg aagcaccagc cttccaaagt 2059  
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cctaragggt ctgtaaccgg cctgactgat gggggcgggg ggttaggaca cgtttctttt 2719



cttttttttc tttttcttat ccttcagtgtagaattcag acacagggt tcacatattg 2779  
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 tgtttggtgc tcctccaatc aaacgtacga ttggacatgt ttgagaaaca ctgcatccac 2899  
 cttttgaagt tgtgtgggtcc atgtttgcca tacaataaaa gttgaactta t 2950

<210> 24

<211> 217

<212> PRT

<213> Mus musculus

<400> 24

Met	Ala	Ala	Gly	Asp	Gly	Asp	Val	Lys	Leu	Ser	Thr	Leu	Gly	Ser	Gly
1				5					10					15	
Gly	Glu	Ser	Gly	Gly	Asp	Gly	Ser	Pro	Gly	Gly	Ala	Gly	Ala	Thr	Ala
				20					25					30	
Val	Arg	Ser	Ser	Trp	Val	Ala	Ala	Leu	Leu	Ala	Thr	Gly	Gly	Glu	Met
				35					40					45	
Leu	Leu	Asn	Val	Ala	Leu	Val	Ala	Leu	Val	Leu	Leu	Gly	Ala	Tyr	Arg
				50					55					60	
Leu	Trp	Val	Arg	Trp	Gly	Arg	Arg	Gly	Leu	Cys	Ser	Gly	Pro	Gly	Ala
				65					70					75	
Gly	Glu	Glu	Ser	Pro	Ala	Ala	Thr	Leu	Pro	Arg	Met	Lys	Lys	Arg	Asp
				85					90					95	
Phe	Ser	Leu	Glu	Gln	Leu	Arg	Gln	Tyr	Asp	Gly	Ala	Arg	Thr	Pro	Arg
				100					105					110	
Ile	Leu	Leu	Ala	Val	Asn	Gly	Lys	Val	Phe	Asp	Val	Thr	Lys	Gly	Ser
				115					120					125	
Lys	Phe	Tyr	Gly	Pro	Ala	Gly	Pro	Tyr	Gly	Ile	Phe	Ala	Gly	Arg	Asp

130                      135                      140  
 Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg  
 145                      150                      155                      160  
 Asp Gly Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser  
                          165                      170                      175  
 Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly  
                          180                      185                      190  
 Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu Glu  
                          195                      200                      205  
 Asp Thr Lys Asp His Ser Lys Gln Asp  
                          210                      215

<210> 25

<211> 1850

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (7).. (675)

<400> 25

ccggtg atg gcg gct ggt gat ggg gac gtg aag cta ggc acc ctg ggg 48

Met Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly

1                      5                      10

agt ggc agc gag agc agc aac gac ggc ggc agc gag agt cca ggc gac 96

Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp

15                      20                      25                      30

gcg gga gcg gca gcg gaa ggg gga ggc tgg gcg gcg gcg gcg ttg gcg 144

Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala  
                             35                            40                            45  
 ctt ctg acg ggg ggc ggg gaa atg ctg ctg aac gtg gcg ctg gtg gct 192  
 Leu Leu Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala  
                             50                            55                            60  
 ctg gtg ctg ctg ggg gcc tac cgg ctg tgg gtg cgc tgg ggg cgg cgg 240  
 Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg  
                             65                            70                            75  
 ggt ctg ggg gcc ggg gcc ggg gcg ggc gag gag agc ccc gcc acc tct 288  
 Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser  
                             80                            85                            90  
 ctg cct cgc atg aag aag cgg gac ttc agc ttg gag cag ctg cgc cag 336  
 Leu Pro Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln  
                             95                            100                            105                            110  
 tac gac ggc tcc cgc aac ccg cgc atc ctg ctc gcg gtc aat ggg aaa 384  
 Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys  
                             115                            120                            125  
 gtc ttc gac gtg acc aaa ggc agc aag ttc tac ggc ccg gcg ggt cca 432  
 Val Phe Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro  
                             130                            135                            140  
 tat gga ata ttt gct ggt agg gat gcc tcc aga gga ctg gcc aca ttt 480  
 Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe  
                             145                            150                            155  
 tgc cta gat aaa gat gca ctt aga gat gaa tat gat gat ctc tca gat 528  
 Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp  
                             160                            165                            170  
 ttg aat gca gta caa atg gag agt gtt cga gaa tgg gaa atg cag ttt 576

Leu Asn Ala Val Gln Met Glu Ser Val Arg Glu Trp Glu Met Gln Phe

175 180 185 190

aaa gaa aaa tat gat tat gta ggc aga ctc cta aaa cca gga gaa gaa 624

Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys Pro Gly Glu Glu

195 200 205

cca tca gaa tat aca gat gaa gaa gat acc aag gat cac aat aaa cag 672

Pro Ser Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp His Asn Lys Gln

210 215 220

gat tgaactttgt aaacaaccaa agtcaggggc cttcagaact gcaattctta 725

Asp

ctccctttca cagactgtcc ggagtctttg ggtttgattc acctgctgcg aaaaacattc 785

aacaaattgt gtacaagata aattaatctc actatgaaga ttgaataac tagacattat 845

ttatgctgcc aaactcattt gttgcagttg tttgtaatgt ctagtggggc ttcattcatcc 905

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gacaaccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga 1085

ctcctgtgtc acatactgtg tttttatattt aacatgggtg aggaggcga cctgatcagg 1145

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ttggaaatta ggagaaggaa tttcaggtgg gtttaagtca gagctagttc cccaacagaa 1325

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ccataaaacc ttgatatcat tctgtgtata tagaatgtaa aaggaatatt acagtgttaa 1565

ctgcatata tgtaatatac acaaactcaa ttagcattgt aatggccaaa tgcattcccc 1625

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ctaatttttag gagtctgacc ctccacatct cactgggtgtg ggtgcatggg gctgtggagt 1745

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 actgtaaata caagtacat ttttaataaag catgtacaat aaacc 1850

<210> 26

<211> 223

<212> PRT

<213> Homo sapiens

<400> 26

Met Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly Ser Gly  
 1 5 10 15  
 Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly  
 20 25 30  
 Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu  
 35 40 45  
 Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala Leu Val  
 50 55 60  
 Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu  
 65 70 75 80  
 Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro  
 85 90 95  
 Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp  
 100 105 110  
 Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe  
 115 120 125  
 Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly  
 130 135 140  
 Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu

145                      150                      155                      160  
 Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn  
                          165                      170                      175  
 Ala Val Gln Met Glu Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu  
                          180                      185                      190  
 Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser  
                          195                      200                      205  
 Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp His Asn Lys Gln Asp  
                          210                      215                      220

<210> 27

<211> 2156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241)..(981)

<400> 27

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 cggccagcga aagaagggag ggggcgggag atccgagaca acgttaccac gtcaacaccc 180  
 aatcaggagc cggcctgacc ccgccccctc ttctcacgtt attggctgag aggccccag 240  
 atg ggc ggg gcc ggc cgt ggg gtt ggg gag ggc agg ggg cgg gga gga 288  
 Met Gly Gly Ala Gly Arg Gly Val Gly Glu Gly Arg Gly Arg Gly Gly  
   1                      5                      10                      15  
 gga gga agg cgc tgg cgg gca gtg atg gcg gct ggt gat ggg gac gtg 336  
 Gly Gly Arg Arg Trp Arg Ala Val Met Ala Ala Gly Asp Gly Asp Val

20	25	30	
aag cta ggc acc ctg ggg agt ggc agc gag agc agc aac gac ggc ggc			384
Lys Leu Gly Thr Leu Gly Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly			
35	40	45	
agc gag agt cca ggc gac gcg gga gcg gca gcg gaa ggg gga ggc tgg			432
Ser Glu Ser Pro Gly Asp Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp			
50	55	60	
gcg gcg gcg gcg ttg gcg ctt ctg acg ggg ggc ggg gaa atg ctg ctg			480
Ala Ala Ala Ala Leu Ala Leu Leu Thr Gly Gly Gly Glu Met Leu Leu			
65	70	75	80
aac gtg gcg ctg gtg gct ctg gtg ctg ctg ggg gcc tac cgg ctg tgg			528
Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp			
85	90	95	
gtg cgc tgg ggg cgg cgg ggt ctg ggg gcc ggg gcc ggg gcg ggc gag			576
Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu			
100	105	110	
gag agc ccc gcc acc tct ctg cct cgc atg aag aag cgg gac ttc agc			624
Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg Asp Phe Ser			
115	120	125	
ttg gag cag ctg cgc cag tac gac ggc tcc cgc aac ccg cgc atc ctg			672
Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu			
130	135	140	
ctc gcg gtc aat ggg aaa gtc ttc gac gtg acc aaa ggc agc aag ttc			720
Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly Ser Lys Phe			
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Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser			

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Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu			
180	185	190	
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Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu			
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Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu Glu Asp Thr			
225	230	235	240
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Lys Asp His Asn Lys Gln Asp			
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<212> PRT

<213> Homo sapiens

<400> 28

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35 40 45

Ser Glu Ser Pro Gly Asp Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp

50 55 60

Ala Ala Ala Ala Leu Ala Leu Leu Thr Gly Gly Gly Glu Met Leu Leu

65 70 75 80

Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp

85 90 95

Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu  
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115 120 125  
Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu  
130 135 140  
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Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser  
165 170 175  
Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu  
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Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser Val Arg  
195 200 205  
Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu  
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<211> 2906

<212> DNA

<213> Mus musculus

<220>

<221> CDS

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&lt;400&gt; 29

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gag aga gag gag gaa tat caa agg gtc cga gag aga ata ttt gcc cga 156
Glu Arg Glu Glu Glu Tyr Gln Arg Val Arg Glu Arg Ile Phe Ala Arg
              20              25              30
gag acc ggc cag aat gga tat ctg aat gac atc agg gga aac cgg gaa 204
Glu Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile Arg Gly Asn Arg Glu
              35              40              45
ggg ctg agc cgt acc tca agc agc cga cag agc agc aca gac agc gag 252
Gly Leu Ser Arg Thr Ser Ser Ser Arg Gln Ser Ser Thr Asp Ser Glu
              50              55              60
ctc aag tcc ctg gag cca cgg cct tgg agc agc aca gac tca gac ggc 300
Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly
              65              70              75              80
tct gtc cgc agc atg cga cct cct gtc acc aaa gcc agc agc ttc agt 348
Ser Val Arg Ser Met Arg Pro Pro Val Thr Lys Ala Ser Ser Phe Ser
              85              90              95
gga atc tcc atc ctc acc cga ggc gac agc att ggc agc agt aaa ggc 396
Gly Ile Ser Ile Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly
              100              105              110
ggc agt gca ggc agg ctc tcc agg cca ggc atg gca cta ggt gcc cca 444
Gly Ser Ala Gly Arg Leu Ser Arg Pro Gly Met Ala Leu Gly Ala Pro
              115              120              125

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 260 265 270

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Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu Ser His Pro Val Ala	
275 280 285	
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Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln Ala Ser Gln Gln Pro	
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Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val Gln Tyr Thr	
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Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser Gln Asn Val	
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Val Gln Pro Ser Phe Gln Gln Pro Met Leu Val Pro Ala Ser Gln Ser	
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Val Gln Gly Gly Leu Pro Thr Gly Gly Val Pro Val Tyr Tyr Ser Met	
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Ile Pro Pro Ala Gln Gln Asn Gly Thr Ser Pro Ser Val Gly Phe Leu	
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cag cct cct ggc tct gag cag tac cag atg cct cag tct ccc tct ccc	1356
Gln Pro Pro Gly Ser Glu Gln Tyr Gln Met Pro Gln Ser Pro Ser Pro	
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Cys Ser Pro Pro Gln Met Ser Gln Gln Tyr Ser Gly Val Ser Pro Ser	
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Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn Gly Pro Gln	
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Ala Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys Lys Tyr Tyr	
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Ser Val Glu Gln Arg Gly Gln Lys Pro Gly Asp Leu Tyr Ser Pro Asp	
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Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu Ser Asn Val	
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tgc act gga ctc agc ccc ctg cct gtc ctc aca cca ttc ccc cgg cct	1692
Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Pro Phe Pro Arg Pro	
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Leu Gln Tyr Asn Leu Ser Ile Cys Pro Pro Leu Leu His Gly Gln Ser	
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act tac acg gtg cac cag gga cag agc gga ttg aag cac gga aac cgg	1836
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Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr Asp Leu Gly Thr Ala	
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Asp Val Val Leu Gly Arg Val Leu Glu Val Thr Asp Leu Pro Glu Gly	
610 615 620	
atc acc cgt acg gag gct gac aaa ctc ttc acc cag ctt gcc atg tct	1980
Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr Gln Leu Ala Met Ser	
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ctc cga gtg gct aaa aag aac tac gac ctg agg atc ctg gaa cga gct 2220  
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<212> PRT

<213> Mus musculus

<400> 30

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25

30

Glu Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile Arg Gly Asn Arg Glu



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Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly		
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Gly Ile Ser Ile Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly		
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Glu Val Cys Asn Gln Val Thr Ser Pro Gln Ser Val Arg Gly Leu Leu		
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Pro Cys Thr Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln		
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Leu Pro Ala Leu Pro Pro Thr Pro Gln His Gln Pro Pro Leu Asn Asn		
165	170	175
His Met Ile Ser Gln Ala Glu Asp Leu Ser Asn Pro Phe Gly Gln Met		
180	185	190
Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala Asp Pro Ser Ser Ala		
195	200	205
Leu Phe Gln Pro Pro Leu Ile Ser Gln His Pro Gln Gln Ala Ser Phe		
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Ile Met Ala Ser Ala Gly Gln Pro Leu Pro Thr Ser Asn Tyr Ser Thr		
225	230	235
Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu Pro Pro Gln Gly Tyr		
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305 310 315 320

Met Leu Gly Val Gln Gln Pro Gln Asn Gln Gly Leu Leu Ser Asn Gln  
325 330 335

Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val Gln Tyr Thr  
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Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser Gln Asn Val  
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Val Gln Pro Ser Phe Gln Gln Pro Met Leu Val Pro Ala Ser Gln Ser  
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Val Gln Gly Gly Leu Pro Thr Gly Gly Val Pro Val Tyr Tyr Ser Met  
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420 425 430

Cys Ser Pro Pro Gln Met Ser Gln Gln Tyr Ser Gly Val Ser Pro Ser  
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Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn Gly Pro Gln  
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Ala Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys Lys Tyr Tyr

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Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu Ser Asn Val			
	515	520	525
Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Pro Phe Pro Arg Pro			
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Leu Gln Tyr Asn Leu Ser Ile Cys Pro Pro Leu Leu His Gly Gln Ser			
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Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu Lys His Gly Asn Arg			
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Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr Gln Leu Ala Met Ser			
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Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln Gly Leu Pro Gly Ala			
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Gly Gly Gly Asp Asn Ser Gly Thr Ala Glu Asn Gly Arg His Pro Asp			
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<213> Homo sapiens

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gac tcc act gga ata gac cta cat gaa ttt ctt gta aat aca ctg aaa 881

Asp Ser Thr Gly Ile Asp Leu His Glu Phe Leu Val Asn Thr Leu Lys

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20

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Lys Asn Pro Arg Asp Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile

30

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105

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110

115

120

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125

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Thr Ser Ser Ser Arg Gln Ser Ser Thr Asp Ser Glu Leu Lys Ser Leu	
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Glu Pro Arg Pro Trp Ser Ser Thr Asp Ser Asp Gly Ser Val Arg Ser	
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atg cga ccc cct gtc acc aaa gct agc agc ttc agt gga atc tct atc	1457
Met Arg Pro Pro Val Thr Lys Ala Ser Ser Phe Ser Gly Ile Ser Ile	
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Leu Thr Arg Gly Asp Ser Ile Gly Ser Ser Lys Gly Gly Ser Ala Gly	
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agg atc tcc agg cca ggt atg gca cta ggt gcc cca gaa gtg tgc aac	1553
Arg Ile Ser Arg Pro Gly Met Ala Leu Gly Ala Pro Glu Val Cys Asn	
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Gln Val Thr Ser Ser Gln Ser Val Arg Gly Leu Leu Pro Cys Thr Ala	
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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Pro Ala Leu Pro Pro	
270                                      275                                      280	

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 Pro Gln Gln Tyr Ser Gly Val Ser Pro Ser Gly Pro Gly Val Val Val  
 560 565 570



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 Gln Lys Pro Gly Asp Leu Tyr Ser Pro Asp Ser Ser Pro Gln Ala Asn  
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 Pro Ser Pro Val Thr Ser Leu Ser Ser Val Cys Thr Gly Leu Ser Pro  
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 Gly Thr Ala Glu Asn Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr  
 780 785 790 795  
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 Ile Val Ala Val Phe Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu  
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 tcactgtaaa tttatttaa tctgtttttt tgtttgtttg ggggttattt ggggggaggt 4290  
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<211> 840

<212> PRT

<213> Homo sapiens

<400> 32

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Asp Leu His Glu Phe Leu Val Asn Thr Leu Lys Lys Asn Pro Arg Asp

20 25 30

Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile Leu Glu Phe Ile Asn

35 40 45

Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln Met Thr Ser Tyr His

50	55	60	
Arg Met Leu Leu His Arg Val Ala Ala Tyr Phe Gly Met Asp His Asn			
65	70	75	80
Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn Lys Thr Ser Asn Thr			
	85	90	95
Arg Ile Pro Glu Gln Arg Phe Ser Glu His Ile Lys Asp Glu Lys Asn			
	100	105	110
Thr Glu Phe Gln Gln Arg Phe Ile Leu Lys Arg Asp Asp Ala Ser Met			
	115	120	125
Asp Arg Asp Asp Asn Gln Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile			
	130	135	140
Arg Leu Ser Lys Glu Ala Phe Ser Ser Ser Ser His Lys Arg Arg Gln			
145	150	155	160
Ile Phe Arg Gly Asn Arg Glu Gly Leu Ser Arg Thr Ser Ser Ser Arg			
	165	170	175
Gln Ser Ser Thr Asp Ser Glu Leu Lys Ser Leu Glu Pro Arg Pro Trp			
	180	185	190
Ser Ser Thr Asp Ser Asp Gly Ser Val Arg Ser Met Arg Pro Pro Val			
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Thr Lys Ala Ser Ser Phe Ser Gly Ile Ser Ile Leu Thr Arg Gly Asp			
	210	215	220
Ser Ile Gly Ser Ser Lys Gly Gly Ser Ala Gly Arg Ile Ser Arg Pro			
225	230	235	240
Gly Met Ala Leu Gly Ala Pro Glu Val Cys Asn Gln Val Thr Ser Ser			
	245	250	255
Gln Ser Val Arg Gly Leu Leu Pro Cys Thr Ala Gln Gln Gln Gln			

260	265	270
Gln Gln Gln Gln Gln Leu Pro Ala Leu Pro Pro Thr Pro Gln Gln Gln		
275	280	285
Pro Pro Leu Asn Asn His Met Ile Ser Gln Ala Asp Asp Leu Ser Asn		
290	295	300
Pro Phe Gly Gln Met Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala		
305	310	315
Asp Pro Ser Ala Ala Leu Phe Gln Thr Pro Leu Ile Ser Gln His Pro		
325	330	335
Gln Gln Thr Ser Phe Ile Met Ala Ser Thr Gly Gln Pro Leu Pro Thr		
340	345	350
Ser Asn Tyr Ser Thr Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu		
355	360	365
Pro Pro Gln Gly Tyr Met Gln Pro Pro Gln Gln Ile Gln Val Ser Tyr		
370	375	380
Tyr Pro Pro Gly Gln Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu		
385	390	395
Ser His Pro Val Ala Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln		
405	410	415
Pro Ser Gln Gln Pro Gly Leu Gln Pro Met Met Pro Asn Gln Gln Gln		
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Ala Ala Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln Asn Gln Gly		
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Leu Leu Ser Ser Gln Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu		
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Val Val Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser		
465	470	475
		480

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Pro	Val	Ser	Gln	Ser	Val	Gln	Gly	Gly	Leu	Pro	Ala	Ala	Gly	Val	Pro
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Val	Tyr	Tyr	Ser	Met	Ile	Pro	Pro	Ala	Gln	Gln	Asn	Gly	Thr	Ser	Pro
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Ser	Val	Gly	Phe	Leu	Gln	Pro	Pro	Gly	Ser	Glu	Gln	Tyr	Gln	Met	Pro
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Gln	Ser	Pro	Ser	Pro	Cys	Ser	Pro	Pro	Gln	Met	Pro	Gln	Gln	Tyr	Ser
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Gly	Val	Ser	Pro	Ser	Gly	Pro	Gly	Val	Val	Val	Met	Gln	Leu	Asn	Val
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Pro	Asn	Gly	Pro	Gln	Pro	Pro	Gln	Asn	Pro	Ser	Met	Val	Gln	Trp	Ser
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His	Cys	Lys	Tyr	Tyr	Ser	Met	Asp	Gln	Arg	Gly	Gln	Lys	Pro	Gly	Asp
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Leu	Tyr	Ser	Pro	Asp	Ser	Ser	Pro	Gln	Ala	Asn	Thr	Gln	Met	Ser	Ser
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Ser	Pro	Val	Thr	Ser	Pro	Thr	Gln	Ser	Pro	Ala	Pro	Ser	Pro	Val	Thr
625						630				635					640
Ser	Leu	Ser	Ser	Val	Cys	Thr	Gly	Leu	Ser	Pro	Leu	Pro	Val	Leu	Thr
					645					650					655
Gln	Phe	Pro	Arg	Pro	Gly	Gly	Pro	Ala	Gln	Gly	Asp	Gly	Arg	Tyr	Ser
				660					665						670
Leu	Leu	Gly	Gln	Pro	Leu	Gln	Tyr	Asn	Leu	Ser	Ile	Cys	Pro	Pro	Leu
				675				680							685

Leu His Gly Gln Ser Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu  
 690 695 700  
 Lys His Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr  
 705 710 715 720  
 Asp Leu Gly Thr Ala Asp Val Val Leu Gly Arg Val Leu Glu Val Thr  
 725 730 735  
 Asp Leu Pro Glu Gly Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr  
 740 745 750  
 Gln Leu Ala Met Ser Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln  
 755 760 765  
 Gly Leu Pro Gly Gly Gly Gly Gly Asp Asn Ser Gly Thr Ala Glu Asn  
 770 775 780  
 Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr Ile Val Ala Val Phe  
 785 790 795 800  
 Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu Arg Leu Asn Asn Ser  
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 Ile Leu Glu Arg Ala Ser Ser Gln  
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Met Leu Ser Arg Asp Ser Ser Gln Glu Tyr Thr

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gac tcc act gga ata gac cta cat gaa ttt ctt gta aat aca ctg aaa 881

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Leu Glu Phe Ile Asn Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln

45

50

55



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Thr Ser Pro Ser Val Gly Phe Leu Gln Pro Pro Gly Ser Glu Gln Tyr	
540 545 550 555	
cag atg cct cag tct ccc tct ccc tgc agt cca cca cag atg cca cag	2513
Gln Met Pro Gln Ser Pro Ser Pro Cys Ser Pro Pro Gln Met Pro Gln	
560 565 570	
cag tac tca gga gtg tca cct tct gga cca ggt gta gtg gtc atg cag	2561
Gln Tyr Ser Gly Val Ser Pro Ser Gly Pro Gly Val Val Val Met Gln	
575 580 585	
ctg aat gtc cct aat gga ccc cag ccc cct cag aac cca tcc atg gtc	2609
Leu Asn Val Pro Asn Gly Pro Gln Pro Pro Gln Asn Pro Ser Met Val	
590 595 600	
cag tgg agt cat tgt aaa tac tac agc atg gac cag cgg ggg cag aag	2657
Gln Trp Ser His Cys Lys Tyr Tyr Ser Met Asp Gln Arg Gly Gln Lys	
605 610 615	
cct gga gac ctg tac agt cct gac agc agc ccc cag gcc aac aca caa	2705
Pro Gly Asp Leu Tyr Ser Pro Asp Ser Ser Pro Gln Ala Asn Thr Gln	
620 625 630 635	

atg agc agc agc cct gtc aca tct cct acc cag tct cca gca ccc tct	2753
Met Ser Ser Ser Pro Val Thr Ser Pro Thr Gln Ser Pro Ala Pro Ser	
640	645
cct gtc acc agc ctc agc agt gtc tgc aca gga ctc agt ccc ctg cct	2801
Pro Val Thr Ser Leu Ser Ser Val Cys Thr Gly Leu Ser Pro Leu Pro	
655	660
gtc ctc aca cag ttc ccc cgg cct ggg ggt cca gca cag ggt gat ggg	2849
Val Leu Thr Gln Phe Pro Arg Pro Gly Gly Pro Ala Gln Gly Asp Gly	
670	675
cgc tac tcc ctt ttg ggc cag cca tta cag tac aat ctg tcc atc tgc	2897
Arg Tyr Ser Leu Leu Gly Gln Pro Leu Gln Tyr Asn Leu Ser Ile Cys	
685	690
cct ccc ttg ctc cat ggc cag tca act tac acg gtg cac cag gga cag	2945
Pro Pro Leu Leu His Gly Gln Ser Thr Tyr Thr Val His Gln Gly Gln	
700	705
agt gga ctg aag cat gga aac cgg ggc aag aga caa gca ctc aaa tct	2993
Ser Gly Leu Lys His Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser	
720	725
gcc tcc act gac ctg ggg aca gca gat gtt gtc ctg ggg cgg gtg ctg	3041
Ala Ser Thr Asp Leu Gly Thr Ala Asp Val Val Leu Gly Arg Val Leu	
735	740
gag gtg aca gat ctc cct gag ggc atc acc cgt act gag gcg gac aaa	3089
Glu Val Thr Asp Leu Pro Glu Gly Ile Thr Arg Thr Glu Ala Asp Lys	
750	755
ctc ttc acg cag ctc gcc atg tct ggc gcc aag atc cag tgg ctc aag	3137
Leu Phe Thr Gln Leu Ala Met Ser Gly Ala Lys Ile Gln Trp Leu Lys	
765	770
	775

gat gct cag ggg ctg cct gga ggg ggt ggg ggg gac aac agt ggg act 3185  
Asp Ala Gln Gly Leu Pro Gly Gly Gly Gly Gly Asp Asn Ser Gly Thr  
780 785 790 795  
gct gag aat ggc cgc cac tcg gac ctc gct gcc ttg tac acc att gtg 3233  
Ala Glu Asn Gly Arg His Ser Asp Leu Ala Ala Leu Tyr Thr Ile Val  
800 805 810  
gct gtg ttc ccc agc ccc ctg gct gcc caa aat gcc tcc ctt cgt ctc 3281  
Ala Val Phe Pro Ser Pro Leu Ala Ala Gln Asn Ala Ser Leu Arg Leu  
815 820 825  
aac aac tcc gtg agt cgc ttc aaa ctt cga atg gcc aaa aag aac tat 3329  
Asn Asn Ser Val Ser Arg Phe Lys Leu Arg Met Ala Lys Lys Asn Tyr  
830 835 840  
gac ctg agg atc ctg gag cga gcc agc tcc caa taaatggagg aggggaaagg 3382  
Asp Leu Arg Ile Leu Glu Arg Ala Ser Ser Gln  
845 850  
gactgtcaca gaagaagcaa gggcaggggtg gaggggggttg aaggatcctg acagaccatg 3442  
gacagaggca ggaagtaagg aaactgatgt taaactggaa cctaagacag tgatgaagat 3502  
ggaaacacag atacctacac tggcattgga ctctttcttg ctcccctgcc atgggtcctc 3562  
tctttttccc tggttgaccc cccttgcatc actcttcttc ccatcctctt cttttttttt 3622  
tttttttttt ttttgagacg gagtttgcgt cttgtcacc cagctggagt gcagtagcac 3682  
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agagacggag tttcaccatg ttggccaggc tggcctcaaa ctcttgacct caggtgatcc 3862  
acctgccttg gccttcaga gtgctgggat tacaggcgtg agccactgtg cctggcttcc 3922  
atcctcttct atcatttttt taaatctctt ctctatcat aaaattaatt tctcattttt 3982  
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tcctttcctt ttttgggtctt tatgaatata tttatatgga cagaattaag ataaacaaaa 4102

ttgattgccc cattctctca cttcccccac ttgtcttcct agaccccaca gagttaaacc 4162  
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 agtaacagac acagtattta attgcacata cagatgtttg ctgggtatat tcactgtaaa 4282  
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 tttaaatata aaaaaaaaaa tctgtcactg g 4373

<210> 34

<211> 854

<212> PRT

<213> Homo sapiens

<400> 34

Met Leu Ser Arg Asp Ser Ser Gln Glu Tyr Thr Asp Ser Thr Gly Ile

1 5 10 15

Asp Leu His Glu Phe Leu Val Asn Thr Leu Lys Lys Asn Pro Arg Asp

20 25 30

Arg Met Met Leu Leu Lys Leu Glu Gln Glu Ile Leu Glu Phe Ile Asn

35 40 45

Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln Met Thr Ser Tyr His

50 55 60

Arg Met Leu Leu His Arg Val Ala Ala Tyr Phe Gly Met Asp His Asn

65 70 75 80

Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn Lys Thr Ser Asn Thr

85 90 95

Arg Ile Pro Glu Gln Arg Phe Ser Glu His Ile Lys Asp Glu Lys Asn

100 105 110

Thr Glu Phe Gln Gln Arg Phe Ile Leu Lys Arg Asp Asp Ala Ser Met

115 120 125

Asp Arg Asp Asp Asn Gln Ile Arg Val Pro Leu Gln Asp Gly Arg Arg  
 130 135 140  
 Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr Gln Arg Val Arg Glu  
 145 150 155 160  
 Arg Ile Phe Ala Arg Glu Thr Gly Gln Asn Gly Tyr Leu Asn Asp Ile  
 165 170 175  
 Arg Gly Asn Arg Glu Gly Leu Ser Arg Thr Ser Ser Ser Arg Gln Ser  
 180 185 190  
 Ser Thr Asp Ser Glu Leu Lys Ser Leu Glu Pro Arg Pro Trp Ser Ser  
 195 200 205  
 Thr Asp Ser Asp Gly Ser Val Arg Ser Met Arg Pro Pro Val Thr Lys  
 210 215 220  
 Ala Ser Ser Phe Ser Gly Ile Ser Ile Leu Thr Arg Gly Asp Ser Ile  
 225 230 235 240  
 Gly Ser Ser Lys Gly Gly Ser Ala Gly Arg Ile Ser Arg Pro Gly Met  
 245 250 255  
 Ala Leu Gly Ala Pro Glu Val Cys Asn Gln Val Thr Ser Ser Gln Ser  
 260 265 270  
 Val Arg Gly Leu Leu Pro Cys Thr Ala Gln Gln Gln Gln Gln Gln  
 275 280 285  
 Gln Gln Gln Leu Pro Ala Leu Pro Pro Thr Pro Gln Gln Gln Pro Pro  
 290 295 300  
 Leu Asn Asn His Met Ile Ser Gln Ala Asp Asp Leu Ser Asn Pro Phe  
 305 310 315 320  
 Gly Gln Met Ser Leu Ser Arg Gln Gly Ser Thr Glu Ala Ala Asp Pro  
 325 330 335  
 Ser Ala Ala Leu Phe Gln Thr Pro Leu Ile Ser Gln His Pro Gln Gln



340	345	350
Thr Ser Phe Ile Met Ala Ser Thr Gly Gln Pro Leu Pro Thr Ser Asn		
355	360	365
Tyr Ser Thr Ser Ser His Ala Pro Pro Thr Gln Gln Val Leu Pro Pro		
370	375	380
Gln Gly Tyr Met Gln Pro Pro Gln Gln Ile Gln Val Ser Tyr Tyr Pro		
385	390	395
Pro Gly Gln Tyr Pro Asn Ser Asn Gln Gln Tyr Arg Pro Leu Ser His		
405	410	415
Pro Val Ala Tyr Ser Pro Gln Arg Gly Gln Gln Leu Pro Gln Pro Ser		
420	425	430
Gln Gln Pro Gly Leu Gln Pro Met Met Pro Asn Gln Gln Gln Ala Ala		
435	440	445
Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln Asn Gln Gly Leu Leu		
450	455	460
Ser Ser Gln Arg Ser Ser Met Gly Gly Gln Met Gln Gly Leu Val Val		
465	470	475
Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro Val Gly Ser Asp Ser		
485	490	495
Gln Asn Val Val Gln Pro Pro Phe Gln Gln Pro Met Leu Val Pro Val		
500	505	510
Ser Gln Ser Val Gln Gly Gly Leu Pro Ala Ala Gly Val Pro Val Tyr		
515	520	525
Tyr Ser Met Ile Pro Pro Ala Gln Gln Asn Gly Thr Ser Pro Ser Val		
530	535	540
Gly Phe Leu Gln Pro Pro Gly Ser Glu Gln Tyr Gln Met Pro Gln Ser		
545	550	555
		560

Pro Ser Pro Cys Ser Pro Pro Gln Met Pro Gln Gln Tyr Ser Gly Val  
 565 570 575  
 Ser Pro Ser Gly Pro Gly Val Val Val Met Gln Leu Asn Val Pro Asn  
 580 585 590  
 Gly Pro Gln Pro Pro Gln Asn Pro Ser Met Val Gln Trp Ser His Cys  
 595 600 605  
 Lys Tyr Tyr Ser Met Asp Gln Arg Gly Gln Lys Pro Gly Asp Leu Tyr  
 610 615 620  
 Ser Pro Asp Ser Ser Pro Gln Ala Asn Thr Gln Met Ser Ser Ser Pro  
 625 630 635 640  
 Val Thr Ser Pro Thr Gln Ser Pro Ala Pro Ser Pro Val Thr Ser Leu  
 645 650 655  
 Ser Ser Val Cys Thr Gly Leu Ser Pro Leu Pro Val Leu Thr Gln Phe  
 660 665 670  
 Pro Arg Pro Gly Gly Pro Ala Gln Gly Asp Gly Arg Tyr Ser Leu Leu  
 675 680 685  
 Gly Gln Pro Leu Gln Tyr Asn Leu Ser Ile Cys Pro Pro Leu Leu His  
 690 695 700  
 Gly Gln Ser Thr Tyr Thr Val His Gln Gly Gln Ser Gly Leu Lys His  
 705 710 715 720  
 Gly Asn Arg Gly Lys Arg Gln Ala Leu Lys Ser Ala Ser Thr Asp Leu  
 725 730 735  
 Gly Thr Ala Asp Val Val Leu Gly Arg Val Leu Glu Val Thr Asp Leu  
 740 745 750  
 Pro Glu Gly Ile Thr Arg Thr Glu Ala Asp Lys Leu Phe Thr Gln Leu  
 755 760 765  
 Ala Met Ser Gly Ala Lys Ile Gln Trp Leu Lys Asp Ala Gln Gly Leu

138/861

ggc ttc gac acc att cct ttg atg acg ccc ctc gat gtc aac cag ctg	211
Gly Phe Asp Thr Ile Pro Leu Met Thr Pro Leu Asp Val Asn Gln Leu	
25 30 35	
cag ttc cca ccc cca gat aag gtc gtg gtg aaa act aag act gaa tat	259
Gln Phe Pro Pro Pro Asp Lys Val Val Val Lys Thr Lys Thr Glu Tyr	
40 45 50	
gaa cct gat cgc aaa aaa gga aaa gca cgt cct ccc aag ata gcc gag	307
Glu Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro Lys Ile Ala Glu	
55 60 65	
ttc acc gtc agc atc acc gag ggt gtc acc gag agg ttt aag gtc tcc	355
Phe Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg Phe Lys Val Ser	
70 75 80	
gtg ctg gtc ctc ttt gcc ctg gcc ttc ctc acc tgt gtc gtc ttt ctg	403
Val Leu Val Leu Phe Ala Leu Ala Phe Leu Thr Cys Val Val Phe Leu	
85 90 95 100	
gtt gtc tac aaa gtg tac aag tat gac cgc gcc tgc cct gat ggg ttt	451
Val Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys Pro Asp Gly Phe	
105 110 115	
gtc ttg aag aac acc cag tgc atc cca gaa ggc ttg gag agc tac tac	499
Val Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu Glu Ser Tyr Tyr	
120 125 130	
acg gag caa gac tcc agt gcc cgg gag aaa ttt tac act gtc ata aac	547
Thr Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr Thr Val Ile Asn	
135 140 145	
cac tac aac gtg gcc aag cag agc atc acc cgc tcc gtg tcg cca tgg	595
His Tyr Asn Val Ala Lys Gln Ser Ile Thr Arg Ser Val Ser Pro Trp	
150 155 160	

atg tca gtt ctg tca gaa gag aag ctg tcg gaa cag gag acc gaa gct 643

Met Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln Glu Thr Glu Ala

165

170

175

180

gca gag aag tca gct tagcgagcag ggcagggtcc ttacgatgtg tcaacttgaag 698

Ala Glu Lys Ser Ala

185

gcaacaaggg gactttgagg gacatttcat taaatataat taccgataat ttagagatta 758

ctcattttacg gtgcaattgc ttctgtttgc taatgctgct ttgcaaatta aacttgctgc 818

ggaccacca caggcgtaag aacaagagca tctcagcatt gcttagagag ctggatgccca 878

ctgtccacgc tgaggagtct tcatttagct ccttcctgg gattcactgg atactgtcaa 938

aaggtaatct acactggcta tgccaggggt ctggccgtca gaacagcaca gctgctgggt 998

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gaaagccac tggttctttt ctttcctgtt atgaatatat ttgcacgtac agccctgaat 1358

gcagggtgcag tttgggtttt ttgttttggt ttgttttgct ttattagcca gtgggcaaag 1418

tgagatgtaa ttttgggtaa gccagggcta ctttagcttt tcttctgtga acagatgtga 1478

ctcctgtgct gtgggaaggg gcaggacggc tggtgggggg ggctgatgtg gcaccttgca 1538

aatagaatat ctaagtccac aatctttgta agaaaagtat gtttatgttt caatctgaat 1598

cttgacatta aagtatatgt ttacaaaatc accagtaggt aaactaaatg tgtaagacaa 1658

ttaaatagaa aaagct 1674

<210> 36

<211> 185

<212> PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 36

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Met Val Lys Leu Gly Asn Asn Phe Ala Glu Lys Gly Thr Lys Gln Pro
  1              5              10              15
Leu Leu Glu Asp Gly Phe Asp Thr Ile Pro Leu Met Thr Pro Leu Asp
              20              25              30
Val Asn Gln Leu Gln Phe Pro Pro Pro Asp Lys Val Val Val Lys Thr
              35              40              45
Lys Thr Glu Tyr Glu Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro
              50              55              60
Lys Ile Ala Glu Phe Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg
              65              70              75              80
Phe Lys Val Ser Val Leu Val Leu Phe Ala Leu Ala Phe Leu Thr Cys
              85              90              95
Val Val Phe Leu Val Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys
              100             105             110
Pro Asp Gly Phe Val Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu
              115             120             125
Glu Ser Tyr Tyr Thr Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr
              130             135             140
Thr Val Ile Asn His Tyr Asn Val Ala Lys Gln Ser Ile Thr Arg Ser
              145             150             155             160
Val Ser Pro Trp Met Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln
              165             170             175
Glu Thr Glu Ala Ala Glu Lys Ser Ala
              180             185

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&lt;210&gt; 37

&lt;211&gt; 1485

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (162)..(716)

&lt;400&gt; 37

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tccgccattg ctgcgagcag gagcaggaga cgcgagctc ggagcgctga gctgacctgc 120
cggagccggg cgtgggctgc agcctcggag ctcccgaac g atg gtg aag ttg ggg 176
                                     Met Val Lys Leu Gly
                                     1           5
aac aat ttc gca gag aag ggc acc aag cag ccg ctg ctg gag gat ggc 224
Asn Asn Phe Ala Glu Lys Gly Thr Lys Gln Pro Leu Leu Glu Asp Gly
          10           15           20
ttc gac acc att ccc ctg atg acg ccc ctc gat gtc aat cag ctg cag 272
Phe Asp Thr Ile Pro Leu Met Thr Pro Leu Asp Val Asn Gln Leu Gln
          25           30           35
ttc ccg ccc ccg gat aag gtg gtc gtg aaa act aag acc gag tat gaa 320
Phe Pro Pro Pro Asp Lys Val Val Val Lys Thr Lys Thr Glu Tyr Glu
          40           45           50
cct gac cgc aag aaa ggg aaa gca cgt cct ccc caa att gct gag ttc 368
Pro Asp Arg Lys Lys Gly Lys Ala Arg Pro Pro Gln Ile Ala Glu Phe
          55           60           65
acc gtc agc atc acg gag ggt gtc acc gag agg ttt aag gtc tcc gtg 416
Thr Val Ser Ile Thr Glu Gly Val Thr Glu Arg Phe Lys Val Ser Val

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70	75	80	85	
ttg gtc ctc ttc gcc ctg gcc ttc ctc acc tgc gtc gtc ttc ctg gtt	464			
Leu Val Leu Phe Ala Leu Ala Phe Leu Thr Cys Val Val Phe Leu Val				
90	95	100		
gtc tac aag gtg tac aag tat gac cgc gcc tgc ccc gat ggg ttc gtc	512			
Val Tyr Lys Val Tyr Lys Tyr Asp Arg Ala Cys Pro Asp Gly Phe Val				
105	110	115		
ctc aag aac acc cag tgc atc cca gaa ggc ttg gag agc tac tac gcg	560			
Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu Glu Ser Tyr Tyr Ala				
120	125	130		
gag caa gac tcc agt gcc cgg gag aaa ttt tac aca gtc ata aac cac	608			
Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr Thr Val Ile Asn His				
135	140	145		
tac aac ctg gcc aag cag agc atc acg cgc tcc gta tcg ccc tgg atg	656			
Tyr Asn Leu Ala Lys Gln Ser Ile Thr Arg Ser Val Ser Pro Trp Met				
150	155	160	165	
tca gtt ctg tca gaa gag aag ctg tcc gag cag gag act gaa gcg gct	704			
Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln Glu Thr Glu Ala Ala				
170	175	180		
gag aag tca gct tagcgggatg ggcaagttcc ttacaatgtg tcacttgcaa	756			
Glu Lys Ser Ala				
185				
ataacaaagg gactttgagg gacatttcat taaatataat tactgatact ttagagggtta	816			
ctcattttacg gtgcaattgc ttctgtttgc taatgctgct ttgcaaataa aacttgctgc	876			
cgaccaccca cgggcataaa atcaagtgca tttcagcatt gcctaaagag ctctgacacc	936			
actttttcatg ttaagatctt catttagctc ctttactggg atttattgga tgctgtaaaa	996			
aaataaattt aactggata tgcgaagggt ttgatctca gataaatgca ttttgtggaa	1056			



ttgattttct gaaccgaccc tgctgtctgc aaaccttcct ccatagccat atctagagtg 1116  
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<210> 38

<211> 185

<212> PRT

<213> Homo sapiens

<400> 38

Met	Val	Lys	Leu	Gly	Asn	Asn	Phe	Ala	Glu	Lys	Gly	Thr	Lys	Gln	Pro
1				5					10					15	
Leu	Leu	Glu	Asp	Gly	Phe	Asp	Thr	Ile	Pro	Leu	Met	Thr	Pro	Leu	Asp
				20				25						30	
Val	Asn	Gln	Leu	Gln	Phe	Pro	Pro	Pro	Asp	Lys	Val	Val	Val	Lys	Thr
				35				40						45	
Lys	Thr	Glu	Tyr	Glu	Pro	Asp	Arg	Lys	Lys	Gly	Lys	Ala	Arg	Pro	Pro
				50				55				60			
Gln	Ile	Ala	Glu	Phe	Thr	Val	Ser	Ile	Thr	Glu	Gly	Val	Thr	Glu	Arg
				65				70				75			80
Phe	Lys	Val	Ser	Val	Leu	Val	Leu	Phe	Ala	Leu	Ala	Phe	Leu	Thr	Cys
				85				90						95	
Val	Val	Phe	Leu	Val	Val	Tyr	Lys	Val	Tyr	Lys	Tyr	Asp	Arg	Ala	Cys

100	105	110
Pro Asp Gly Phe Val Leu Lys Asn Thr Gln Cys Ile Pro Glu Gly Leu		
115	120	125
Glu Ser Tyr Tyr Ala Glu Gln Asp Ser Ser Ala Arg Glu Lys Phe Tyr		
130	135	140
Thr Val Ile Asn His Tyr Asn Leu Ala Lys Gln Ser Ile Thr Arg Ser		
145	150	155
Val Ser Pro Trp Met Ser Val Leu Ser Glu Glu Lys Leu Ser Glu Gln		
165	170	175
Glu Thr Glu Ala Ala Glu Lys Ser Ala		
180	185	

&lt;210&gt; 39

&lt;211&gt; 2676

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (35).. (2488)

&lt;400&gt; 39

actgcgagag gggcctggcg gccgtgcggg agcc atg gcg gcc acg gag gcg gcg 55

Met Ala Ala Thr Glu Ala Ala

1

5

gcg gcc gat tct gcg ggt ccg gcc ccg ggt gtc ccg gcc acg ccg gcg 103

Ala Ala Asp Ser Ala Gly Pro Ala Pro Gly Val Pro Ala Thr Pro Ala

10

15

20

agc acg cgg gga gcc gct gcc gcc tct agc ccg tgg agg ccg ccc gag 151

Ser Thr Arg Gly Ala Ala Ala Ala Ser Ser Pro Trp Arg Pro Pro Glu  
 25 30 35  
 tcg cga ctg caa ggc agc cgg ccg aga ccg gcc agg gct cgg gcc gcg 199  
 Ser Arg Leu Gln Gly Ser Arg Pro Arg Pro Ala Arg Ala Arg Ala Ala  
 40 45 50 55  
 gcc ccg gtg cca ccg gcc cgg gag ctg atc cag ccg act gtg agc gag 247  
 Ala Pro Val Pro Pro Ala Arg Glu Leu Ile Gln Pro Thr Val Ser Glu  
 60 65 70  
 ctg tcc cgg gct gtg cgc acc aat att ctg tgc acc gtg cgc ggc tgc 295  
 Leu Ser Arg Ala Val Arg Thr Asn Ile Leu Cys Thr Val Arg Gly Cys  
 75 80 85  
 ggc aag atc ctg ccc aac agc cct gcg ctc aac atg cac ctc gtc aag 343  
 Gly Lys Ile Leu Pro Asn Ser Pro Ala Leu Asn Met His Leu Val Lys  
 90 95 100  
 agc cac cga ctg cag gat ggc ata gta aac ccg aca ata agg aaa gac 391  
 Ser His Arg Leu Gln Asp Gly Ile Val Asn Pro Thr Ile Arg Lys Asp  
 105 110 115  
 ttg aca act gca ccg aaa ttc tac tgt tgt cca atc aaa gga tgt cct 439  
 Leu Thr Thr Ala Pro Lys Phe Tyr Cys Cys Pro Ile Lys Gly Cys Pro  
 120 125 130 135  
 cga ggc ccc gac cga ccg ttt tct cag ttt tct ctg gtt aaa cag cac 487  
 Arg Gly Pro Asp Arg Pro Phe Ser Gln Phe Ser Leu Val Lys Gln His  
 140 145 150  
 ttt atg aaa atg cat gca gag aag aag cac aaa tgc agt aag tgc agt 535  
 Phe Met Lys Met His Ala Glu Lys Lys His Lys Cys Ser Lys Cys Ser  
 155 160 165  
 aat tcc tac ggc acc gag tgg gac ctg aaa aga cac gag gag gat tgt 583

Asn Ser Tyr Gly Thr Glu Trp Asp Leu Lys Arg His Glu Glu Asp Cys	
170	175
180	
ggc aag acc ttc cag tgt acg tgc ggc tgt ccc tac gcc agc aga acc	631
Gly Lys Thr Phe Gln Cys Thr Cys Gly Cys Pro Tyr Ala Ser Arg Thr	
185	190
195	
gca ctg cag tct cac atc tac cga act ggc cac gag atc cct gca gag	679
Ala Leu Gln Ser His Ile Tyr Arg Thr Gly His Glu Ile Pro Ala Glu	
200	205
210	215
cac aga gac cca cct agt aaa aaa agg aaa atg gaa agc tac ctg caa	727
His Arg Asp Pro Pro Ser Lys Lys Arg Lys Met Glu Ser Tyr Leu Gln	
220	225
230	
aac caa aag ttg tcc agt aaa acc act gaa cca ctg agc gac caa gca	775
Asn Gln Lys Leu Ser Ser Lys Thr Thr Glu Pro Leu Ser Asp Gln Ala	
235	240
245	
gcc ccg cgc caa gat gct gct gaa ccg gat gct ccg gag gtc aag cct	823
Ala Pro Arg Gln Asp Ala Ala Glu Pro Asp Ala Pro Glu Val Lys Pro	
250	255
260	
gca gca tcc ctc gaa gac tcc tgt agc gcc cac acc aaa aag cag agc	871
Ala Ala Ser Leu Glu Asp Ser Cys Ser Ala His Thr Lys Lys Gln Ser	
265	270
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gtc gcg acg cct ccc cgg tgt ccc cag aag ttg ctg tta cca aag ccc	919
Val Ala Thr Pro Pro Arg Cys Pro Gln Lys Leu Leu Leu Pro Lys Pro	
280	285
290	295
aag gtg gct ctg gtt aaa ctc cca gtc atg cag ttt tcc ccc gtg cct	967
Lys Val Ala Leu Val Lys Leu Pro Val Met Gln Phe Ser Pro Val Pro	
300	305
310	
gtc ttt gtg cct aca gcg gag tcc tcg gcc cag cct gtg gtg tta ggt	1015

Val Phe Val Pro Thr Ala Glu Ser Ser Ala Gln Pro Val Val Leu Gly  
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 gtg gat cac agt tct gca gcc ggt act gtg cac tta gta cct ctg tcg 1063  
 Val Asp His Ser Ser Ala Ala Gly Thr Val His Leu Val Pro Leu Ser  
 330 335 340  
 gta gga gcc ctg atc ctc agc ctg gac tca gag gcc tgc tct ctg aag 1111  
 Val Gly Ala Leu Ile Leu Ser Leu Asp Ser Glu Ala Cys Ser Leu Lys  
 345 350 355  
 gag agc cta ccc ctc tca aaa att atc agt cct gtt gtt gag cca atg 1159  
 Glu Ser Leu Pro Leu Ser Lys Ile Ile Ser Pro Val Val Glu Pro Met  
 360 365 370 375  
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 Asn Thr Gly Val Gln Val Asn Leu Gly Lys Ser Leu Cys Ser Pro Leu  
 380 385 390  
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 Gln Glu Val Gly Ser Val Cys Gln Arg Thr Ser Ile Ser Ser Ser Asn  
 395 400 405  
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 Val Gln Thr Asp Leu Thr Tyr Ala Ser Ala Asn Leu Ile Pro Ser Ala  
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 Gln Trp Leu Gly Pro Asp Ser Ser Val Ser Ser Cys Ser Gln Thr Asp  
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 ctg tcg ttt gat tct caa gtg tcc ctt cct gtt agt gtc cac acc cag 1399  
 Leu Ser Phe Asp Ser Gln Val Ser Leu Pro Val Ser Val His Thr Gln  
 440 445 450 455  
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Thr Leu Val Pro Ser Ser Lys Val Thr Ser Ser Ile Ala Ala Gln Thr  
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 gat gca ttt ata gac gcc tgt ttc cag cct ggt ggg gtc tcc agg gaa 1495  
 Asp Ala Phe Ile Asp Ala Cys Phe Gln Pro Gly Gly Val Ser Arg Glu  
 475 480 485  
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 Thr Gln Thr Ser Arg Met Gln Asn Arg Thr Asn Asp Ser Val Pro Val  
 490 495 500  
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 Gly His Thr Gly Leu Cys Gly Asp Ile Phe Glu Ser Val His Ala Ser  
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 Tyr Ser Val Pro Thr Asp Thr Ile Met Ser Ser Ser Leu Val Ala Glu  
 520 525 530 535  
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 Thr Gly Thr His Gly Leu Pro Pro Gln Ser Asp Pro Lys Ile Leu Gly  
 540 545 550  
 caa gtc atg gaa aag tct gca ccc gtg tta aac ttc agc acc cag aac 1735  
 Gln Val Met Glu Lys Ser Ala Pro Val Leu Asn Phe Ser Thr Gln Asn  
 555 560 565  
 ggc ttg ctt cct gca cac acc atg aca gat aat cag acc caa acc ata 1783  
 Gly Leu Leu Pro Ala His Thr Met Thr Asp Asn Gln Thr Gln Thr Ile  
 570 575 580  
 gat ctg ctg agc gac ttg gaa aac atc ttg tca agt aac ctg cca ggt 1831  
 Asp Leu Leu Ser Asp Leu Glu Asn Ile Leu Ser Ser Asn Leu Pro Gly  
 585 590 595  
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Gln Thr Leu Asp Asn Arg Gly Leu Leu Ser Asp Thr Asn Pro Gly Pro	
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gac gcc cag ctc cca gct ggc tca gcg cag aat tct ggg att gat ttt	1927
Asp Ala Gln Leu Pro Ala Gly Ser Ala Gln Asn Ser Gly Ile Asp Phe	
620	625
630	
gat att gaa gag ttc ctc tca gcc tcc aat atc cag act cag act gag	1975
Asp Ile Glu Glu Phe Leu Ser Ala Ser Asn Ile Gln Thr Gln Thr Glu	
635	640
645	
gag agt gag ctc agc tcc atg agc act gag ccg gtc ctg gag tcc ctg	2023
Glu Ser Glu Leu Ser Ser Met Ser Thr Glu Pro Val Leu Glu Ser Leu	
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gac atc gag acg cag acc gac gtc ctc ctc tca gat ccc tcc aca cag	2071
Asp Ile Glu Thr Gln Thr Asp Val Leu Leu Ser Asp Pro Ser Thr Gln	
665	670
675	
ccc tat ggc ttc aga gcg ggg tca ggc ttc ctg ggc ctt gag atg ttc	2119
Pro Tyr Gly Phe Arg Ala Gly Ser Gly Phe Leu Gly Leu Glu Met Phe	
680	685
690	695
gac aca cag aca caa aca gac tta aac ttc ttc tta gac agt agt cct	2167
Asp Thr Gln Thr Gln Thr Asp Leu Asn Phe Phe Leu Asp Ser Ser Pro	
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710	
cac ctg ccc ctg ggc agc atc ctg aaa cac tcc agc ttc tcc atg agt	2215
His Leu Pro Leu Gly Ser Ile Leu Lys His Ser Ser Phe Ser Met Ser	
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acc gac tcc tct gac aca gag acc caa act gaa gga gcc tgc cct gct	2263
Thr Asp Ser Ser Asp Thr Glu Thr Gln Thr Glu Gly Ala Cys Pro Ala	
730	735
740	
cgg cac ctg cct gct ctg gag agc aag gtc cag ttg agc agc aca gaa	2311

Arg His Leu Pro Ala Leu Glu Ser Lys Val Gln Leu Ser Ser Thr Glu  
 745 750 755  
 aca caa acc atg agt tct ggc ttc gag ccc ctg ggg aac ttg ttc ctc 2359  
 Thr Gln Thr Met Ser Ser Gly Phe Glu Pro Leu Gly Asn Leu Phe Leu  
 760 765 770 775  
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 Leu Ala Trp Asn Thr Met Glu Ser Gln Phe Ser Ser Val Glu Thr Gln  
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 Thr Cys Ala Glu Leu His Ala Val Ser Ser Phe  
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 tcagtggggc agctgttttag attctcttca gttcttggtg ttttgtactc gtgaccacaa 2628  
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&lt;210&gt; 40

&lt;211&gt; 818

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 40

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Ser Pro Trp Arg Pro Pro Glu Ser Arg Leu Gln Gly Ser Arg Pro Arg  
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 Pro Ala Arg Ala Arg Ala Ala Ala Pro Val Pro Pro Ala Arg Glu Leu  
 50 55 60  
 Ile Gln Pro Thr Val Ser Glu Leu Ser Arg Ala Val Arg Thr Asn Ile  
 65 70 75 80  
 Leu Cys Thr Val Arg Gly Cys Gly Lys Ile Leu Pro Asn Ser Pro Ala  
 85 90 95  
 Leu Asn Met His Leu Val Lys Ser His Arg Leu Gln Asp Gly Ile Val  
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 Asn Pro Thr Ile Arg Lys Asp Leu Thr Thr Ala Pro Lys Phe Tyr Cys  
 115 120 125  
 Cys Pro Ile Lys Gly Cys Pro Arg Gly Pro Asp Arg Pro Phe Ser Gln  
 130 135 140  
 Phe Ser Leu Val Lys Gln His Phe Met Lys Met His Ala Glu Lys Lys  
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 His Lys Cys Ser Lys Cys Ser Asn Ser Tyr Gly Thr Glu Trp Asp Leu  
 165 170 175  
 Lys Arg His Glu Glu Asp Cys Gly Lys Thr Phe Gln Cys Thr Cys Gly  
 180 185 190  
 Cys Pro Tyr Ala Ser Arg Thr Ala Leu Gln Ser His Ile Tyr Arg Thr  
 195 200 205  
 Gly His Glu Ile Pro Ala Glu His Arg Asp Pro Pro Ser Lys Lys Arg  
 210 215 220  
 Lys Met Glu Ser Tyr Leu Gln Asn Gln Lys Leu Ser Ser Lys Thr Thr  
 225 230 235 240  
 Glu Pro Leu Ser Asp Gln Ala Ala Pro Arg Gln Asp Ala Ala Glu Pro

245 250 255  
Asp Ala Pro Glu Val Lys Pro Ala Ala Ser Leu Glu Asp Ser Cys Ser  
260 265 270  
Ala His Thr Lys Lys Gln Ser Val Ala Thr Pro Pro Arg Cys Pro Gln  
275 280 285  
Lys Leu Leu Leu Pro Lys Pro Lys Val Ala Leu Val Lys Leu Pro Val  
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Met Gln Phe Ser Pro Val Pro Val Phe Val Pro Thr Ala Glu Ser Ser  
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325 330 335  
Val His Leu Val Pro Leu Ser Val Gly Ala Leu Ile Leu Ser Leu Asp  
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Ser Glu Ala Cys Ser Leu Lys Glu Ser Leu Pro Leu Ser Lys Ile Ile  
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Ser Pro Val Val Glu Pro Met Asn Thr Gly Val Gln Val Asn Leu Gly  
370 375 380  
Lys Ser Leu Cys Ser Pro Leu Gln Glu Val Gly Ser Val Cys Gln Arg  
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Thr Ser Ile Ser Ser Ser Asn Val Gln Thr Asp Leu Thr Tyr Ala Ser  
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Ala Asn Leu Ile Pro Ser Ala Gln Trp Leu Gly Pro Asp Ser Ser Val  
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450 455 460

Ser Ser Ile Ala Ala Gln Thr Asp Ala Phe Ile Asp Ala Cys Phe Gln  
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 Pro Gly Gly Val Ser Arg Glu Thr Gln Thr Ser Arg Met Gln Asn Arg  
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 Thr Asn Asp Ser Val Pro Val Gly His Thr Gly Leu Cys Gly Asp Ile  
                          500                      505                      510  
 Phe Glu Ser Val His Ala Ser Tyr Ser Val Pro Thr Asp Thr Ile Met  
                          515                      520                      525  
 Ser Ser Ser Leu Val Ala Glu Thr Gly Thr His Gly Leu Pro Pro Gln  
                          530                      535                      540  
 Ser Asp Pro Lys Ile Leu Gly Gln Val Met Glu Lys Ser Ala Pro Val  
 545                      550                      555                      560  
 Leu Asn Phe Ser Thr Gln Asn Gly Leu Leu Pro Ala His Thr Met Thr  
                          565                      570                      575  
 Asp Asn Gln Thr Gln Thr Ile Asp Leu Leu Ser Asp Leu Glu Asn Ile  
                          580                      585                      590  
 Leu Ser Ser Asn Leu Pro Gly Gln Thr Leu Asp Asn Arg Gly Leu Leu  
                          595                      600                      605  
 Ser Asp Thr Asn Pro Gly Pro Asp Ala Gln Leu Pro Ala Gly Ser Ala  
                          610                      615                      620  
 Gln Asn Ser Gly Ile Asp Phe Asp Ile Glu Glu Phe Leu Ser Ala Ser  
 625                      630                      635                      640  
 Asn Ile Gln Thr Gln Thr Glu Glu Ser Glu Leu Ser Ser Met Ser Thr  
                          645                      650                      655  
 Glu Pro Val Leu Glu Ser Leu Asp Ile Glu Thr Gln Thr Asp Val Leu  
                          660                      665                      670  
 Leu Ser Asp Pro Ser Thr Gln Pro Tyr Gly Phe Arg Ala Gly Ser Gly

675                      680                      685  
 Phe Leu Gly Leu Glu Met Phe Asp Thr Gln Thr Gln Thr Asp Leu Asn  
 690                      695                      700  
 Phe Phe Leu Asp Ser Ser Pro His Leu Pro Leu Gly Ser Ile Leu Lys  
 705                      710                      715                      720  
 His Ser Ser Phe Ser Met Ser Thr Asp Ser Ser Asp Thr Glu Thr Gln  
 725                      730                      735  
 Thr Glu Gly Ala Cys Pro Ala Arg His Leu Pro Ala Leu Glu Ser Lys  
 740                      745                      750  
 Val Gln Leu Ser Ser Thr Glu Thr Gln Thr Met Ser Ser Gly Phe Glu  
 755                      760                      765  
 Pro Leu Gly Asn Leu Phe Leu Thr Ser Asn Glu Thr Gln Thr Ala Met  
 770                      775                      780  
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<210> 41

<211> 2700

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25).. (2493)

<400> 41

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 Ala Gly Ser Ala Ala Leu Ala Ala Gly Ala Arg Ala Val Pro Ala Ala  
 10 15 20 25  
 acg aca gga gcc gcc gcc gcc gcc tcg ggc ccg tgg gtg ccc ccg gga 147  
 Thr Thr Gly Ala Ala Ala Ala Ala Ser Gly Pro Trp Val Pro Pro Gly  
 30 35 40  
 ccc cga ctg agg ggc agc cgg ccg cgg ccc gcg ggg gcg acg cag cag 195  
 Pro Arg Leu Arg Gly Ser Arg Pro Arg Pro Ala Gly Ala Thr Gln Gln  
 45 50 55  
 ccc gct gtc ccc gcg ccg ccg gcg ggg gag ctg atc cag ccg tcg gtg 243  
 Pro Ala Val Pro Ala Pro Pro Ala Gly Glu Leu Ile Gln Pro Ser Val  
 60 65 70  
 agc gag ctg tcc cgg gcc gtg cgg acc aac atc ctg tgc acc gtg cgc 291  
 Ser Glu Leu Ser Arg Ala Val Arg Thr Asn Ile Leu Cys Thr Val Arg  
 75 80 85  
 ggc tgc ggc aag atc ctg ccc aac agc ccc gcg ctc aac atg cac cta 339  
 Gly Cys Gly Lys Ile Leu Pro Asn Ser Pro Ala Leu Asn Met His Leu  
 90 95 100 105  
 gtc aag agc cac cgc ctg cag gat ggc ata gtc aat cca aca ata aga 387  
 Val Lys Ser His Arg Leu Gln Asp Gly Ile Val Asn Pro Thr Ile Arg  
 110 115 120  
 aaa gat ttg aaa act gga ccg aaa ttc tac tgc tgt cca att gaa ggc 435  
 Lys Asp Leu Lys Thr Gly Pro Lys Phe Tyr Cys Cys Pro Ile Glu Gly  
 125 130 135

tgc ccc aga ggc cct gag aga ccg ttt tct cag ttt tct ctc gta aaa	483
Cys Pro Arg Gly Pro Glu Arg Pro Phe Ser Gln Phe Ser Leu Val Lys	
140 145 150	
cag cac ttt atg aaa atg cat gct gag aag aag cac aaa tgt agt aag	531
Gln His Phe Met Lys Met His Ala Glu Lys Lys His Lys Cys Ser Lys	
155 160 165	
tgc agc aat tcg tac ggt aca gaa tgg gac ctg aaa aga cat gca gag	579
Cys Ser Asn Ser Tyr Gly Thr Glu Trp Asp Leu Lys Arg His Ala Glu	
170 175 180 185	
gac tgt ggc aag acc ttc cgg tgc aca tgc ggc tgt ccc tac gcc agt	627
Asp Cys Gly Lys Thr Phe Arg Cys Thr Cys Gly Cys Pro Tyr Ala Ser	
190 195 200	
aga aca gca ctg cag tct cac atc tac cga act ggg cac gag ata cct	675
Arg Thr Ala Leu Gln Ser His Ile Tyr Arg Thr Gly His Glu Ile Pro	
205 210 215	
gca gaa cac agg gac cca cct agt aag aaa agg aaa atg gaa aac tgt	723
Ala Glu His Arg Asp Pro Pro Ser Lys Lys Arg Lys Met Glu Asn Cys	
220 225 230	
gca caa aac cag aag tta tcc aac aag acc att gaa tca ttg aac aac	771
Ala Gln Asn Gln Lys Leu Ser Asn Lys Thr Ile Glu Ser Leu Asn Asn	
235 240 245	
caa cca atc cct aga cca gac act caa gaa cta gaa gct tca gaa ata	819
Gln Pro Ile Pro Arg Pro Asp Thr Gln Glu Leu Glu Ala Ser Glu Ile	
250 255 260 265	
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Lys Leu Glu Pro Ser Phe Glu Asp Ser Cys Gly Ser Asn Thr Asp Lys	
270 275 280	

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 Gln Thr Leu Thr Thr Pro Pro Arg Tyr Pro Gln Lys Leu Leu Leu Pro  
 285 290 295  
 aag ccc aaa gtg gct ttg gtt aaa cta ccc gtg atg cag ttt tct gtc 963  
 Lys Pro Lys Val Ala Leu Val Lys Leu Pro Val Met Gln Phe Ser Val  
 300 305 310  
 atg cct gtc ttt gtg cct aca gcc gac tcc tca gcc cag cct gtg gtg 1011  
 Met Pro Val Phe Val Pro Thr Ala Asp Ser Ser Ala Gln Pro Val Val  
 315 320 325  
 tta ggt gtt gat cag ggc tct gcc aca ggg gct gtg cac tta atg ccc 1059  
 Leu Gly Val Asp Gln Gly Ser Ala Thr Gly Ala Val His Leu Met Pro  
 330 335 340 345  
 ttg tca gta gga acc ctg atc ctc ggc cta gat tca gag gct tgc tct 1107  
 Leu Ser Val Gly Thr Leu Ile Leu Gly Leu Asp Ser Glu Ala Cys Ser  
 350 355 360  
 ctt aag gag agc cta cct ctt ttc aaa att gct aat cct att gct ggt 1155  
 Leu Lys Glu Ser Leu Pro Leu Phe Lys Ile Ala Asn Pro Ile Ala Gly  
 365 370 375  
 gag cca ata agt act ggt gtt caa gtg aac ttt ggt aaa agt cca tct 1203  
 Glu Pro Ile Ser Thr Gly Val Gln Val Asn Phe Gly Lys Ser Pro Ser  
 380 385 390  
 aat cct tta caa gaa cta ggg aac acg tgt caa aag aat agc att tct 1251  
 Asn Pro Leu Gln Glu Leu Gly Asn Thr Cys Gln Lys Asn Ser Ile Ser  
 395 400 405  
 tca atc aac gtg cag aca gat ctg tct tat gcc tca caa aac ttt ata 1299  
 Ser Ile Asn Val Gln Thr Asp Leu Ser Tyr Ala Ser Gln Asn Phe Ile  
 410 415 420 425

cct tct gca cag tgg gcc act gct gat tcc tct gtg tgg tct tgt tct	1347
Pro Ser Ala Gln Trp Ala Thr Ala Asp Ser Ser Val Ser Ser Cys Ser	
430 435 440	
caa act gat ttg tgg ttt gat tct caa gtg tct ctt ccc att agt gtt	1395
Gln Thr Asp Leu Ser Phe Asp Ser Gln Val Ser Leu Pro Ile Ser Val	
445 450 455	
cac act cag aca ttt ttg ccc agc tct aag gta act tca tct ata gct	1443
His Thr Gln Thr Phe Leu Pro Ser Ser Lys Val Thr Ser Ser Ile Ala	
460 465 470	
gct cag act gat gca ttt atg gac acc tgt ttc cag tca ggt ggg gtc	1491
Ala Gln Thr Asp Ala Phe Met Asp Thr Cys Phe Gln Ser Gly Gly Val	
475 480 485	
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Ser Arg Glu Thr Gln Thr Ser Gly Ile Glu Ser Pro Thr Asp Asp His	
490 495 500 505	
gta cag atg gac caa gct gga atg tgc gga gac att ttt gag agt gtt	1587
Val Gln Met Asp Gln Ala Gly Met Cys Gly Asp Ile Phe Glu Ser Val	
510 515 520	
cat tca tca tat aat gtt gct aca ggt aac att ata agc aac agt tta	1635
His Ser Ser Tyr Asn Val Ala Thr Gly Asn Ile Ile Ser Asn Ser Leu	
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Val Ala Glu Thr Val Thr His Ser Leu Leu Pro Gln Asn Glu Pro Lys	
540 545 550	
act tta aat caa gat att gag aaa tct gca cca att ata aat ttc agt	1731
Thr Leu Asn Gln Asp Ile Glu Lys Ser Ala Pro Ile Ile Asn Phe Ser	
555 560 565	



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 caa acc ata gat tta tta agt gat ttg gaa aac atc ttg tca agt aat 1827  
 Gln Thr Ile Asp Leu Leu Ser Asp Leu Glu Asn Ile Leu Ser Ser Asn  
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 ctg cct gcc cag aca ttg gat cat cgt agt ctt ttg tct gac aca aat 1875  
 Leu Pro Ala Gln Thr Leu Asp His Arg Ser Leu Leu Ser Asp Thr Asn  
 605 610 615  
 cct gga cct gac acc cag ctc cca tct ggc cca gcc cag aac ccc gga 1923  
 Pro Gly Pro Asp Thr Gln Leu Pro Ser Gly Pro Ala Gln Asn Pro Gly  
 620 625 630  
 atc gat ttt gat atc gaa gag ttc ttt tcg gcc tca aat atc cag act 1971  
 Ile Asp Phe Asp Ile Glu Glu Phe Phe Ser Ala Ser Asn Ile Gln Thr  
 635 640 645  
 caa act gaa gag agt gaa ctt agc acc atg acc acc gag cca gtc ttg 2019  
 Gln Thr Glu Glu Ser Glu Leu Ser Thr Met Thr Thr Glu Pro Val Leu  
 650 655 660 665  
 gag tca ctg gac ata gag act caa acg gac ttc tta ctc gca gat acc 2067  
 Glu Ser Leu Asp Ile Glu Thr Gln Thr Asp Phe Leu Leu Ala Asp Thr  
 670 675 680  
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 Ser Ala Gln Ser Tyr Gly Cys Arg Gly Asn Ser Asn Phe Leu Gly Leu  
 685 690 695  
 gag atg ttt gac aca cag aca cag aca gac tta aac ttt ttc tta gac 2163  
 Glu Met Phe Asp Thr Gln Thr Gln Thr Asp Leu Asn Phe Phe Leu Asp  
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agt agc cct cat ctg cct ctg gga agt att ctg aaa cac tcc agc ttt 2211  
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 715 720 725  
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 730 735 740 745  
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 750 755 760  
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 765 770 775  
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&lt;210&gt; 42

&lt;211&gt; 823

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

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20 25 30

Ala Ser Gly Pro Trp Val Pro Pro Gly Pro Arg Leu Arg Gly Ser Arg

35 40 45

Pro Arg Pro Ala Gly Ala Thr Gln Gln Pro Ala Val Pro Ala Pro Pro

50 55 60

Ala Gly Glu Leu Ile Gln Pro Ser Val Ser Glu Leu Ser Arg Ala Val

65 70 75 80

Arg Thr Asn Ile Leu Cys Thr Val Arg Gly Cys Gly Lys Ile Leu Pro

85 90 95

Asn Ser Pro Ala Leu Asn Met His Leu Val Lys Ser His Arg Leu Gln

100 105 110

Asp Gly Ile Val Asn Pro Thr Ile Arg Lys Asp Leu Lys Thr Gly Pro

115 120 125

Lys Phe Tyr Cys Cys Pro Ile Glu Gly Cys Pro Arg Gly Pro Glu Arg

130 135 140

Pro Phe Ser Gln Phe Ser Leu Val Lys Gln His Phe Met Lys Met His

145 150 155 160

Ala Glu Lys Lys His Lys Cys Ser Lys Cys Ser Asn Ser Tyr Gly Thr

165 170 175

Glu Trp Asp Leu Lys Arg His Ala Glu Asp Cys Gly Lys Thr Phe Arg

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Cys Thr Cys Gly Cys Pro Tyr Ala Ser Arg Thr Ala Leu Gln Ser His		
195	200	205
Ile Tyr Arg Thr Gly His Glu Ile Pro Ala Glu His Arg Asp Pro Pro		
210	215	220
Ser Lys Lys Arg Lys Met Glu Asn Cys Ala Gln Asn Gln Lys Leu Ser		
225	230	235
Asn Lys Thr Ile Glu Ser Leu Asn Asn Gln Pro Ile Pro Arg Pro Asp		
245	250	255
Thr Gln Glu Leu Glu Ala Ser Glu Ile Lys Leu Glu Pro Ser Phe Glu		
260	265	270
Asp Ser Cys Gly Ser Asn Thr Asp Lys Gln Thr Leu Thr Thr Pro Pro		
275	280	285
Arg Tyr Pro Gln Lys Leu Leu Leu Pro Lys Pro Lys Val Ala Leu Val		
290	295	300
Lys Leu Pro Val Met Gln Phe Ser Val Met Pro Val Phe Val Pro Thr		
305	310	315
Ala Asp Ser Ser Ala Gln Pro Val Val Leu Gly Val Asp Gln Gly Ser		
325	330	335
Ala Thr Gly Ala Val His Leu Met Pro Leu Ser Val Gly Thr Leu Ile		
340	345	350
Leu Gly Leu Asp Ser Glu Ala Cys Ser Leu Lys Glu Ser Leu Pro Leu		
355	360	365
Phe Lys Ile Ala Asn Pro Ile Ala Gly Glu Pro Ile Ser Thr Gly Val		
370	375	380
Gln Val Asn Phe Gly Lys Ser Pro Ser Asn Pro Leu Gln Glu Leu Gly		

385	390	395	400
Asn Thr Cys Gln Lys Asn Ser Ile Ser Ser Ile Asn Val Gln Thr Asp			
	405	410	415
Leu Ser Tyr Ala Ser Gln Asn Phe Ile Pro Ser Ala Gln Trp Ala Thr			
	420	425	430
Ala Asp Ser Ser Val Ser Ser Cys Ser Gln Thr Asp Leu Ser Phe Asp			
	435	440	445
Ser Gln Val Ser Leu Pro Ile Ser Val His Thr Gln Thr Phe Leu Pro			
	450	455	460
Ser Ser Lys Val Thr Ser Ser Ile Ala Ala Gln Thr Asp Ala Phe Met			
465	470	475	480
Asp Thr Cys Phe Gln Ser Gly Gly Val Ser Arg Glu Thr Gln Thr Ser			
	485	490	495
Gly Ile Glu Ser Pro Thr Asp Asp His Val Gln Met Asp Gln Ala Gly			
	500	505	510
Met Cys Gly Asp Ile Phe Glu Ser Val His Ser Ser Tyr Asn Val Ala			
	515	520	525
Thr Gly Asn Ile Ile Ser Asn Ser Leu Val Ala Glu Thr Val Thr His			
	530	535	540
Ser Leu Leu Pro Gln Asn Glu Pro Lys Thr Leu Asn Gln Asp Ile Glu			
545	550	555	560
Lys Ser Ala Pro Ile Ile Asn Phe Ser Ala Gln Asn Ser Met Leu Pro			
	565	570	575
Ser Gln Asn Met Thr Asp Asn Gln Thr Gln Thr Ile Asp Leu Leu Ser			
	580	585	590
Asp Leu Glu Asn Ile Leu Ser Ser Asn Leu Pro Ala Gln Thr Leu Asp			
	595	600	605

His Arg Ser Leu Leu Ser Asp Thr Asn Pro Gly Pro Asp Thr Gln Leu  
 610 615 620  
 Pro Ser Gly Pro Ala Gln Asn Pro Gly Ile Asp Phe Asp Ile Glu Glu  
 625 630 635 640  
 Phe Phe Ser Ala Ser Asn Ile Gln Thr Gln Thr Glu Glu Ser Glu Leu  
 645 650 655  
 Ser Thr Met Thr Thr Glu Pro Val Leu Glu Ser Leu Asp Ile Glu Thr  
 660 665 670  
 Gln Thr Asp Phe Leu Leu Ala Asp Thr Ser Ala Gln Ser Tyr Gly Cys  
 675 680 685  
 Arg Gly Asn Ser Asn Phe Leu Gly Leu Glu Met Phe Asp Thr Gln Thr  
 690 695 700  
 Gln Thr Asp Leu Asn Phe Phe Leu Asp Ser Ser Pro His Leu Pro Leu  
 705 710 715 720  
 Gly Ser Ile Leu Lys His Ser Ser Phe Ser Val Ser Thr Asp Ser Ser  
 725 730 735  
 Asp Thr Glu Thr Gln Thr Glu Gly Val Ser Thr Ala Lys Asn Ile Pro  
 740 745 750  
 Ala Leu Glu Ser Lys Val Gln Leu Asn Ser Thr Glu Thr Gln Thr Met  
 755 760 765  
 Ser Ser Gly Phe Glu Thr Leu Gly Ser Leu Phe Phe Thr Ser Asn Glu  
 770 775 780  
 Thr Gln Thr Ala Met Asp Asp Phe Leu Leu Ala Asp Leu Ala Trp Asn  
 785 790 795 800  
 Thr Met Glu Ser Gln Phe Ser Ser Val Glu Thr Gln Thr Ser Ala Glu  
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820

&lt;210&gt; 43

&lt;211&gt; 2845

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1609)

&lt;400&gt; 43

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                                     Met Thr Phe Ala Glu
                                     1           5
gac aag acc tat aag tat atc cga gac aac cac agc aag ttt tgc tgt 163
Asp Lys Thr Tyr Lys Tyr Ile Arg Asp Asn His Ser Lys Phe Cys Cys
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gtt gac gtt ctg gag atc ctg cct tac ctg tcc tgc ctc aca gct agt 211
Val Asp Val Leu Glu Ile Leu Pro Tyr Leu Ser Cys Leu Thr Ala Ser
                25                30                35
gac cag gat cga ctg cgg gct tcc tac agg cag atc ggg aac cgg gac 259
Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln Ile Gly Asn Arg Asp
                40                45                50
aca ctc tgg gga ctc ttc aat aat ctc cag cgc cgg cct ggc tgg gtg 307
Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg Arg Pro Gly Trp Val
                55                60                65
gag gtc ttc atc cgg gca ctg cag atc tgt gag ctg cct ggg ctg tct 355

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Ala Thr Tyr Gly Pro Val Ser Pro Thr Val Ser Phe Gln Pro Leu Pro  
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 Arg Thr Ala Leu Arg Thr Asn Leu Leu Ser Gly Val Thr Val Ser Ala  
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 Ala Lys Gly Ala Gly Asp Gln Ala Lys Ala Ala Thr Cys Phe Ser Thr  
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 Thr Leu Thr Asn Ser Val Thr Thr Ser Ser Ala Pro Ser Pro Arg Leu  
 280 285 290  
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 Val Pro Val Lys Thr Met Ser Ser Lys Leu Pro Leu Ser Ser Lys Ser  
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 Ala Ser Val Ala Lys Ala Pro Ala Asn Thr Ile Pro Pro Glu Arg Asn  
 345 350 355  
 agc aag caa gcc aag gag acc ccg gag ggt cca gca acc aaa gtc acc 1219

Ser Lys Gln Ala Lys Glu Thr Pro Glu Gly Pro Ala Thr Lys Val Thr  
 360 365 370  
 act gga ggc aac cag act gga cca aat agc agt atc agg agc ttg cac 1267  
 Thr Gly Gly Asn Gln Thr Gly Pro Asn Ser Ser Ile Arg Ser Leu His  
 375 380 385  
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 Ser Gly Pro Glu Met Ser Lys Pro Gly Val Leu Val Ser Gln Leu Asp  
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 gag cca ttc tca gcc tgc tct gtg gac ctt gcc att agc cct agc agc 1363  
 Glu Pro Phe Ser Ala Cys Ser Val Asp Leu Ala Ile Ser Pro Ser Ser  
 410 415 420  
 tcc ttg gtc tca gaa ccc aac cat ggt cca gag gag aat gag tat tcg 1411  
 Ser Leu Val Ser Glu Pro Asn His Gly Pro Glu Glu Asn Glu Tyr Ser  
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 Ser Phe Arg Ile Gln Val Asp Glu Ser Pro Ser Ala Asp Leu Leu Gly  
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 Ser Pro Glu Pro Leu Ala Thr Gln Gln Pro Gln Glu Glu Glu Glu His  
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 Cys Ala Ser Ser Met Pro Trp Ala Lys Trp Leu Gly Ala Thr Ser Ala  
 470 475 480 485  
 ctc ttg gct gta ttc ctg gca gtg atg ctg tac cgt agt agg cgc ctg 1603  
 Leu Leu Ala Val Phe Leu Ala Val Met Leu Tyr Arg Ser Arg Arg Leu  
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 gcc cag tgaagcctca gctgtatgct gttctcttgc tcagttctgc caagcatggt 1659

Ala Gln

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&lt;210&gt; 44

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 44

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Cys Leu Thr Ala Ser Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln  
35 40 45  
Ile Gly Asn Arg Asp Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg  
50 55 60  
Arg Pro Gly Trp Val Glu Val Phe Ile Arg Ala Leu Gln Ile Cys Glu  
65 70 75 80  
Leu Pro Gly Leu Ser Asp Gln Val Thr Arg Val Tyr Gln Ser Tyr Leu  
85 90 95  
Pro Pro Gly Thr Ser Leu Arg Ser Leu Glu Pro Leu Gln Leu Pro Asp  
100 105 110  
Phe Pro Ala Ala Val Ser Gly Pro Ser Ala Phe Ala Pro Gly His Asn  
115 120 125  
Ile Pro Gly His Gly Leu Arg Glu Thr Pro Ser Cys Pro Lys Pro Val  
130 135 140  
Gln Asp Thr Gln Pro Pro Glu Ser Pro Val Glu Asn Ser Glu Gln Leu  
145 150 155 160  
Leu Gln Thr Asn Ser Gly Ala Val Ala Arg Met Ser Gly Gly Ser Leu  
165 170 175  
Ile Pro Ser Pro Asn Gln Gln Ala Leu Ser Pro Gln Pro Ser Arg Glu  
180 185 190  
His Gln Glu Gln Glu Pro Glu Leu Gly Gly Ala His Ala Ala Asn Val  
195 200 205  
Ala Ser Val Pro Ile Ala Thr Tyr Gly Pro Val Ser Pro Thr Val Ser

210	215	220	
Phe Gln Pro Leu Pro Arg Thr Ala Leu Arg Thr Asn Leu Leu Ser Gly			
225	230	235	240
Val Thr Val Ser Ala Leu Ser Ala Asp Thr Ser Leu Ser Ser Ser Ser			
	245	250	255
Thr Gly Ser Ala Phe Ala Lys Gly Ala Gly Asp Gln Ala Lys Ala Ala			
	260	265	270
Thr Cys Phe Ser Thr Thr Leu Thr Asn Ser Val Thr Thr Ser Ser Ala			
	275	280	285
Pro Ser Pro Arg Leu Val Pro Val Lys Thr Met Ser Ser Lys Leu Pro			
	290	295	300
Leu Ser Ser Lys Ser Thr Ala Ala Met Thr Ser Thr Val Leu Thr Asn			
305	310	315	320
Thr Ala Pro Ser Lys Leu Pro Ser Asn Ser Val Tyr Ala Gly Thr Val			
	325	330	335
Pro Ser Arg Val Pro Ala Ser Val Ala Lys Ala Pro Ala Asn Thr Ile			
	340	345	350
Pro Pro Glu Arg Asn Ser Lys Gln Ala Lys Glu Thr Pro Glu Gly Pro			
	355	360	365
Ala Thr Lys Val Thr Thr Gly Gly Asn Gln Thr Gly Pro Asn Ser Ser			
	370	375	380
Ile Arg Ser Leu His Ser Gly Pro Glu Met Ser Lys Pro Gly Val Leu			
385	390	395	400
Val Ser Gln Leu Asp Glu Pro Phe Ser Ala Cys Ser Val Asp Leu Ala			
	405	410	415
Ile Ser Pro Ser Ser Ser Leu Val Ser Glu Pro Asn His Gly Pro Glu			
	420	425	430

Glu Asn Glu Tyr Ser Ser Phe Arg Ile Gln Val Asp Glu Ser Pro Ser  
                   435                                  440                                  445  
 Ala Asp Leu Leu Gly Ser Pro Glu Pro Leu Ala Thr Gln Gln Pro Gln  
                   450                                  455                                  460  
 Glu Glu Glu Glu His Cys Ala Ser Ser Met Pro Trp Ala Lys Trp Leu  
 465                                  470                                  475                                  480  
 Gly Ala Thr Ser Ala Leu Leu Ala Val Phe Leu Ala Val Met Leu Tyr  
                                   485                                  490                                  495  
 Arg Ser Arg Arg Leu Ala Gln  
                                   500

<210> 45

<211> 3929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129).. (1748)

<400> 45

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 gtctcgtttc ctctcagtcc atccaccctt catggggcca gagccctctc tccagaatct 120  
 gagcagca atg ccg ttt gct gaa gac aag acc tat aag tat atc tgc cgc 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg

1

5

10

aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg cct tac 218

Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr

15

20

25

30

ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc acc tgc	266
Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys	
35 40 45	
aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat acc ctt	314
Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu	
50 55 60	
cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg agg ggc	362
Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly	
65 70 75	
tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac cag agc	410
Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser	
80 85 90	
tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag cca ccg	458
Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro	
95 100 105 110	
tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg gcc cac	506
Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His	
115 120 125	
agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac ccc atg	554
Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met	
130 135 140	
cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat tca gag	602
Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu	
145 150 155	
caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat cca gat	650
Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp	
160 165 170	

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 Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu  
 175 180 185 190  
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 Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His  
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 Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser  
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 Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser  
 225 230 235  
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 Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe  
 240 245 250  
 tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag ggt aaa 938  
 Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys  
 255 260 265 270  
 cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc agt ggg 986  
 Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly  
 275 280 285  
 gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc acc ttg 1034  
 Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu  
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 atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca gca tct 1082  
 Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser  
 305 310 315



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 Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly  
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 Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser  
 355 360 365  
 atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac ggg agc 1274  
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 Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr  
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 Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser  
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 450 455 460

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&lt;211&gt; 540

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

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Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu  
35 40 45  
Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg  
50 55 60  
Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu  
65 70 75 80  
Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln  
85 90 95  
Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu  
100 105 110  
Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile  
115 120 125  
Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val  
130 135 140  
Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala  
145 150 155 160  
Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly  
165 170 175  
Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser

180	185	190
Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala		
195	200	205
Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser		
210	215	220
Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu		
225	230	235
Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser		
245	250	255
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly		
260	265	270
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu		
275	280	285
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro		
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Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser		
305	310	315
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val		
325	330	335
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn		
340	345	350
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val		
355	360	365
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg		
370	375	380
Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly		
385	390	395
		400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser  
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Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe  
420 425 430  
Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly  
435 440 445  
Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly  
450 455 460  
Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu  
465 470 475 480  
Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln  
485 490 495  
Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser  
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Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val  
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Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His  
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<210> 47

<211> 3173

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (144).. (2108)

<400> 47

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 caggaacctt cactggaaga gca atg gct gcg gct gca gca gct tct cac ctg 173

Met Ala Ala Ala Ala Ala Ala Ser His Leu

1 5 10  
 aac ctg gat gcc ctc cgg gaa gtg cta gaa tgt ccc atc tgc atg gag 221  
 Asn Leu Asp Ala Leu Arg Glu Val Leu Glu Cys Pro Ile Cys Met Glu

15 20 25  
 tcc ttc act gaa gag cag ctg cga ccc aag ctg ctg cac tgt ggc cat 269  
 Ser Phe Thr Glu Glu Gln Leu Arg Pro Lys Leu Leu His Cys Gly His

30 35 40  
 acc atc tgc cgc cag tgt ctg gag aag ctc ctg gcc agc agc atc aat 317  
 Thr Ile Cys Arg Gln Cys Leu Glu Lys Leu Leu Ala Ser Ser Ile Asn

45 50 55  
 ggc gtc cgc tgc ccc ttt tgc agc aag att act cgc atc acc agc ctg 365  
 Gly Val Arg Cys Pro Phe Cys Ser Lys Ile Thr Arg Ile Thr Ser Leu

60 65 70  
 acc cag ctg acc gac aac ctg acg gtg ctg aag atc att gac aca gct 413  
 Thr Gln Leu Thr Asp Asn Leu Thr Val Leu Lys Ile Ile Asp Thr Ala

75 80 85 90  
 ggg ctc agt gag gcc gtc ggc ctg ctc atg tgc cga ggc tgt ggc cgg 461  
 Gly Leu Ser Glu Ala Val Gly Leu Leu Met Cys Arg Gly Cys Gly Arg

95 100 105  
 cgg ctg cct cgg cag ttc tgc cga agc tgt ggt gtg gtg ttg tgt gaa 509  
 Arg Leu Pro Arg Gln Phe Cys Arg Ser Cys Gly Val Val Leu Cys Glu

110 115 120  
 ccc tgc cgg gag gca gat cac caa ccc cct ggc cac tgc aca ctt ccg 557

Pro Cys Arg Glu Ala Asp His Gln Pro Pro Gly His Cys Thr Leu Pro  
 125 130 135  
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 Val Lys Glu Ala Ala Glu Glu Arg Arg Arg Asp Phe Gly Glu Lys Leu  
 140 145 150  
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 Thr Arg Leu Arg Glu Leu Thr Gly Glu Leu Gln Arg Arg Lys Ala Ala  
 155 160 165 170  
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 Leu Glu Gly Val Ser Arg Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu  
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 Gln Glu Tyr Gly His Glu Glu Arg Arg Ile Gln Glu Glu Leu Ala Arg  
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 Ser Gln Val Val Glu Glu Gln Ser Tyr Leu Leu Asn Ile Ala Glu Val  
 220 225 230  
 cag gcc gtg tct cgc tgt gac tac ttt cta gcg aag atc aag caa gct 893  
 Gln Ala Val Ser Arg Cys Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala  
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 Asp Val Ala Leu Leu Glu Glu Ala Ala Asp Glu Glu Glu Pro Glu Leu  
 255 260 265  
 act gcc agc cta ccc cgg gag ctt acc ctg caa gat gtg gag ctc ctt 989



Thr Ala Ser Leu Pro Arg Glu Leu Thr Leu Gln Asp Val Glu Leu Leu  
 270 275 280  
 aag gta gga cac gtt ggt cct ctg caa att ggc cag gct gtt aag aag 1037  
 Lys Val Gly His Val Gly Pro Leu Gln Ile Gly Gln Ala Val Lys Lys  
 285 290 295  
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 cct gag gaa gta gct ccc agc cct agg gct tcc ccc gcg aaa cag cgg 1181  
 Pro Glu Glu Val Ala Pro Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg  
 335 340 345  
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 Ser Ser Glu Ala Ala Ser Gly Ile Gln Gln Cys Leu Phe Leu Lys Lys  
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 Met Gly Ala Lys Gly Ser Thr Pro Gly Met Phe Asn Leu Pro Val Ser  
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 Leu Tyr Val Thr Ser Gln Ser Glu Val Leu Val Ala Asp Arg Gly Asn  
 380 385 390  
 tat cgt atc caa gtg ttc aac cgc aaa ggc ttt ttg aag gag atc cgc 1373  
 Tyr Arg Ile Gln Val Phe Asn Arg Lys Gly Phe Leu Lys Glu Ile Arg  
 395 400 405 410  
 cgc agc ccc agc ggc att gat agc ttc gtg cta agc ttc ctt gga gcc 1421

Arg Ser Pro Ser Gly Ile Asp Ser Phe Val Leu Ser Phe Leu Gly Ala  
 415 420 425  
 gac ttg ccc aat ctc act cca ctt tca gtg gcc atg aac tgc cat ggg 1469  
 Asp Leu Pro Asn Leu Thr Pro Leu Ser Val Ala Met Asn Cys His Gly  
 430 435 440  
 ctg att ggt gtc act gat agc tac gac aac tcc ctt aaa gtc tat acc 1517  
 Leu Ile Gly Val Thr Asp Ser Tyr Asp Asn Ser Leu Lys Val Tyr Thr  
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 Trp Gly Ile Thr Ala Leu Pro Ser Gly Gln Phe Val Val Thr Asp Val  
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 Glu Gly Gly Lys Leu Trp Cys Phe Thr Val Asp Arg Gly Ala Gly Val  
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 Val Lys Tyr Ser Cys Leu Cys Ser Ala Val Arg Pro Lys Phe Val Thr  
 510 515 520  
 tgt gat gct gaa ggc aca gtc tac ttc acc caa ggc ttg ggg ctc aat 1757  
 Cys Asp Ala Glu Gly Thr Val Tyr Phe Thr Gln Gly Leu Gly Leu Asn  
 525 530 535  
 gtg gaa aac cga cag aat gaa cac cac ctg gag ggt ggc ttc tcc atc 1805  
 Val Glu Asn Arg Gln Asn Glu His His Leu Glu Gly Gly Phe Ser Ile  
 540 545 550  
 ggt tct gtt ggc ccc gat ggg cag ctg ggc cgg caa atc agc cac ttc 1853

Gly Ser Val Gly Pro Asp Gly Gln Leu Gly Arg Gln Ile Ser His Phe			
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ttc tct gag aat gaa gat ttc cgc tgc atc gct ggc atg tgt gta gat	1901		
Phe Ser Glu Asn Glu Asp Phe Arg Cys Ile Ala Gly Met Cys Val Asp			
575	580	585	
gct cgg ggc gac ctg att gtg gca gat agc agc cgc aag gaa att ctg	1949		
Ala Arg Gly Asp Leu Ile Val Ala Asp Ser Ser Arg Lys Glu Ile Leu			
590	595	600	
cat ttt ccc aag ggc ggt ggc tac agc gtc ctt att cga gag ggc ctt	1997		
His Phe Pro Lys Gly Gly Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu			
605	610	615	
acc tgt cca gtg ggc atc gcc ctg aca ccc aag ggg cag ctg ctg gtc	2045		
Thr Cys Pro Val Gly Ile Ala Leu Thr Pro Lys Gly Gln Leu Leu Val			
620	625	630	
ttg gac tgt tgg gat cac tgc gtc aag atc tac agc tat cat ctg aga	2093		
Leu Asp Cys Trp Asp His Cys Val Lys Ile Tyr Ser Tyr His Leu Arg			
635	640	645	650
aga tat tcc acc cct taaaagatga ggagaaatac cactttcttc ttccctcaa	2148		
Arg Tyr Ser Thr Pro			
655			
tagagtttcc ttccctttcc ttctttcggt gttgatgggt ccgtagagta gatgtggcct	2208		
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tagtctactg tctccttcct gttacagtgt gcttcgtctg tggctttaaa tctggctgca	2568		

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 ctaaagaaca aactgttagg tagctagctc tgtattttct tcaagtgagt gcatattgtt 3108  
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<210> 48

<211> 655

<212> PRT

<213> Mus musculus

<400> 48

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				20						25				30	
Leu	Arg	Pro	Lys	Leu	Leu	His	Cys	Gly	His	Thr	Ile	Cys	Arg	Gln	Cys
				35						40				45	
Leu	Glu	Lys	Leu	Leu	Ala	Ser	Ser	Ile	Asn	Gly	Val	Arg	Cys	Pro	Phe
				50						55				60	
Cys	Ser	Lys	Ile	Thr	Arg	Ile	Thr	Ser	Leu	Thr	Gln	Leu	Thr	Asp	Asn
65					70					75				80	

Leu Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu Ala Val  
85 90 95  
Gly Leu Leu Met Cys Arg Gly Cys Gly Arg Arg Leu Pro Arg Gln Phe  
100 105 110  
Cys Arg Ser Cys Gly Val Val Leu Cys Glu Pro Cys Arg Glu Ala Asp  
115 120 125  
His Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala Ala Glu  
130 135 140  
Glu Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg Glu Leu  
145 150 155 160  
Thr Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val Ser Arg  
165 170 175  
Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly His Glu  
180 185 190  
Glu Arg Arg Ile Gln Glu Glu Leu Ala Arg Ser Arg Lys Phe Phe Thr  
195 200 205  
Gly Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val Glu Glu  
210 215 220  
Gln Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser Arg Cys  
225 230 235 240  
Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu Leu Glu  
245 250 255  
Glu Ala Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu Pro Arg  
260 265 270  
Glu Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His Val Gly  
275 280 285  
Pro Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val Asn Met

290	295	300	
Glu Asp Ser Trp Ala Gly Glu Glu Gly Ala Ala Ser Ser Ala Ser Ala			
305	310	315	320
Ser Val Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Ala Pro			
	325	330	335
Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg Ser Ser Glu Ala Ala Ser			
	340	345	350
Gly Ile Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly Ser			
	355	360	365
Thr Pro Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser Gln			
	370	375	380
Ser Glu Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val Phe			
385	390	395	400
Asn Arg Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly Ile			
	405	410	415
Asp Ser Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu Thr			
	420	425	430
Pro Leu Ser Val Ala Met Asn Cys His Gly Leu Ile Gly Val Thr Asp			
	435	440	445
Ser Tyr Asp Asn Ser Leu Lys Val Tyr Thr Met Asp Gly His Cys Val			
	450	455	460
Ala Cys His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala Leu			
465	470	475	480
Pro Ser Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu Trp			
	485	490	495
Cys Phe Thr Val Asp Arg Gly Ala Gly Val Val Lys Tyr Ser Cys Leu			
	500	505	510

Cys Ser Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly Thr  
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 545 550 555 560  
 Gly Gln Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu Asp  
 565 570 575  
 Phe Arg Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu Ile  
 580 585 590  
 Val Ala Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly Gly  
 595 600 605  
 Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly Ile  
 610 615 620  
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<210> 49

<211> 3137

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (131).. (2089)

<400> 49

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aggaagagca atg gct gca gca gca gct tct cac ctg aac ctg gat gcc 169
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ctc cgg gaa gtg cta gaa tgc ccc atc tgc atg gag tcc ttc aca gaa 217
Leu Arg Glu Val Leu Glu Cys Pro Ile Cys Met Glu Ser Phe Thr Glu
      15             20             25
gag cag ctg cgt ccc aag ctt ctg cac tgt ggc cat acc atc tgc cgc 265
Glu Gln Leu Arg Pro Lys Leu Leu His Cys Gly His Thr Ile Cys Arg
      30             35             40             45
cag tgc ctg gag aag cta ttg gcc agt agc atc aat ggt gtc cgc tgt 313
Gln Cys Leu Glu Lys Leu Leu Ala Ser Ser Ile Asn Gly Val Arg Cys
            50             55             60
ccc ttt tgc agc aag att acc cgc ata acc agc ttg acc cag ctg aca 361
Pro Phe Cys Ser Lys Ile Thr Arg Ile Thr Ser Leu Thr Gln Leu Thr
            65             70             75
gac aat ctg aca gtg cta aag atc att gat aca gct ggg ctc agc gag 409
Asp Asn Leu Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu
            80             85             90
gct gtg ggg ctg ctc atg tgt cgg tcc tgt ggg cgg cgt ctg ccc cgg 457
Ala Val Gly Leu Leu Met Cys Arg Ser Cys Gly Arg Arg Leu Pro Arg
            95             100             105
caa ttc tgc cgg agc tgt ggt ttg gtg tta tgt gag ccc tgc cgg gag 505
Gln Phe Cys Arg Ser Cys Gly Leu Val Leu Cys Glu Pro Cys Arg Glu
110             115             120             125
gca gac cat cag cct cct ggc cac tgt aca ctc cct gtc aaa gaa gca 553

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Ala Asp His Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala	
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140	
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Ala Glu Glu Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg	
145	150
155	
gaa ctt atg ggg gag ctg cag cgg cgg aag gca gcc ttg gaa ggt gtc	649
Glu Leu Met Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val	
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tcc aag gac ctt cag gca agg tat aaa gca gtt ctc cag gag tat ggg	697
Ser Lys Asp Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly	
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cat gag gag cgc agg gtc cag gat gag ctg gct cgc tct cgg aag ttc	745
His Glu Glu Arg Arg Val Gln Asp Glu Leu Ala Arg Ser Arg Lys Phe	
190	195
200	205
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Phe Thr Gly Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val	
210	215
220	
gag gag cag agt tac ctg ctt aac att gca gag gtg cag gct gtg tct	841
Glu Glu Gln Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser	
225	230
235	
cgc tgt gac tac ttc ctg gcc aag atc aag cag gca gat gta gca cta	889
Arg Cys Asp Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu	
240	245
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ctg gag gag aca gct gat gag gag gag cca gag ctc act gcc agc ttg	937
Leu Glu Glu Thr Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu	
255	260
265	
cct cgg gag ctc acc ctg caa gat gtg gag ctc ctt aag gta ggt cat	985

Pro Arg Glu Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His	
270	275
280	285
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Val Gly Pro Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val	
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aac gtg gaa gat tcc tgg gcc atg gag gcc aca gcg tct gct gcc tct	1081
Asn Val Glu Asp Ser Trp Ala Met Glu Ala Thr Ala Ser Ala Ala Ser	
305	310
315	
acc tct gtt act ttt aga gag atg gac atg agc ccg gag gaa gtg gtt	1129
Thr Ser Val Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Val	
320	325
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Ala Ser Pro Arg Ala Ser Pro Ala Lys Gln Arg Gly Pro Glu Ala Ala	
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Ser Asn Ile Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly	
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360	365
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Ser Thr Pro Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser	
370	375
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caa ggt gaa gta cta gtc gct gac cgt ggt aac tat cgt ata caa gtc	1321
Gln Gly Glu Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val	
385	390
395	
ttt acc cgc aaa ggc ttt ttg aag gaa atc cgc cgc agc ccc agt ggc	1369
Phe Thr Arg Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly	
400	405
410	
att gat agc ttt gtg cta agc ttc ctt ggg gca gat cta ccc aac ctc	1417

Ile Asp Ser Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu  
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 Thr Pro Leu Ser Val Ala Met Asn Cys Gln Gly Leu Ile Gly Val Thr  
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 Asp Ser Tyr Asp Asn Ser Leu Lys Val Tyr Thr Leu Asp Gly His Cys  
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 gtg gcc tgt cac agg agc cag ctg agc aaa cca tgg ggt atc aca gcc 1561  
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 465 470 475  
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 Leu Pro Ser Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu  
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 Trp Cys Phe Thr Val Asp Arg Gly Ser Gly Val Val Lys Tyr Ser Cys  
 495 500 505  
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 Leu Cys Ser Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly  
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 Thr Val Tyr Phe Thr Gln Gly Leu Gly Leu Asn Leu Glu Asn Arg Gln  
 530 535 540  
 aat gag cac cac ctg gag ggt ggc ttt tcc att ggc tct gta ggc cct 1801  
 Asn Glu His His Leu Glu Gly Gly Phe Ser Ile Gly Ser Val Gly Pro  
 545 550 555  
 gat ggg cag ctg ggt cgc cag att agc cac ttc ttc tcg gag aat gag 1849

Asp Gly Gln Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu  
 560 565 570  
 gat ttc cgc tgc att gct ggc atg tgt gtg gat gct cgt ggt gat ctc 1897  
 Asp Phe Arg Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu  
 575 580 585  
 atc gtg gct gac agt agt cgc aag gaa att ctc cat ttt cct aag ggt 1945  
 Ile Val Ala Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly  
 590 595 600 605  
 ggg ggc tat agt gtc ctt att cga gag gga ctt acc tgt ccg gtg ggc 1993  
 Gly Gly Tyr Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly  
 610 615 620  
 ata gcc cta act cct aag ggg cag ctg ctg gtc ttg gac tgt tgg gat 2041  
 Ile Ala Leu Thr Pro Lys Gly Gln Leu Leu Val Leu Asp Cys Trp Asp  
 625 630 635  
 cat tgc atc aag atc tac agc tac cat ctg aga aga tat tcc acc cca 2089  
 His Cys Ile Lys Ile Tyr Ser Tyr His Leu Arg Arg Tyr Ser Thr Pro  
 640 645 650  
 taggggatga gaaattatca gtttcttctg ctcccaagcc aacttccctt cccttagttc 2149  
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 ttctagaact ttagaagctc catcttttaa tgtttttatt tgttatgtcc ccttccccgc 2269  
 ttcccaccta aatttagagc tttaaaagat gcactgcca aataggacac acgatggtgt 2329  
 tagctgaagt ttgattagca attaggcact tccaaggctt tagtagagag agccacttta 2389  
 gccctttgtg ccatgtttga aatttgcct tgtattaaat ccttgatttt ttcccatttg 2449  
 gctttgatgc ccttgatcca ttgtttcctt cctactataa tgtgcttcat ctgtgacact 2509  
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 gtatgaaagt cattcattta gtgctaccaa aggggataca caagcccttt aggaagcagt 2689

acctctcgcc tggaggatct gtgccatctt ggattgagaa ttgcagatgt gacagaatgg 2749  
 attgacccta gttggttggt attgatgact tcagcctgga aattgcttgc cttttaaaga 2809  
 agcatatatg ggttgaatt atgcaaagc ataggaagct gggaataagc aaacaaatgc 2869  
 tgatatagtc agcaaatttg gatagtctct agggctcatc atttttcata ctacctctct 2929  
 cttctggcct gtgtctaagg aattgtacaa cataggccag ggccaacaaa gtggagaggt 2989  
 ggacacattt tcatgttcat tactaaaaca aacagcaaaa ctattggttt gttattctgt 3049  
 gttttcctca agtcagtaca tactatttgg tttcaggatt tctttccatt tctctatcaa 3109  
 gcattaaata attgagaact gtttcttc 3137

<210> 50

<211> 653

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Ala Ala Ala Ala Ser His Leu Asn Leu Asp Ala Leu Arg Glu

1 5 10 15

Val Leu Glu Cys Pro Ile Cys Met Glu Ser Phe Thr Glu Glu Gln Leu

20 25 30

Arg Pro Lys Leu Leu His Cys Gly His Thr Ile Cys Arg Gln Cys Leu

35 40 45

Glu Lys Leu Leu Ala Ser Ser Ile Asn Gly Val Arg Cys Pro Phe Cys

50 55 60

Ser Lys Ile Thr Arg Ile Thr Ser Leu Thr Gln Leu Thr Asp Asn Leu

65 70 75 80

Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu Ala Val Gly

85 90 95

Leu Leu Met Cys Arg Ser Cys Gly Arg Arg Leu Pro Arg Gln Phe Cys

100	105	110
Arg Ser Cys Gly Leu Val Leu Cys Glu Pro Cys Arg Glu Ala Asp His		
115	120	125
Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala Ala Glu Glu		
130	135	140
Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg Glu Leu Met		
145	150	155
Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val Ser Lys Asp		
165	170	175
Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly His Glu Glu		
180	185	190
Arg Arg Val Gln Asp Glu Leu Ala Arg Ser Arg Lys Phe Phe Thr Gly		
195	200	205
Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val Glu Glu Gln		
210	215	220
Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser Arg Cys Asp		
225	230	235
Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu Leu Glu Glu		
245	250	255
Thr Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu Pro Arg Glu		
260	265	270
Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His Val Gly Pro		
275	280	285
Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val Asn Val Glu		
290	295	300
Asp Ser Trp Ala Met Glu Ala Thr Ala Ser Ala Ala Ser Thr Ser Val		
305	310	315
		320

Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Val Ala Ser Pro  
 325 330 335  
 Arg Ala Ser Pro Ala Lys Gln Arg Gly Pro Glu Ala Ala Ser Asn Ile  
 340 345 350  
 Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly Ser Thr Pro  
 355 360 365  
 Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser Gln Gly Glu  
 370 375 380  
 Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val Phe Thr Arg  
 385 390 395 400  
 Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly Ile Asp Ser  
 405 410 415  
 Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu Thr Pro Leu  
 420 425 430  
 Ser Val Ala Met Asn Cys Gln Gly Leu Ile Gly Val Thr Asp Ser Tyr  
 435 440 445  
 Asp Asn Ser Leu Lys Val Tyr Thr Leu Asp Gly His Cys Val Ala Cys  
 450 455 460  
 His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala Leu Pro Ser  
 465 470 475 480  
 Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu Trp Cys Phe  
 485 490 495  
 Thr Val Asp Arg Gly Ser Gly Val Val Lys Tyr Ser Cys Leu Cys Ser  
 500 505 510  
 Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly Thr Val Tyr  
 515 520 525  
 Phe Thr Gln Gly Leu Gly Leu Asn Leu Glu Asn Arg Gln Asn Glu His

530                      535                      540  
 His Leu Glu Gly Gly Phe Ser Ile Gly Ser Val Gly Pro Asp Gly Gln  
 545                      550                      555                      560  
 Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu Asp Phe Arg  
                     565                      570                      575  
 Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu Ile Val Ala  
                     580                      585                      590  
 Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly Gly Gly Tyr  
                     595                      600                      605  
 Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly Ile Ala Leu  
                     610                      615                      620  
 Thr Pro Lys Gly Gln Leu Leu Val Leu Asp Cys Trp Asp His Cys Ile  
 625                      630                      635                      640  
 Lys Ile Tyr Ser Tyr His Leu Arg Arg Tyr Ser Thr Pro  
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<210> 51

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (357)

<400> 51

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 cctcctcagc cagcc atg ctg gag cat ctg agc tcg ctg ccc acg cag atg 171



Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met  
1 5 10  
gtg agg gcg caa ccc ggg gac ctc tgc acg ccg ttc ttg tgc ctg gca 219  
Val Arg Ala Gln Pro Gly Asp Leu Cys Thr Pro Phe Leu Cys Leu Ala  
15 20 25  
gct tcg aag ccc atg ttg gag cac cga ccc ggt gct gcg ctg ttc cgg 267  
Ala Ser Lys Pro Met Leu Glu His Arg Pro Gly Ala Ala Leu Phe Arg  
30 35 40  
gcc cgg atg gtt acc gtc cac cct ctt tcc cga att gcc tcc tgg gtc 315  
Ala Arg Met Val Thr Val His Pro Leu Ser Arg Ile Ala Ser Trp Val  
45 50 55 60  
ccc ttc tct tct act ccg cga gaa tct cct gtc cat tct cgg 357  
Pro Phe Ser Ser Thr Pro Arg Glu Ser Pro Val His Ser Pro  
65 70  
tgagggtggt tcagttcctc ccgggaagcc cagaatttaa tatcttgccc aggcccttag 417  
gagagcggga gaccctgatg ttgggggttac cctgtgccag agttgtgagg tcagggcagg 477  
aattgtatgt tctcggcggg ggaaccaatt ctttttttcc tctgcttcac ccaggatta 537  
caagggccag aagctagctg aacagatggt tcagggaatt attctttttt ctgcagtaag 597  
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ttaatatact tcatttgtct ctagatagtt ggatttatct acgggtacgt ggctgaacag 717  
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agtagtgaga ccaaagcca acgtttccct catccttcca aacagcgttt ccctttgcta 897  
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gacggagttt cactcttggt gccaggctg cagtgcactg gggcgatttc ggctcactgc 1137

accttctgcc tcccgggttt aatagatttt cctgcctcag cctcccagagt agctgtgact 1197  
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 tacaggcgag agccaccacg cctggccccc acctttcttt taggtcttaa agccatttgt 1377  
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 ctttatagga atatggattt ttttttgtt tttttgttcc ctcagcatag gagtcatattg 1497  
 ggaacctggc attatacgta atgatttttt aaacttttaa tagctataat ttatgcattt 1557  
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 agtgggtacc tgttcaagaa tcaagcacag acgacaagaa accaggggaa agaaaaatta 1677  
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 gatgagctaa attgctttca taccacagat aagggtctaaa accacctaata gctcttatgg 1797  
 cacagctgtg tatagattta gttctcttta tacttcattt ctagcccagt tgggttttga 1857  
 tttatataag tagtttagac cttctcttca taatcttgct ctgagatggg gaacagaaca 1917  
 cacaagtatg aagtttcttt cagggtgtaaa taatgaaaaa taaatgcctc ataatgata 1977  
 gtacaatgta actatcaaag ttttataatt cattatgagt taaccatttt aatgtttcca 2037  
 attaaacctc atagtgc 2054

<210> 52

<211> 74

<212> PRT

<213> Homo sapiens

<400> 52

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Val Arg Ala Gln

1

5

10

15

Pro Gly Asp Leu Cys Thr Pro Phe Leu Cys Leu Ala Ala Ser Lys Pro

20

25

30

Met Leu Glu His Arg Pro Gly Ala Ala Leu Phe Arg Ala Arg Met Val

35                      40                      45  
 Thr Val His Pro Leu Ser Arg Ile Ala Ser Trp Val Pro Phe Ser Ser  
 50                      55                      60  
 Thr Pro Arg Glu Ser Pro Val His Ser Pro  
 65                      70

<210> 53

<211> 798

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (441)

<400> 53

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 acggtcctta agtctcggtc gccctcgct cgcagcctgc caccgcgct cagctgcccg 120  
 cctctcagc cagcc atg ctg gag cat ctg agc tcg ctg ccc acg cag atg 171

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met

1

5

10

gat tac aag ggc cag aag cta gct gaa cag atg ttt cag gga att att 219

Asp Tyr Lys Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile

15

20

25

ctt ttt tct gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag 267

Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln

30

35

40

ttc ggg tgg act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt 315

Phe Gly Trp Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys

45                                      50                                      55                                      60  
 ttg ctg aca ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag 363  
 Leu Leu Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys  
                                     65                                      70                                      75  
 tgg tta cct gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa 411  
 Trp Leu Pro Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu  
                                     80                                      85                                      90  
 aga aaa att aag agg cat gct aaa aat aat tgaggttttc atgattcagc 461  
 Arg Lys Ile Lys Arg His Ala Lys Asn Asn  
                                     95                                      100  
 acctgctttt gtttctgtga gatgagctaa attgctttca taccccagat aagggtctaaa 521  
 accacctaata gctcttatgg cacagctgtg tatagattta gttctcttta tacttcattt 581  
 ctagcccagt tgggttttga tttatataag tagtttagac cttctcttca taatcttgct 641  
 ctgagatggg gaacagaaca cacaagtatg aagtttcttt caggtgtaaa taatgaaaaa 701  
 taaatgcctc ataaatgata gtacaatgta actatcaaag tttataatt cattatgagt 761  
 taaccatttt aatgtttcca attaaacctc atagtgc 798

<210> 54

<211> 102

<212> PRT

<213> Homo sapiens

<400> 54

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly  
     1                                      5                                      10                                      15  
 Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala  
                                     20                                      25                                      30  
 Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr

35	40	45
Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu		
50	55	60
Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val		
65	70	75
Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys		
	85	90
		95
Arg His Ala Lys Asn Asn		
100		

&lt;210&gt; 55

&lt;211&gt; 1583

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (513).. (1226)

&lt;400&gt; 55

caggctaatac cagctgtcat gtatttctgg cgtgatgtgg ctgtctccct tgacacgctc 60  
tgggctcttc ccaaggcaac agcctgggtc tggttaacaac cgtgtcctcg ggtctgctgt 120  
actttgaagt gatcggaag tgatgtgacg ctccggggat cccaccaggc tcagagacac 180  
ccctggtttag ggctccgaca agtcgttccc ctcaaaggct cgccgcggcc gcccttactg 240  
caggcgatgg aggagatgcg gatgcagccc gcgccccgac ccgccctgcc agctcagcgc 300  
ccgcgcgcga ggccccggag ccagcccgt tgtctggcgc cccgcgttcc ctgcacgctg 360  
ggccgagcac acttgccctc tagctccgtg gcagccgcgc agccccacta cgcccagcca 420  
gcccgcagcg gtaaccgcta gagcgtcgcg ccaagcaggc gccgcggggc agccctgccg 480  
ccgggggtcct cgcagggaaa aaggccgtcg cc atg gag acg cgg ggg cgc cgg 533

										Met	Glu	Thr	Arg	Gly	Arg	Arg				
										1						5				
cgg	ccg	ttg	ggc	cgc	gca	agt	act	gtc	aag	gac	agt	ttt	cgg	gac	ggg		581			
Arg	Pro	Leu	Gly	Arg	Ala	Ser	Thr	Val	Lys	Asp	Ser	Phe	Arg	Asp	Gly					
			10				15				20									
gga	cgc	ggc	tcc	agg	cac	cca	aca	gca	ctg	acg	gcg	aac	act	tca	cgg		629			
Gly	Arg	Gly	Ser	Arg	His	Pro	Thr	Ala	Leu	Thr	Ala	Asn	Thr	Ser	Arg					
			25				30				35									
gcg	cgc	gat	gcc	tcg	aca	agg	cgg	ccg	cca	cca	cca	cct	cag	ctg	ccc		677			
Ala	Arg	Asp	Ala	Ser	Thr	Arg	Arg	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Pro					
			40				45				50				55					
tcg	cgg	gca	gca	cgg	cgc	ggc	aaa	agc	gca	cgt	cgc	cta	gcg	atg	gcg		725			
Ser	Arg	Ala	Ala	Arg	Arg	Gly	Lys	Ser	Ala	Arg	Arg	Leu	Ala	Met	Ala					
						60				65				70						
cgg	ggc	ggg	gac	acg	ggc	tgt	acc	ggc	ccg	tcg	gag	act	tcc	gct	tcc		773			
Arg	Gly	Gly	Asp	Thr	Gly	Cys	Thr	Gly	Pro	Ser	Glu	Thr	Ser	Ala	Ser					
			75				80				85									
ggg	gcc	gcc	gcc	atc	gct	ctc	ccg	ggc	tta	gaa	ggc	ccg	gct	act	gac		821			
Gly	Ala	Ala	Ala	Ile	Ala	Leu	Pro	Gly	Leu	Glu	Gly	Pro	Ala	Thr	Asp					
			90				95				100									
gcg	cag	tgc	cag	acc	tta	gcc	ctc	acg	gtc	ctt	aag	tct	cgg	tcg	ccc		869			
Ala	Gln	Cys	Gln	Thr	Leu	Ala	Leu	Thr	Val	Leu	Lys	Ser	Arg	Ser	Pro					
			105				110				115									
tcg	cct	cgc	agc	ctg	cca	ccc	gcg	ctc	agc	tgc	ccg	cct	cct	cag	cca		917			
Ser	Pro	Arg	Ser	Leu	Pro	Pro	Ala	Leu	Ser	Cys	Pro	Pro	Pro	Gln	Pro					
			120				125				130				135					
gcc	atg	ctg	gag	cat	ctg	agc	tcg	ctg	ccc	acg	cag	atg	gat	tac	aag		965			

Ala Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys  
                             140                            145                            150  
 ggc cag aag cta gct gaa cag atg ttt cag gga att att ctt ttt tct 1013  
 Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser  
                             155                            160                            165  
 gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg 1061  
 Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp  
                             170                            175                            180  
 act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt ttg ctg aca 1109  
 Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr  
                             185                            190                            195  
 ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct 1157  
 Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro  
 200                            205                            210                            215  
 gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att 1205  
 Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile  
                             220                            225                            230  
 aag agg cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt 1256  
 Lys Arg His Ala Lys Asn Asn  
                             235  
 gtttctgtga gatgagctaa attgctttca taccacagat aagggctaaa accacctaatt 1316  
 gctcttatgg cacagctgtg tatagattta gttctcttta tacttcattt ctagcccagt 1376  
 tgggttttga tttatataag tagtttagac cttctcttca taatcttgct ctgagatggg 1436  
 gaacagaaca cacaagtatg aagtttcttt cagggtgtaaa taatgaaaaa taaatgcctc 1496  
 ataaatgata gtacaatgta actatcaaag ttttataatt cattatgagt taaccatttt 1556  
 aatgtttcca attaaacctc atagtgc 1583

&lt;210&gt; 56

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

Met Glu Thr Arg Gly Arg Arg Arg Pro Leu Gly Arg Ala Ser Thr Val  
1 5 10 15  
Lys Asp Ser Phe Arg Asp Gly Gly Arg Gly Ser Arg His Pro Thr Ala  
20 25 30  
Leu Thr Ala Asn Thr Ser Arg Ala Arg Asp Ala Ser Thr Arg Arg Pro  
35 40 45  
Pro Pro Pro Pro Gln Leu Pro Ser Arg Ala Ala Arg Arg Gly Lys Ser  
50 55 60  
Ala Arg Arg Leu Ala Met Ala Arg Gly Gly Asp Thr Gly Cys Thr Gly  
65 70 75 80  
Pro Ser Glu Thr Ser Ala Ser Gly Ala Ala Ala Ile Ala Leu Pro Gly  
85 90 95  
Leu Glu Gly Pro Ala Thr Asp Ala Gln Cys Gln Thr Leu Ala Leu Thr  
100 105 110  
Val Leu Lys Ser Arg Ser Pro Ser Pro Arg Ser Leu Pro Pro Ala Leu  
115 120 125  
Ser Cys Pro Pro Pro Gln Pro Ala Met Leu Glu His Leu Ser Ser Leu  
130 135 140  
Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Glu Gln Met Phe  
145 150 155 160  
Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr Gly Tyr  
165 170 175



Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala Gly Phe

180

185

190

Ala Phe Ser Cys Leu Leu Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg

195

200

205

His Pro Leu Lys Trp Leu Pro Val Gln Glu Ser Ser Thr Asp Asp Lys

210

215

220

Lys Pro Gly Glu Arg Lys Ile Lys Arg His Ala Lys Asn Asn

225

230

235

&lt;210&gt; 57

&lt;211&gt; 782

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (110).. (421)

&lt;400&gt; 57

ggctactgac ggcagtgcc agaccttagc cctcacggtc cttaagtctc ggctgcacctc 60

gcctcgcagc ctgccaccgc cgtcagctg cccgcctcct cagccagcc atg ctg gag 118

Met Leu Glu

1

cat ctg agc tcg ctg ccc acg cag atg gat tac aag ggc cag aag cta 166

His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu

5

10

15

gct gaa cag atg ttt cag gga att att ctt ttt tct gca ata gtt gga 214

Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly

20

25

30

35

ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg act gtc tat ata 262  
 Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile  
                     40                    45                    50  
 gtt atg gcc gga ttt gct ttt tca tgt ttg gcc cag ctg aca ctt cct 310  
 Val Met Ala Gly Phe Ala Phe Ser Cys Leu Ala Gln Leu Thr Leu Pro  
                     55                    60                    65  
 cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct gtt caa 358  
 Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val Gln  
                     70                    75                    80  
 gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att aag agg 406  
 Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys Arg  
                     85                    90                    95  
 cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt gtttctgtga 461  
 His Ala Lys Asn Asn  
 100  
 gatgagctaa attgctttca taccacagat aagagctaaa accacctaata gctcttatgg 521  
 cacagctgtg tatagattta gttctcttta tacttcattt ctagccagcagg tgggttttga 581  
 tttatataag tagtttagac cttctcttca taatcttgct ctgagatggg gaacagaaca 641  
 cacaagtatg aagtttcttt caggtgtaaa taatgaaaaa taaatgcctc ataatgata 701  
 gtacaatgta actatcaaag ttttataatt cattatgagt taaccatttt aatgtttcca 761  
 attaaacctc atagtgaag t 782

&lt;210&gt; 58

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly  
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 Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala  
 20 25 30  
 Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr  
 35 40 45  
 Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Ala Gln Leu  
 50 55 60  
 Thr Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu  
 65 70 75 80  
 Pro Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys  
 85 90 95  
 Ile Lys Arg His Ala Lys Asn Asn  
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<210> 59

<211> 2402

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(450)

<400> 59

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 1 5 10  
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Ala Glu Leu Pro Pro Gln Pro Ala Ala Gly Gln Tyr Gly Pro Gly Asp  
 15 20 25  
 tcg gca gat gca ccc aac ccc tgg tcg agg gag ccg cgt gac cga tca 147  
 Ser Ala Asp Ala Pro Asn Pro Trp Ser Arg Glu Pro Arg Asp Arg Ser  
 30 35 40  
 ggg cat ctg tcc caa aca cca aga agc cct gaa gct ctt ctg cga ggt 195  
 Gly His Leu Ser Gln Thr Pro Arg Ser Pro Glu Ala Leu Leu Arg Gly  
 45 50 55  
 aga cga aga ggc cat ctg tgt ggt gtg ccg aga atc cag gag cca caa 243  
 Arg Arg Arg Gly His Leu Cys Gly Val Pro Arg Ile Gln Glu Pro Gln  
 60 65 70  
 aca gca cag cgt ggt gcc att gga gga ggt ggt gca gga gta caa ggc 291  
 Thr Ala Gln Arg Gly Ala Ile Gly Gly Gly Gly Ala Gly Val Gln Gly  
 75 80 85 90  
 caa act gca ggg gca cgt gga acc act gag gaa gca cct gga ggc agt 339  
 Gln Thr Ala Gly Ala Arg Gly Thr Thr Glu Glu Ala Pro Gly Gly Ser  
 95 100 105  
 gca gaa gat gaa agc caa gga gga gag gcg agt gac aga act gaa gag 387  
 Ala Glu Asp Glu Ser Gln Gly Gly Glu Ala Ser Asp Arg Thr Glu Glu  
 110 115 120  
 cca gat gaa gtc aga gct ggc agc ggt ggc ctc gga gtt tgg gcg act 435  
 Pro Asp Glu Val Arg Ala Gly Ser Gly Gly Leu Gly Val Trp Ala Thr  
 125 130 135  
 gac acg gtt tct ggc tgaagagcag gcagggctgg aacggcgtct cagagagatg 490  
 Asp Thr Val Ser Gly  
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 catgaagccc agctggggcg tgcgggagcc gcggctagtc gccttgcaga acaggccgcc 550

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aatttctacc tccatagacc ggccagaatt tagcttctact tgagagagat ctggaatggt 1990  
cgccatgatt gaaaccacgc accattacat catcattaca ttaattacat caacataaat 2050  
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 cttgccttgt cacttgcagc tttcgccctc tgctttgatg gctgaggtga actcatgttc 2350  
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<210> 60

<211> 143

<212> PRT

<213> Homo sapiens

<400> 60

Met Pro Ser Val Gln Lys Glu Leu Ser Ser Ala Glu Leu Pro Pro Gln  
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 20 25 30  
 Pro Trp Ser Arg Glu Pro Arg Asp Arg Ser Gly His Leu Ser Gln Thr  
 35 40 45  
 Pro Arg Ser Pro Glu Ala Leu Leu Arg Gly Arg Arg Arg Gly His Leu  
 50 55 60  
 Cys Gly Val Pro Arg Ile Gln Glu Pro Gln Thr Ala Gln Arg Gly Ala  
 65 70 75 80  
 Ile Gly Gly Gly Gly Ala Gly Val Gln Gly Gln Thr Ala Gly Ala Arg  
 85 90 95  
 Gly Thr Thr Glu Glu Ala Pro Gly Gly Ser Ala Glu Asp Glu Ser Gln  
 100 105 110  
 Gly Gly Glu Ala Ser Asp Arg Thr Glu Glu Pro Asp Glu Val Arg Ala  
 115 120 125  
 Gly Ser Gly Gly Leu Gly Val Trp Ala Thr Asp Thr Val Ser Gly

130

135

140

&lt;210&gt; 61

&lt;211&gt; 2402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (86).. (1366)

&lt;400&gt; 61

agccccctcgg aggtgcttca catgccctca gtgcagaaag agctttcctc ggcggagctt 60

ccgcccccaac ctgcagctgg ccaat atg gtc cag gtg att cgg cag atg cac 112

Met Val Gln Val Ile Arg Gln Met His

1

5

cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc tgt ccc 160

Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro

10

15

20

25

aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa gag gcc 208

Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala

30

35

40

atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac agc gtg 256

Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val

45

50

55

gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg cag ggg 304

Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly

60

65

70

cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag atg aaa 352

His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys  
 75 80 85  
 gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg aag tca 400  
 Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser  
 90 95 100 105  
 gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg ttt ctg 448  
 Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu  
 110 115 120  
 gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg cat gaa 496  
 Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu  
 125 130 135  
 gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca gaa cag 544  
 Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln  
 140 145 150  
 gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg agc cag 592  
 Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln  
 155 160 165  
 cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc aat agg 640  
 Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg  
 170 175 180 185  
 tgt gaa gag gta cag ctg cag ccc cca gag gtc tgg tcc cct gac ccg 688  
 Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro  
 190 195 200  
 tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg agg aaa 736  
 Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys  
 205 210 215  
 atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg ctg gac 784



Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp  
 220 225 230  
 cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc cgg ggg 832  
 Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly  
 235 240 245  
 gtc cgc ctg gca gag cgg cgg cag gag gtt gct gac cat ccc aag cgc 880  
 Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg  
 250 255 260 265  
 ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag ggc ttc cgc tcc ggc 928  
 Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly  
 270 275 280  
 cgg cac tac tgg gag gta gag gtg ggc ggg cgg cgg ggc tgg gcg gtg 976  
 Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp Ala Val  
 285 290 295  
 ggt gct gcc cgt gaa tca acc cat cat aag gaa aag gtg ggc cct ggg 1024  
 Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly Pro Gly  
 300 305 310  
 ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc tcg cgc cat cac cat 1072  
 Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His His His  
 315 320 325  
 cgc cgc cgc cgg ctc cac ctg ccc cag cag ccc ctg ctc cag cgg gaa 1120  
 Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln Arg Glu  
 330 335 340 345  
 gtg tgg tgc gtg ggc acc aac ggc aaa cgc tat cag gcc cag agc tcc 1168  
 Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln Ser Ser  
 350 355 360  
 aca gaa cag acg ctg ctg agc ccc agt gag aaa cca agg cgc ttt ggt 1216

Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg Phe Gly  
 365 370 375  
 gtg tac ctg gac tat gaa gct ggg cgc ctg ggc ttc tac aac gca gag 1264  
 Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn Ala Glu  
 380 385 390  
 act cta gcc cac gtg cac acc ttc tcg gct gcc ttc ctg ggc gag cgt 1312  
 Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly Glu Arg  
 395 400 405  
 gtc ttt cct ttc ttc cgg gtg ctc tcc aag ggc acc cgc atc aag ctc 1360  
 Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr Arg Ile Lys Leu  
 410 415 420 425  
 tgc cct tgattatcct gccaccgca ggggccctc tgtcagcact tggggggtg 1416  
 Cys Pro  
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 aatttagctt cacttgagag agatctggaa tggtcgccat gattgaaacc acgcaccatt 2016  
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 aggctcctct cccctttgtt cagtggagct ggcttttctc ccagcccctt tccatgcctt 2196  
 tcactccatt tggcaagctc tgagggggag cctggggacg ggtttgggtc ccaggagga 2256

218/861

Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu  
145 150 155 160  
Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu  
165 170 175  
Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln  
180 185 190  
Pro Pro Glu Val Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp  
195 200 205  
Phe Leu Thr Asp Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln  
210 215 220  
Ala Ala Arg Val Asp Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala  
225 230 235 240  
Leu Met Leu Ser Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg  
245 250 255  
Gln Glu Val Ala Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val  
260 265 270  
Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu  
275 280 285  
Val Gly Gly Arg Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr  
290 295 300  
His His Lys Glu Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly  
305 310 315 320  
Asp Ala Ser Ser Ser Arg His His His Arg Arg Arg Arg Leu His Leu  
325 330 335  
Pro Gln Gln Pro Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn  
340 345 350  
Gly Lys Arg Tyr Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser

355	360	365
Pro Ser Glu Lys Pro Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala		
370	375	380
Gly Arg Leu Gly Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr		
385	390	395
Phe Ser Ala Ala Phe Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val		
405	410	415
Leu Ser Lys Gly Thr Arg Ile Lys Leu Cys Pro		
420	425	

&lt;210&gt; 63

&lt;211&gt; 2691

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (711).. (2264)

&lt;400&gt; 63

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cgggtggcgcc cagcactgtc ccctcccctc gtagagacac ggttgtcgtt tgggagtagg 540

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 Met Ala  
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 gcc gtt gcc atg aca ccc aac cct gtg cag acc ctt cag gag gag gcg 764  
 Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu Glu Ala  
 5 10 15  
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 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly  
 20 25 30  
 tgc ggg cac aac ttc tgc cga gtt tgt gta acc cag ttg tgg ggt ggg 860  
 Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp Gly Gly  
 35 40 45 50  
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 Asp Gly Glu Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala Gly Trp  
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 85 90 95  
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 Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg  
 100 105 110  
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Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu  
 115 120 125 130  
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 Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg  
 135 140 145  
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 Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu  
 150 155 160  
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 Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg  
 165 170 175  
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 Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser  
 180 185 190  
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 Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln  
 195 200 205 210  
 atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc 1388  
 Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile  
 215 220 225  
 tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa 1436  
 Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu  
 230 235 240  
 gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac 1484  
 Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His  
 245 250 255  
 agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg 1532

Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu  
 260 265 270  
 cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag 1580  
 Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys  
 275 280 285 290  
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 Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met  
 295 300 305  
 aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg 1676  
 Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg  
 310 315 320  
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 Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met  
 325 330 335  
 cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca 1772  
 His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala  
 340 345 350  
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 355 360 365 370  
 agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc 1868  
 Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe  
 375 380 385  
 aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc tgg tcc cct 1916  
 Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro  
 390 395 400  
 gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg 1964



Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val  
 405 410 415  
 agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg 2012  
 Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr  
 420 425 430  
 ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc 2060  
 Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg  
 435 440 445 450  
 cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct gac cat ccc 2108  
 Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro  
 455 460 465  
 aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag ggc ttc cgc 2156  
 Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg  
 470 475 480  
 tcc ggc cgg cac tac tgg gag gag cct aaa gaa ccc tcc tgg cct cca 2204  
 Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp Pro Pro  
 485 490 495  
 gct cag cct tct ctc acc tac tat gtc tgt cca aca gac cgg cca gaa 2252  
 Ala Gln Pro Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp Arg Pro Glu  
 500 505 510  
 ttt agc ttc act tgagagagat ctggaatggt cgccatgatt gaaaccacgc 2304  
 Phe Ser Phe Thr  
 515  
 accattacat catcattaca ttaattacat caacataaat tattttcttcc cccttcctt 2364  
 ttccagcact caaccaagga gcaaagctca tcccacccca caccctccc aggtctgctc 2424  
 actgccaggc tcctctcccc tttgttcagt ggagctggct tttctcccag cccctttcca 2484  
 tgcctttcac tccatttggc aagctctgag ggggagcctg gggacggggt tgggtcccca 2544

ggaggagagc cttgggtata atctatTTTT ctaggagcct cttgccttgt cacttgcagc 2604  
 tttcgccctc tgctttgatg gctgaggtga actcatgttc tttgggaaga gggaaggcgt 2664  
 gctgtggaaa taaaatgttt atttgct 2691

<210> 64

<211> 518

<212> PRT

<213> Homo sapiens

<400> 64

Met	Ala	Ala	Val	Ala	Met	Thr	Pro	Asn	Pro	Val	Gln	Thr	Leu	Gln	Glu
1				5						10				15	
Glu	Ala	Val	Cys	Ala	Ile	Cys	Leu	Asp	Tyr	Phe	Thr	Asp	Pro	Val	Ser
			20					25					30		
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
			35					40					45		
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
		50				55					60				
Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Val	Glu	Ala	Val	Gly	Ala	Gly	Ala
	65				70					75				80	
Gly	Trp	Asp	Thr	Pro	Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu
				85					90					95	
Glu	Glu	Val	Glu	Glu	Glu	Glu	Glu	Gly	Val	Phe	Trp	Thr	Ser	Gly	Met
			100						105					110	
Ser	Arg	Ser	Ser	Trp	Asp	Asn	Met	Asp	Tyr	Val	Trp	Glu	Glu	Glu	Asp
		115					120						125		
Glu	Glu	Glu	Asp	Leu	Asp	Tyr	Tyr	Leu	Gly	Asp	Met	Glu	Glu	Glu	Asp
	130						135					140			

Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val  
145 150 155 160  
Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala  
165 170 175  
Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg  
180 185 190  
Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile  
195 200 205  
Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln  
210 215 220  
Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val  
225 230 235 240  
Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys  
245 250 255  
Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala  
260 265 270  
Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val  
275 280 285  
Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser  
290 295 300  
Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu  
305 310 315 320  
Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg  
325 330 335  
Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg  
340 345 350  
Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln

355                                      360                                      365  
 Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu  
 370                                      375                                      380  
 Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp  
 385                                      390                                      395                                      400  
 Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala  
 405                                      410                                      415  
 Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp  
 420                                      425                                      430  
 Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro  
 435                                      440                                      445  
 Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp  
 450                                      455                                      460  
 His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly  
 465                                      470                                      475                                      480  
 Phe Arg Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp  
 485                                      490                                      495  
 Pro Pro Ala Gln Pro Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp Arg  
 500                                      505                                      510  
 Pro Glu Phe Ser Phe Thr  
 515

&lt;210&gt; 65

&lt;211&gt; 1749

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (24).. (1322)

&lt;400&gt; 65

ctggcgcggg gtgggacacc ccc atg cgg gat gaa gac tac gag ggt gac atg 53

Met Arg Asp Glu Asp Tyr Glu Gly Asp Met

1

5

10

gag gag gag gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc 101

Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15

20

25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu

30

35

40

gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag 197

Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu

45

50

55

gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag 245

Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu

60

65

70

gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca 293

Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro

75

80

85

90

gcc cct cgg agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct 341

Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro

95

100

105

cgg cgg agc ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg 389

Arg Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val

110

115

120

att cgg cag atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat 437  
 Ile Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp  
 125 130 135  
 cag ggc atc tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag 485  
 Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu  
 140 145 150  
 gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac 533  
 Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His  
 155 160 165 170  
 aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag 581  
 Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys  
 175 180 185  
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629  
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala  
 190 195 200  
 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677  
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys  
 205 210 215  
 agc cag atg aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga 725  
 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg  
 220 225 230  
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773  
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu  
 235 240 245 250  
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821  
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser  
 255 260 265

cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869  
 Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala  
 270 275 280  
 cag gag cgg agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag 917  
 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys  
 285 290 295  
 gag act ttc aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc 965  
 Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val  
 300 305 310  
 tgg tcc cct gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat 1013  
 Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp  
 315 320 325 330  
 gcc atc gtg agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg 1061  
 Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val  
 335 340 345  
 gac ctg acg ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc 1109  
 Asp Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser  
 350 355 360  
 cct gac cgc cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct 1157  
 Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala  
 365 370 375  
 gac cat ccc aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag 1205  
 Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln  
 380 385 390  
 ggc ttc cgc tcc ggc cgg cac tac tgg gag gag cct aaa gaa ccc tcc 1253  
 Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Glu Pro Lys Glu Pro Ser  
 395 400 405 410

tgg cct cca gct cag cct tct ctc acc tac tat gtc tgt cca aca gac 1301  
 Trp Pro Pro Ala Gln Pro Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp

415

420

425

cgg cca gaa ttt agc ttc act tgagagagat ctggaatggt cgccatgatt 1352  
 Arg Pro Glu Phe Ser Phe Thr

430

gaaaccacgc accattacat catcattaca ttaattacat caacataaat tattttcttcc 1412  
 cccttccctt ttccagcaact caaccaagga gcaaagctca tcccacccca caccctccc 1472  
 aggtctgctc actgccaggc tcctctcccc ttgtttcagt ggagctggct tttctcccag 1532  
 cccctttcca tgcctttcac tccatttggc aagctctgag ggggagcctg gggacgggtt 1592  
 tgggtcccca ggaggagagc cttgggtata atctatTTTT ctaggagcct cttgccttgt 1652  
 cacttgcagc tttcgccctc tgctttgatg gctgaggtga actcatgttc tttgggaaga 1712  
 gggaaggcgt gctgtggaaa taaaatgttt atttgct 1749

&lt;210&gt; 66

&lt;211&gt; 433

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu Val Glu Glu  
 1 5 10 15  
 Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg Ser Ser Trp  
 20 25 30  
 Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu Glu Asp Leu  
 35 40 45  
 Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg Gly Glu Asp  
 50 55 60



Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu Glu Asp Leu  
 65 70 75 80  
 Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg Arg Cys Phe  
 85 90 95  
 Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser Phe Arg Pro  
 100 105 110  
 Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln Met His Pro  
 115 120 125  
 Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro Lys  
 130 135 140  
 His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala Ile  
 145 150 155 160  
 Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val Val  
 165 170 175  
 Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly His  
 180 185 190  
 Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys Ala  
 195 200 205  
 Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser Glu  
 210 215 220  
 Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu Ala  
 225 230 235 240  
 Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu Ala  
 245 250 255  
 Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala  
 260 265 270  
 Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln

275 280 285  
Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys  
290 295 300  
Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro Cys  
305 310 315 320  
Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys Met  
325 330 335  
Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp Pro  
340 345 350  
Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly Val  
355 360 365  
Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg Phe  
370 375 380  
Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg  
385 390 395 400  
His Tyr Trp Glu Glu Pro Lys Glu Pro Ser Trp Pro Pro Ala Gln Pro  
405 410 415  
Ser Leu Thr Tyr Tyr Val Cys Pro Thr Asp Arg Pro Glu Phe Ser Phe  
420 425 430  
Thr

&lt;210&gt; 67

&lt;211&gt; 2694

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (24)..(1658)

&lt;400&gt; 67

ctggcgcggg gtgggacacc ccc atg cgg gat gaa gac tac gag ggt gac atg 53

Met Arg Asp Glu Asp Tyr Glu Gly Asp Met

1

5

10

gag gag gag gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc 101

Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15

20

25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu

30

35

40

gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag 197

Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu

45

50

55

gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag 245

Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu

60

65

70

gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca 293

Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro

75

80

85

90

gcc cct cgg agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct 341

Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro

95

100

105

cgg cgg agc ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg 389

Arg Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val

110

115

120

att cgg cag atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat 437

Ile Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp  
           125                          130                          135  
 cag ggc atc tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag 485  
 Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu  
           140                          145                          150  
 gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac 533  
 Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His  
 155                          160                          165                          170  
 aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag 581  
 Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys  
                           175                          180                          185  
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629  
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala  
                           190                          195                          200  
 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677  
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys  
                           205                          210                          215  
 agc cag atg aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga 725  
 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg  
           220                          225                          230  
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773  
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu  
 235                          240                          245                          250  
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821  
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser  
                           255                          260                          265  
 cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869

Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala  
 270 275 280  
 cag gag cgg agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag 917  
 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys  
 285 290 295  
 gag act ttc aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc 965  
 Glu Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val  
 300 305 310  
 tgg tcc cct gac cgg tgc caa ccc cat agc cat gac ttc ctg aca gat 1013  
 Trp Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp  
 315 320 325 330  
 gcc atc gtg agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg 1061  
 Ala Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val  
 335 340 345  
 gac ctg acg ctg gac cct gac acg gct cac cgg gcc ctg atg ctg tcc 1109  
 Asp Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser  
 350 355 360  
 cct gac cgc cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct 1157  
 Pro Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala  
 365 370 375  
 gac cat ccc aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag 1205  
 Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln  
 380 385 390  
 ggc ttc cgc tcc ggc cgg cac tac tgg gag gta gag gtg ggc ggg cgg 1253  
 Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg  
 395 400 405 410  
 cgg ggc tgg gcg gtg ggt gct gcc cgt gaa tca acc cat cat aag gaa 1301

Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu  
 415 420 425  
 aag gtg ggc cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc 1349  
 Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser  
 430 435 440  
 tcg cgc cat cac cat cgc cgc cgc cgg ctc cac ctg ccc cag cag ccc 1397  
 Ser Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro  
 445 450 455  
 ctg ctc cag cgg gaa gtg tgg tgc gtg ggc acc aac ggc aaa cgc tat 1445  
 Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr  
 460 465 470  
 cag gcc cag agc tcc aca gaa cag acg ctg ctg agc ccc agt gag aaa 1493  
 Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys  
 475 480 485 490  
 cca agg cgc ttt ggt gtg tac ctg gac tat gaa gct ggg cgc ctg ggc 1541  
 Pro Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly  
 495 500 505  
 ttc tac aac gca gag act cta gcc cac gtg cac acc ttc tcg gct gcc 1589  
 Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala  
 510 515 520  
 ttc ctg ggc gag cgt gtc ttt cct ttc ttc cgg gtg ctc tcc aag ggc 1637  
 Phe Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly  
 525 530 535  
 acc cgc atc aag ctc tgc cct tgattatcct gccaccgca ggggcccctc 1688  
 Thr Arg Ile Lys Leu Cys Pro  
 540 545  
 tgtcagcact tgggggggtgg gtggtggagg gtggcccgtta agtttgaggg ctcaaaggct 1748

cttcccactg cttgttactg tgttgettcc cactccccct tgaccccagg cccctgcttc 1808  
 tccctctagg agcctaaaga accctcctgg cctccagctc agccttctct cacctactat 1868  
 gtctgtccaa caggtctgca tgggtccctg ataatgagaa cagctgcctg gtcttctctc 1928  
 ccagtctgcc tagcccagcc ctgggactgg aatttgagta ggggatgagg ggaaattgta 1988  
 atttcattcc ttaacttcct tttccccacc cctgctcttc aacctcttta tcagttctga 2048  
 ggctggaggg tttgggcaag gcaacatccc cattccaatt ccattttctg atgcagattt 2108  
 tagctgaggg atttgaagc catttgggga ggcaggtctg gccaaagggt agagctgggt 2168  
 aataaatgtc tattctcctg gggaggaggg attctaaact ttccttccgt cctcaatttc 2228  
 tacctccata gaccggccag aatttagctt cacttgagag agatctggaa tggtcgccat 2288  
 gattgaaacc acgcaccatt acatcatcat tacattaatt acatcaacat aaattatttc 2348  
 ttcccccttc cttttccag cactcaacca aggagcaaag ctcatccac cccacacccc 2408  
 tcccagatct gctcactgcc aggtcctct cccctttgtt cagtggagct ggcttttctc 2468  
 ccagccccctt tccatgcctt tcactccatt tggcaagctc tgagggggag cctggggacg 2528  
 ggtttgggtc ccaggagga ggccttggg tataatctat ttttctagga gcctcttgcc 2588  
 ttgtcacttg cagctttgc cctctgcttt gatggctgag gtgaactcat gttctttggg 2648  
 aaaagggaag gcgtgctgtg gaaataaaat gtttatttgc ttctct 2694

<210> 68

<211> 545

<212> PRT

<213> Homo sapiens

<400> 68

Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu Val Glu Glu

1

5

10

15

Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg Ser Ser Trp

20

25

30

Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu Glu Asp Leu

35 40 45  
Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg Gly Glu Asp  
50 55 60  
Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu Glu Asp Leu  
65 70 75 80  
Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg Arg Cys Phe  
85 90 95  
Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser Phe Arg Pro  
100 105 110  
Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln Met His Pro  
115 120 125  
Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro Lys  
130 135 140  
His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala Ile  
145 150 155 160  
Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val Val  
165 170 175  
Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly His  
180 185 190  
Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys Ala  
195 200 205  
Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser Glu  
210 215 220  
Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu Ala  
225 230 235 240  
Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu Ala  
245 250 255



Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala  
                   260                          265                          270  
 Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln  
                   275                          280                          285  
 Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys  
                   290                          295                          300  
 Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro Asp Pro Cys  
 305                          310                          315                          320  
 Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val Arg Lys Met  
                   325                          330                          335  
 Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr Leu Asp Pro  
                   340                          345                          350  
 Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg Arg Gly Val  
                   355                          360                          365  
 Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro Lys Arg Phe  
                   370                          375                          380  
 Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg Ser Gly Arg  
 385                          390                          395                          400  
 His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp Ala Val Gly  
                   405                          410                          415  
 Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly Pro Gly Gly  
                   420                          425                          430  
 Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His His His Arg  
                   435                          440                          445  
 Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln Arg Glu Val  
                   450                          455                          460  
 Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln Ser Ser Thr

465                      470                      475                      480  
 Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg Phe Gly Val  
                     485                      490                      495  
 Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn Ala Glu Thr  
                     500                      505                      510  
 Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly Glu Arg Val  
                     515                      520                      525  
 Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr Arg Ile Lys Leu Cys  
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 Pro  
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<210> 69

<211> 3636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (711).. (2600)

<400> 69

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 tttctcccca gcggcggggg atgggggtag gcggttcctc tggttctttct gcgttccccg 180  
 cggcctctta ccacagagac gcgggcctcc accgtcctag ccctcccgcc ctgttctcta 240  
 gtgcggacta gagcgtctcc tcgccatttc ctgtcgccct ggggccccgc ggggaaaaag 300  
 ggggagtagc aggacagcgg agggaagtgc cgagcttagg tggtgtgtag acgccggaag 360  
 tggttggaag gaggccggaa gctaggggcg gggccaggaa gtgaggaggg gcgggggttt 420

atgaggagtc caagggagca ttggggcaga cttgcactca gagccacctg agggacttgg 480  
 cgggtggcgcc cagcactgtc ccctccctc gtagagacac ggttgtcgtt tgggagtagg 540  
 gaacactgtg ttgggggtggg ttgtcggcag gacatctctc tggctgctct tggggcgagg 600  
 tgtggagggg cagggctggg ggtggagccg ggtcgccagg gcgtcggtag ggaagacccc 660  
 cgccccctgc cccccaccg aacctctaca ctggctggct ggacactaag atg gct 716

Met Ala

1

gcc gtt gcc atg aca ccc aac cct gtg cag acc ctt cag gag gag gcg 764  
 Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu Glu Ala

5

10

15

gtg tgc gcc atc tgc ctc gat tac ttc acg gac ccc gtg tcc atc ggc 812  
 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly

20

25

30

tgc ggg cac aac ttc tgc cga gtt tgt gta acc cag ttg tgg ggt ggg 860  
 Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp Gly Gly

35

40

45

50

gag gat gag gag gac aga gat gag tta gat cgg gag gag gag gag gag 908  
 Glu Asp Glu Glu Asp Arg Asp Glu Leu Asp Arg Glu Glu Glu Glu Glu

55

60

65

gac gga gag gag gag gaa gtg gag gct gtg ggg gct ggc gcg ggg tgg 956  
 Asp Gly Glu Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala Gly Trp

70

75

80

gac acc ccc atg cgg gat gaa gac tac gag ggt gac atg gag gag gag 1004  
 Asp Thr Pro Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu

85

90

95

gtc gag gag gaa gaa gag ggt gtg ttc tgg acc agt ggc atg agc agg 1052  
 Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg

100	105	110	
tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag gac gag gag			1100
Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu			
115	120	125	130
gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag gac ctg agg			1148
Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg			
135	140	145	
ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag gtt gag gaa			1196
Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu			
150	155	160	
gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca gcc cct cgg			1244
Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg			
165	170	175	
agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct cgg cgg agc			1292
Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser			
180	185	190	
ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg att cgg cag			1340
Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln			
195	200	205	210
atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc			1388
Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile			
215	220	225	
tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa			1436
Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu			
230	235	240	
gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac aaa cag cac			1484
Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His			

245	250	255	
agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag gcc aaa ctg			1532
Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu			
260	265	270	
cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag			1580
Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys			
275	280	285	290
atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg			1628
Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met			
	295	300	305
aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg			1676
Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg			
	310	315	320
ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg			1724
Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met			
	325	330	335
cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca			1772
His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala			
	340	345	350
gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg			1820
Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg			
	355	360	365
agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc			1868
Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe			
	375	380	385
aat agg tgt gaa gag gta cag ctg cag ccc cca gag gtc tgg tcc cct			1916
Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp Ser Pro			

390	395	400	
gac ccg tgc caa ccc cat agc cat gac ttc ctg aca gat gcc atc gtg			1964
Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala Ile Val			
405	410	415	
agg aaa atg agc cgg atg ttc tgt cag gct gcg aga gtg gac ctg acg			2012
Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp Leu Thr			
420	425	430	
ctg gac cct gac acg gct cac ccg gcc ctg atg ctg tcc cct gac cgc			2060
Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro Asp Arg			
435	440	445	450
cgg ggg gtc cgc ctg gca gag cgg cgg cag gag gtt gct gac cat ccc			2108
Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp His Pro			
455	460	465	
aag cgc ttc tcg gcc gac tgc tgc gta ctg ggg gcc cag ggc ttc cgc			2156
Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly Phe Arg			
470	475	480	
tcc ggc cgg cac tac tgg gag gta gag gtg ggc ggg cgg cgg ggc tgg			2204
Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg Gly Trp			
485	490	495	
gcg gtg ggt gct gcc cgt gaa tca acc cat cat aag gaa aag gtg ggc			2252
Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys Val Gly			
500	505	510	
cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc agc tcc tcg cgc cat			2300
Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser Arg His			
515	520	525	530
cac cat cgc cgc cgc cgg ctc cac ctg ccc cag cag ccc ctg ctc cag			2348
His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu Leu Gln			

535	540	545	
cgg gaa gtg tgg tgc gtg ggc acc aac ggc aaa cgc tat cag gcc cag			2396
Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln Ala Gln			
550	555	560	
agc tcc aca gaa cag acg ctg ctg agc ccc agt gag aaa cca agg cgc			2444
Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro Arg Arg			
565	570	575	
ttt ggt gtg tac ctg gac tat gaa gct ggg cgc ctg ggc ttc tac aac			2492
Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe Tyr Asn			
580	585	590	
gca gag act cta gcc cac gtg cac acc ttc tgc gct gcc ttc ctg ggc			2540
Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe Leu Gly			
595	600	605	610
gag cgt gtc ttt cct ttc ttc cgg gtg ctc tcc aag ggc acc cgc atc			2588
Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr Arg Ile			
615	620	625	
aag ctc tgc cct tgattatcct gccaccgca ggggccctc tgtcagcact			2640
Lys Leu Cys Pro			
630			
tggggggtgg gtggtggagg gtggcccgta agtttgagg ctcaaaggct cttcccactg			2700
cttggttactg tggtgcttcc cactccccct tgaccccagg cccctgcttc tccctctagg			2760
agcctaaaga accctcctgg cctccagctc agccttctct cacctactat gtctgtccaa			2820
caggctctgca tgggtccctg ataatgagaa cagctgcctg gtcttctctc ccagtctgcc			2880
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tttgggcaag gcaacatccc cattccaatt ccattttctg atgcagattt tagctgaggg			3060
atttggaagc catttgggga ggcaggctgg gccaaagggt agagctgggt aataaatgtc			3120

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 gaccggccag aatttagctt cacttgagag agatctggaa tggtcgccat gattgaaacc 3240  
 acgcaccatt acatcatcat tacattaatt acatcaacat aaattatttc ttcccccttc 3300  
 ccttttccag cactcaacca aggagcaaag ctcatccac cccacacccc tcccagatct 3360  
 gctcactgcc aggtcctctt cccctttgtt cagtggagct ggcttttctc ccagcccctt 3420  
 tccatgcctt tcactccatt tggcaagctc tgagggggag cctggggacg ggtttgggtc 3480  
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 cagctttcgc cctctgcttt gatggctgag gtgaactcat gttctttggg aaaagggaag 3600  
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<210> 70

<211> 630

<212> PRT

<213> Homo sapiens

<400> 70

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Glu	Ala	Val	Cys	Ala	Ile	Cys	Leu	Asp	Tyr	Phe	Thr	Asp	Pro	Val	Ser
				20					25					30	
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
				35					40					45	
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
				50					55					60	
Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Val	Glu	Ala	Val	Gly	Ala	Gly	Ala
				65					70					75	
Gly	Trp	Asp	Thr	Pro	Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu
				85					90					95	



Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met  
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 Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp  
                   115                          120                          125  
 Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp  
                   130                          135                          140  
 Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val  
 145                          150                          155                          160  
 Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala  
                           165                          170                          175  
 Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg  
                           180                          185                          190  
 Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile  
                   195                          200                          205  
 Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln  
                   210                          215                          220  
 Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val  
 225                          230                          235                          240  
 Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys  
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 Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala  
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 Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val  
                   275                          280                          285  
 Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser  
                   290                          295                          300  
 Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu

305	310	315	320
Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg			
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Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg			
	340	345	350
Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln			
	355	360	365
Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu			
	370	375	380
Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp			
385	390	395	400
Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala			
	405	410	415
Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp			
	420	425	430
Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro			
	435	440	445
Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp			
	450	455	460
His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly			
465	470	475	480
Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg			
	485	490	495
Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys			
	500	505	510
Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser			
	515	520	525

Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu  
 530 535 540  
 Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln  
 545 550 555 560  
 Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro  
 565 570 575  
 Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe  
 580 585 590  
 Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe  
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 610 615 620  
 Arg Ile Lys Leu Cys Pro  
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<210> 71

<211> 3833

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (711)..(1898)

<400> 71

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 cgcccctcgc cccccaccg aacctctaca ctggctggct ggacactaag atg gct 716

Met Ala

1

gcc gtt gcc atg aca ccc aac cct gtg cag acc ctt cag gag gag gcg 764  
 Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu Glu Ala

5

10

15

gtg tgc gcc atc tgc ctc gat tac ttc acg gac ccc gtg tcc atc ggc 812  
 Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser Ile Gly

20

25

30

tgc ggg cac aac ttc tgc cga gtt tgt gta acc cag ttg tgg ggt ggg 860  
 Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp Gly Gly

35

40

45

50

gag gat gag gag gac aga gat gag tta gat cgg gag gag gag gag gag 908  
 Glu Asp Glu Glu Asp Arg Asp Glu Leu Asp Arg Glu Glu Glu Glu Glu

55

60

65

gac gga gag gag gag gaa gtg gag gct gtg ggg gct ggc gcg ggg tgg 956  
 Asp Gly Glu Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala Gly Trp

70

75

80

gac acc ccc atg cgg gat gaa gac tac gag ggt gac atg gag gag gag 1004  
 Asp Thr Pro Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu Glu Glu

85	90	95	
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Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met Ser Arg			
100	105	110	
tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag gac gag gag	1100		
Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp Glu Glu			
115	120	125	130
gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag gac ctg agg	1148		
Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp Leu Arg			
	135	140	145
ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag gtt gag gaa	1196		
Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val Glu Glu			
	150	155	160
gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca gcc cct cgg	1244		
Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala Pro Arg			
	165	170	175
agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct cgg cgg agc	1292		
Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg Arg Ser			
180	185	190	
ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg att cgg cag	1340		
Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile Arg Gln			
195	200	205	210
atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat cag ggc atc	1388		
Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile			
	215	220	225
tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag gta gac gaa	1436		
Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu			

230	235	240	
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Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His			
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Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu			
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cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca gtg cag aag 1580			
Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys			
275	280	285	290
atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag agc cag atg 1628			
Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met			
295	300	305	
aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga ctg aca cgg 1676			
Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg			
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ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc aga gag atg 1724			
Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met			
325	330	335	
cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt cgc ctt gca 1772			
His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala			
340	345	350	
gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc cag gag cgg 1820			
Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg			
355	360	365	370
agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag gag act ttc 1868			
Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe			

375	380	385	
aat agg tgt gtt ccc agt ctt tgc cct tcg tgacccagtg gcatctggtt			1918
Asn Arg Cys Val Pro Ser Leu Cys Pro Ser			
390	395		
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tccatctcct ggaccctcct ctcttcccc tcagcttttg cttttccctc tgggaatatc			2038
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<210> 72

<211> 396

<212> PRT

<213> Homo sapiens

<400> 72

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				20					25					30	
Ile	Gly	Cys	Gly	His	Asn	Phe	Cys	Arg	Val	Cys	Val	Thr	Gln	Leu	Trp
				35					40					45	
Gly	Gly	Glu	Asp	Glu	Glu	Asp	Arg	Asp	Glu	Leu	Asp	Arg	Glu	Glu	Glu
				50					55					60	
Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Val	Glu	Ala	Val	Gly	Ala	Gly	Ala
				65					70					75	
Gly	Trp	Asp	Thr	Pro	Met	Arg	Asp	Glu	Asp	Tyr	Glu	Gly	Asp	Met	Glu
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Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met  
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 Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp  
 115 120 125  
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 130 135 140  
 Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val  
 145 150 155 160  
 Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala  
 165 170 175  
 Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg  
 180 185 190  
 Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile  
 195 200 205  
 Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln  
 210 215 220  
 Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val  
 225 230 235 240  
 Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys  
 245 250 255  
 Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala  
 260 265 270  
 Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val  
 275 280 285  
 Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser  
 290 295 300  
 Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu

305                      310                      315                      320  
 Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg  
                          325                      330                      335  
 Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg  
                          340                      345                      350  
 Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln  
                          355                      360                      365  
 Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu  
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 Thr Phe Asn Arg Cys Val Pro Ser Leu Cys Pro Ser  
 385                      390                      395

<210> 73

<211> 2891

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24).. (956)

<400> 73

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Glu Glu Glu Val Glu Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly

15                      20                      25

atg agc agg tcc agc tgg gac aac atg gac tat gtg tgg gag gag gag 149

Met Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu	
30 35 40	
gac gag gag gaa gac ctg gac tac tac ttg ggg gac atg gag gag gag	197
Asp Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu	
45 50 55	
gac ctg agg ggg gag gat gag gag gac gag gag gaa gtg ctg gag gag	245
Asp Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu	
60 65 70	
gtt gag gaa gag gat cta gac ccc gtc acc cca ctg ccc ccg cct cca	293
Val Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro	
75 80 85 90	
gcc cct cgg agg tgc ttc aca tgc cct cag tgc cga aag agc ttt cct	341
Ala Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro	
95 100 105	
cgg cgg agc ttc cgc ccc aac ctg cag ctg gcc aat atg gtc cag gtg	389
Arg Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val	
110 115 120	
att cgg cag atg cac cca acc cct ggt cga ggg agc cgc gtg acc gat	437
Ile Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp	
125 130 135	
cag ggc atc tgt ccc aaa cac caa gaa gcc ctg aag ctc ttc tgc gag	485
Gln Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu	
140 145 150	
gta gac gaa gag gcc atc tgt gtg gtg tgc cga gaa tcc agg agc cac	533
Val Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His	
155 160 165 170	
aaa cag cac agc gtg gtg cca ttg gag gag gtg gtg cag gag tac aag	581

Lys Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys  
 175 180 185  
 gcc aaa ctg cag ggg cac gtg gaa cca ctg agg aag cac ctg gag gca 629  
 Ala Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala  
 190 195 200  
 gtg cag aag atg aaa gcc aag gag gag agg cga gtg aca gaa ctg aag 677  
 Val Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys  
 205 210 215  
 agc cag atg aag tca gag ctg gca gcg gtg gcc tcg gag ttt ggg cga 725  
 Ser Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg  
 220 225 230  
 ctg aca cgg ttt ctg gct gaa gag cag gca ggg ctg gaa cgg cgt ctc 773  
 Leu Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu  
 235 240 245 250  
 aga gag atg cat gaa gcc cag ctg ggg cgt gcg gga gcc gcg gct agt 821  
 Arg Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser  
 255 260 265  
 cgc ctt gca gaa cag gcc gcc cag ctc agc cgc ctg ctg gca gag gcc 869  
 Arg Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala  
 270 275 280  
 cag gag cgg agc cag cag ggg ggt ctc cgg ctg ctc cag gac atc aag 917  
 Gln Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys  
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 gag act ttc aat agg tgt gtt ccc agt ctt tgc cct tcg tgacccagt 966  
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 gcttc 2891

<210> 74

<211> 311

<212> PRT

<213> Homo sapiens

<400> 74

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				20				25					30		
Asp	Asn	Met	Asp	Tyr	Val	Trp	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Leu
				35				40					45		
Asp	Tyr	Tyr	Leu	Gly	Asp	Met	Glu	Glu	Glu	Asp	Leu	Arg	Gly	Glu	Asp
				50				55					60		
Glu	Glu	Asp	Glu	Glu	Glu	Val	Leu	Glu	Glu	Val	Glu	Glu	Glu	Asp	Leu
				65				70					75		80
Asp	Pro	Val	Thr	Pro	Leu	Pro	Pro	Pro	Pro	Ala	Pro	Arg	Arg	Cys	Phe
				85				90					95		
Thr	Cys	Pro	Gln	Cys	Arg	Lys	Ser	Phe	Pro	Arg	Arg	Ser	Phe	Arg	Pro
				100				105					110		
Asn	Leu	Gln	Leu	Ala	Asn	Met	Val	Gln	Val	Ile	Arg	Gln	Met	His	Pro
				115				120					125		

Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln Gly Ile Cys Pro Lys  
130 135 140  
His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Glu Glu Ala Ile  
145 150 155 160  
Cys Val Val Cys Arg Glu Ser Arg Ser His Lys Gln His Ser Val Val  
165 170 175  
Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala Lys Leu Gln Gly His  
180 185 190  
Val Glu Pro Leu Arg Lys His Leu Glu Ala Val Gln Lys Met Lys Ala  
195 200 205  
Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser Gln Met Lys Ser Glu  
210 215 220  
Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu Thr Arg Phe Leu Ala  
225 230 235 240  
Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg Glu Met His Glu Ala  
245 250 255  
Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg Leu Ala Glu Gln Ala  
260 265 270  
Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln Glu Arg Ser Gln Gln  
275 280 285  
Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu Thr Phe Asn Arg Cys  
290 295 300  
Val Pro Ser Leu Cys Pro Ser  
305 310

&lt;210&gt; 75

&lt;211&gt; 3070

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (267).. (1295)

&lt;400&gt; 75

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acacagattt gctgccacag aggctg atg gac aac cag gcg gag aga gaa agt 293

Met Asp Asn Gln Ala Glu Arg Glu Ser

1

5

gag gct ggt gtt ggt ttg caa agg gat gag gat gac gct cct ctg tgt 341  
Glu Ala Gly Val Gly Leu Gln Arg Asp Glu Asp Asp Ala Pro Leu Cys

10

15

20

25

gaa gac gtg gag cta caa gac gga gat ctg tcc ccc gaa gaa aaa ata 389  
Glu Asp Val Glu Leu Gln Asp Gly Asp Leu Ser Pro Glu Glu Lys Ile

30

35

40

ttt ttg aga gaa ttt ccc aga ttg aaa gaa gat ctg aaa ggg aac att 437  
Phe Leu Arg Glu Phe Pro Arg Leu Lys Glu Asp Leu Lys Gly Asn Ile

45

50

55

gac aag ctc cgt gcc ctc gca gac gat att gac aaa acc cac aag aaa 485  
Asp Lys Leu Arg Ala Leu Ala Asp Asp Ile Asp Lys Thr His Lys Lys

60

65

70

ttc acc aag gct aac atg gtg gcc acc tct act gct gtc atc tct gga 533  
Phe Thr Lys Ala Asn Met Val Ala Thr Ser Thr Ala Val Ile Ser Gly



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Val Met Ser Leu Leu Gly Leu Ala Leu Ala Pro Ala Thr Gly Gly Gly			
90	95	100	105
agc ctg ctg ctc tcc acc gct ggt caa ggt ttg gca aca gca gct ggg	629		
Ser Leu Leu Leu Ser Thr Ala Gly Gln Gly Leu Ala Thr Ala Ala Gly			
110	115	120	
gtc acc agc atc gtg agt ggt acg ttg gaa cgc tcc aaa aat aaa gaa	677		
Val Thr Ser Ile Val Ser Gly Thr Leu Glu Arg Ser Lys Asn Lys Glu			
125	130	135	
gcc caa gca cgg gcg gaa gac ata ctg ccc acc tac gac caa gag gac	725		
Ala Gln Ala Arg Ala Glu Asp Ile Leu Pro Thr Tyr Asp Gln Glu Asp			
140	145	150	
agg gag gat gag gaa gag aag gca gac tat gtc aca gct gct gga aag	773		
Arg Glu Asp Glu Glu Glu Lys Ala Asp Tyr Val Thr Ala Ala Gly Lys			
155	160	165	
att atc tat aat ctt aga aac acc ttg aag tat gcc aag aaa aac gtc	821		
Ile Ile Tyr Asn Leu Arg Asn Thr Leu Lys Tyr Ala Lys Lys Asn Val			
170	175	180	185
cgt gca ttt tgg aaa ctc aga gcc aac cca cgc ttg gcc aat gct acc	869		
Arg Ala Phe Trp Lys Leu Arg Ala Asn Pro Arg Leu Ala Asn Ala Thr			
190	195	200	
aag cgt ctt ctg acc act ggc caa gtc tcc tcc cgg agc cgc gtg cag	917		
Lys Arg Leu Leu Thr Thr Gly Gln Val Ser Ser Arg Ser Arg Val Gln			
205	210	215	
gtg caa aag gcc ttt gcg gga aca aca ctg gcg atg acc aaa aat gct	965		
Val Gln Lys Ala Phe Ala Gly Thr Thr Leu Ala Met Thr Lys Asn Ala			

220	225	230	
cgc gtg ctg gga ggt gtg atg tcc gcc ttc tcc ctt ggc tat gac ttg			1013
Arg Val Leu Gly Gly Val Met Ser Ala Phe Ser Leu Gly Tyr Asp Leu			
235	240	245	
gcc act ctc tca aag gaa tgg aag cac ctg aag gaa gga gca agg aca			1061
Ala Thr Leu Ser Lys Glu Trp Lys His Leu Lys Glu Gly Ala Arg Thr			
250	255	260	265
aag ttt gcg gaa gag ttg aga gcc aag gcc ttg gag ctg gag agg aaa			1109
Lys Phe Ala Glu Glu Leu Arg Ala Lys Ala Leu Glu Leu Glu Arg Lys			
270	275	280	
ctc aca gaa ctc acc cag ctc tac aag agc ttg cag cag aaa gtg agg			1157
Leu Thr Glu Leu Thr Gln Leu Tyr Lys Ser Leu Gln Gln Lys Val Arg			
285	290	295	
tca agg gcc aga ggg gtg ggg aag gat tta act ggg acc tgc gaa acc			1205
Ser Arg Ala Arg Gly Val Gly Lys Asp Leu Thr Gly Thr Cys Glu Thr			
300	305	310	
gag gct tac tgg aag gag tta agg gag cat gtg tgg atg tgg ctg tgg			1253
Glu Ala Tyr Trp Lys Glu Leu Arg Glu His Val Trp Met Trp Leu Trp			
315	320	325	
ctg tgt gtg tgt ctg tgt gtc tgt gtg tat gta cag ttt aca			1295
Leu Cys Val Cys Leu Cys Val Cys Val Tyr Val Gln Phe Thr			
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&lt;210&gt; 76

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

Met Asp Asn Gln Ala Glu Arg Glu Ser Glu Ala Gly Val Gly Leu Gln

1 5 10 15

Arg Asp Glu Asp Asp Ala Pro Leu Cys Glu Asp Val Glu Leu Gln Asp

20 25 30

Gly Asp Leu Ser Pro Glu Glu Lys Ile Phe Leu Arg Glu Phe Pro Arg

35 40 45

Leu Lys Glu Asp Leu Lys Gly Asn Ile Asp Lys Leu Arg Ala Leu Ala

50 55 60

Asp Asp Ile Asp Lys Thr His Lys Lys Phe Thr Lys Ala Asn Met Val

65 70 75 80

Ala Thr Ser Thr Ala Val Ile Ser Gly Val Met Ser Leu Leu Gly Leu

85 90 95

Ala Leu Ala Pro Ala Thr Gly Gly Gly Ser Leu Leu Leu Ser Thr Ala

100 105 110

Gly Gln Gly Leu Ala Thr Ala Ala Gly Val Thr Ser Ile Val Ser Gly

115 120 125

Thr Leu Glu Arg Ser Lys Asn Lys Glu Ala Gln Ala Arg Ala Glu Asp

130 135 140

Ile Leu Pro Thr Tyr Asp Gln Glu Asp Arg Glu Asp Glu Glu Glu Lys

145 150 155 160

Ala Asp Tyr Val Thr Ala Ala Gly Lys Ile Ile Tyr Asn Leu Arg Asn

165 170 175

Thr Leu Lys Tyr Ala Lys Lys Asn Val Arg Ala Phe Trp Lys Leu Arg

	180		185		190
Ala Asn Pro Arg Leu Ala Asn Ala Thr Lys Arg Leu Leu Thr Thr Gly					
195		200		205	
Gln Val Ser Ser Arg Ser Arg Val Gln Val Gln Lys Ala Phe Ala Gly					
210		215		220	
Thr Thr Leu Ala Met Thr Lys Asn Ala Arg Val Leu Gly Gly Val Met					
225		230		235	240
Ser Ala Phe Ser Leu Gly Tyr Asp Leu Ala Thr Leu Ser Lys Glu Trp					
	245		250		255
Lys His Leu Lys Glu Gly Ala Arg Thr Lys Phe Ala Glu Glu Leu Arg					
	260		265		270
Ala Lys Ala Leu Glu Leu Glu Arg Lys Leu Thr Glu Leu Thr Gln Leu					
	275		280		285
Tyr Lys Ser Leu Gln Gln Lys Val Arg Ser Arg Ala Arg Gly Val Gly					
	290		295		300
Lys Asp Leu Thr Gly Thr Cys Glu Thr Glu Ala Tyr Trp Lys Glu Leu					
305		310		315	320
Arg Glu His Val Trp Met Trp Leu Trp Leu Cys Val Cys Leu Cys Val					
	325		330		335
Cys Val Tyr Val Gln Phe Thr					
	340				

&lt;210&gt; 77

&lt;211&gt; 2506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (108).. (1607)

&lt;400&gt; 77

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cgc gtc ttt ctc gca ttc tgt gtc tgg ctg act ctg ccg gga gct gaa 164
Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu
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acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 212
Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser
      20              25              30              35

tgt gtc aat gcc acc gcc tgt cgc tgc aat cca ggg ttc ggc tct ttt 260
Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Gly Ser Phe
              40              45              50

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Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp Ile Asn Glu
              55              60              65

tgt gca aca ccg tcg aaa gtg tca tgc gga aaa ttc tcg gac tgc tgg 356
Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp
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aac aca gag ggg agc tac gac tgc gtg tgc agc ccg gga tat gag cct 404
Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly Tyr Glu Pro
              85              90              95

gtt tct ggg gca aaa aca ttc aag aat gag agc gag aac acc tgt caa 452
Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn Thr Cys Gln

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gat gtg gac gaa tgt cag cag aac cca agg ctc tgt aaa agc tac ggc				500
Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly				
	120	125	130	
acc tgc gtc aac acc ctt ggc agc tat acc tgc cag tgc ctg cct ggc				548
Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly				
	135	140	145	
ttc aag ttc ata cct gag gat ccg aag gtc tgc aca gat gtg gac gag				596
Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp Val Asp Glu				
	150	155	160	
tgc agc tcc ggg cag cat cag tgt gac agc tcc acc gag ggc tgc cag				644
Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu Gly Cys Gln				
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gtg ctg ggc agc aag aac ggc agc acc acc tgc caa tgc agc cac ctg				692
Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu				
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Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys				
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ctg acc ctg atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg				788
Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu				
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ctg ctg tgc atc ctc act ttc ctg ctg gtg cgg ccc atc cag ggc tcg				836
Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser				
	230	235	240	
cgc acc acc ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc				884
Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser				

245	250	255	
acc atc ttc ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg	932		
Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu			
260	265	270	275
cgc tgc cgc ctg gtg gcc ggg ctg ctg cac tac tgt ttc ctg gcc gcc	980		
Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala			
280	285	290	
ttc tgc tgg atg agc ctc gaa ggc ctg gag ctc tac ttt ctt gtg gtg	1028		
Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val			
295	300	305	
cgc gtg ttc caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc	1076		
Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile			
310	315	320	
ggc tat ggc gtg ccc ctg ctc atc gtg ggc gtc tcg gct gcc atc tac	1124		
Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr			
325	330	335	
agc aag ggc tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag	1172		
Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln			
340	345	350	355
ggc ttc ctc tgg agc ttc ttg gga cct gtg acc ttc atc att ttg tgc	1220		
Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys			
360	365	370	
aat gct gtc att ttc gtg act acc gtc tgg aag ctc act cag aag ttt	1268		
Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe			
375	380	385	
tct gaa atc aat cca gac atg aag aaa tta aag aag gcg agg gcg ctg	1316		
Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu			



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 acc atc acg gcc atc gcg cag ctc ttc ctg ttg ggc tgc acc tgg gtc 1364  
 Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr Trp Val  
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 Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val  
 420 425 430 435  
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 Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu Leu His  
 440 445 450  
 tgc ctg ctc aac aag aag gtt cgg gaa gaa tac cgg aag tgg gcc tgc 1508  
 Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys  
 455 460 465  
 cta gtt gct ggg ggg agc aag tac tca gaa ttc acc tcc acc acg tct 1556  
 Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr Thr Ser  
 470 475 480  
 ggc act ggc cac aat cag acc cgg gcc ctc agg gca tca gag tcc ggc 1604  
 Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly  
 485 490 495  
 ata tgaaggcgca tggttctgga cggcccagca gctcctgtgg ccacagcagc 1657  
 Ile  
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 gaggcctgcc ctgcctggcc gggcaggagg ttctcactgt tgtgaaggtt gtagacgttg 2437  
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<210> 78

<211> 500

<212> PRT

<213> Homo sapiens

<400> 78

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Gly	Ala	Glu	Thr	Gln	Asp	Ser	Arg	Gly	Cys	Ala	Arg	Trp	Cys	Pro	Gln
				20					25					30	
Asn	Ser	Ser	Cys	Val	Asn	Ala	Thr	Ala	Cys	Arg	Cys	Asn	Pro	Gly	Phe
				35					40					45	
Gly	Ser	Phe	Ser	Glu	Ile	Ile	Thr	Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp
				50					55					60	
Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser	Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser
				65					70					75	
Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser	Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly

	85	90	95
Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn			
	100	105	110
Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys			
	115	120	125
Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys			
	130	135	140
Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp			
145	150	155	160
Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu			
	165	170	175
Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys			
	180	185	190
Ser His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu			
	195	200	205
Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu			
	210	215	220
Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile			
225	230	235	240
Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe			
	245	250	255
Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln			
	260	265	270
Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe			
	275	280	285
Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe			
	290	295	300

Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu  
305 310 315 320  
Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala  
325 330 335  
Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp  
340 345 350  
Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile  
355 360 365  
Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr  
370 375 380  
Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala  
385 390 395 400  
Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys  
405 410 415  
Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu  
420 425 430  
Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr  
435 440 445  
Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys  
450 455 460  
Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser  
465 470 475 480  
Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser  
485 490 495  
Glu Ser Gly Ile  
500

&lt;210&gt; 79

&lt;211&gt; 2506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (108)..(1607)

&lt;400&gt; 79

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Met Gly Gly

1

cgc gtc ttt ctc gca ttc tgt gtc tgg ctg act ctg ccg gga gct gaa 164  
 Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu

5

10

15

acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 212  
 Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser

20

25

30

35

tgt gtc aat gcc acc gcc tgt cgc tgc aat cca ggg ttc agc tct ttt 260  
 Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe

40

45

50

tct gag atc atc acc acc ccg acg gag act tgt gac gac atc aac gag 308  
 Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp Ile Asn Glu

55

60

65

tgt gca aca ccg tcg aaa gtg tca tgc gga aaa ttc tcg gac tgc tgg 356  
 Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp

70

75

80

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aac aca gag ggg agc tac gac tgc gtg tgc agc ccg gga tat gag cct 404
Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly Tyr Glu Pro
      85              90              95
gtt tct ggg gca aaa aca ttc aag aat gag agc gag aac acc tgt caa 452
Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn Thr Cys Gln
100              105              110              115
gat gtg gac gaa tgt cag cag aac cca agg ctc tgt aaa agc tac ggc 500
Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly
      120              125              130
acc tgc gtc aac acc ctt ggc agc tat acc tgc cag tgc ctg cct ggc 548
Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly
      135              140              145
ttc aag ttc ata cct gag gat ccg aag gtc tgc aca gat gtg gac gag 596
Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp Val Asp Glu
      150              155              160
tgc agc tcc ggg cag cat cag tgt gac agc tcc acc gag ggc tgc cag 644
Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu Gly Cys Gln
      165              170              175
gtg ctg ggc agc aag aac ggc agc acc acc tgc caa tgc agc cac ctg 692
Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu
180              185              190              195
agc agc ttt gcg atc ctt atg gct cat tat gac gtg gag gac tgg aag 740
Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys
      200              205              210
ctg acc ctg atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg 788
Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu
      215              220              225

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Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser	
230 235 240	
cgc acc acc ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc	884
Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser	
245 250 255	
acc atc ttc ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg	932
Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu	
260 265 270 275	
cgc tgc cgc ctg gtg gcc ggg ctg ctg cac tac tgt ttc ctg gcc gcc	980
Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala	
280 285 290	
ttc tgc tgg atg agc ctc gaa ggc ctg gag ctc tac ttt ctt gtg gtg	1028
Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val	
295 300 305	
cgc gtg ttc caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc	1076
Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile	
310 315 320	
ggc tat ggc gtg ccc ctg ctc atc gtg ggc gtc tgc gct gcc atc tac	1124
Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr	
325 330 335	
agc aag ggc tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag	1172
Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln	
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Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys	
360 365 370	

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 Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu  
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 Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val  
 420 425 430 435  
 ttt acc atc ctc aac tgc ctg cag ggc gcc ttc ctc tac ctg ctg cac 1460  
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 Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys  
 455 460 465  
 cta gtt gct ggg ggg agc aag tac tca gaa ttc acc tcc acc acg tct 1556  
 Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr Thr Ser  
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 ggc act ggc cac aat cag acc cgg gcc ctc agg gca tca gag tcc ggc 1604  
 Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly  
 485 490 495  
 ata tgaaggcgca tggttctgga cggcccagca gctcctgtgg ccacagcagc 1657  
 Ile  
 500



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<210> 80

<211> 500

<212> PRT

<213> Homo sapiens

<400> 80

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5

10

15

Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln

20

25

30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe

35

40

45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp  
 50 55 60  
 Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser  
 65 70 75 80  
 Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly  
 85 90 95  
 Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn  
 100 105 110  
 Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys  
 115 120 125  
 Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys  
 130 135 140  
 Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp  
 145 150 155 160  
 Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Glu  
 165 170 175  
 Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys  
 180 185 190  
 Ser His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu  
 195 200 205  
 Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu  
 210 215 220  
 Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile  
 225 230 235 240  
 Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe  
 245 250 255  
 Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln

260	265	270
Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe		
275	280	285
Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe		
290	295	300
Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu		
305	310	315
Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala		
325	330	335
Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp		
340	345	350
Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile		
355	360	365
Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr		
370	375	380
Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala		
385	390	395
Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys		
405	410	415
Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu		
420	425	430
Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr		
435	440	445
Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys		
450	455	460
Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser		
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485

490

495

Glu Ser Gly Ile

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<210> 81

<211> 2917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (2314)

<400> 81

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cctgccgctc ctgccggcag ctccaacc atg gga ggc cgc gtc ttt ctc gca    112
                                Met Gly Gly Arg Val Phe Leu Ala
                                1              5

ttc tgt gtc tgg ctg act ctg ccg gga gct gaa acc cag gac tcc agg    160
Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu Thr Gln Asp Ser Arg
    10              15              20

ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg tgt gtc aat gcc acc    208
Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser Cys Val Asn Ala Thr
    25              30              35              40

gcc tgt cgc tgc aat cca ggg ttc agc tct ttt tct gag atc atc acc    256
Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe Ser Glu Ile Ile Thr
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acc ccg acg gag act tgt gac gac atc aac gag tgt gca aca ccg tcg    304

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Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp	Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser		
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Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser	Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser		
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Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly	Tyr	Glu	Pro	Val	Ser	Gly	Ala	Lys		
aca	ttc	aag	aat	gag	agc	gag	aac	acc	tgt	caa	gat	gtg	gac	gag	tgc	448	
Thr	Phe	Lys	Asn	Glu	Ser	Glu	Asn	Thr	Cys	Gln	Asp	Val	Asp	Glu	Cys		
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Ser	Ser	Gly	Gln	His	Gln	Cys	Asp	Ser	Ser	Thr	Val	Cys	Phe	Asn	Thr		
gtg	ggt	tca	tac	agc	tgc	cgc	tgc	cgc	cca	ggc	tgg	aag	ccc	aga	cac	544	
Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro	Gly	Trp	Lys	Pro	Arg	His		
gga	atc	ccg	aat	aac	caa	aag	gac	act	gtc	tgt	gaa	gat	atg	act	ttc	592	
Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val	Cys	Glu	Asp	Met	Thr	Phe		
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Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His	Ser	Gln	Thr	Leu	Ser	Arg		
ttc	ttc	gac	aaa	gtc	cag	gac	ctg	ggc	aga	gac	tcc	aag	aca	agc	tca	688	
Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg	Asp	Ser	Lys	Thr	Ser	Ser		
gcc	gag	gtc	acc	atc	cag	aat	gtc	atc	aaa	ttg	gtg	gat	gaa	ctg	atg	736	

Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu Val Asp Glu Leu Met	
205	210
gaa gct cct gga gac gta gag gcc ctg gcg cca cct gtc cgg cac ctc	784
Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro Pro Val Arg His Leu	
220	225
ata gcc acc cag ctg ctc tca aac ctt gaa gat atc atg agg atc ctg	832
Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp Ile Met Arg Ile Leu	
235	240
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Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr Tyr Ile Ser Pro Ser Asn	
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aca gag ctg acc ctg atg atc cag gag cgg ggg gac aag aac gtc act	928
Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly Asp Lys Asn Val Thr	
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gga gcc gag gat cca ggc ccc gcc gtg gcg ggc atc ctc tcc atc cag	1024
Gly Ala Glu Asp Pro Gly Pro Ala Val Ala Gly Ile Leu Ser Ile Gln	
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aac atg acg aca ttg ctg gcc aat gcc tcc ttg aac ctg cat tcc aag	1072
Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu Asn Leu His Ser Lys	
315	320
aag caa gcc gaa ctg gag gag ata tat gaa agc agc atc cgt ggt gtc	1120
Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser Ser Ile Arg Gly Val	
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caa ctc aga cgc ctc tct gcc gtc aac tcc atc ttt ctg agc cac aac	1168

Gln Leu Arg Arg Leu Ser Ala Val Asn Ser Ile Phe Leu Ser His Asn  
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 Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe Ala Phe Ser His Leu  
                     365                      370                      375  
 gag tcc tcc gat ggg gag gcg gga aga gac cct cct gcc aag gac gtg 1264  
 Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro Pro Ala Lys Asp Val  
                     380                      385                      390  
 atg cct ggg cca cgg cag gag ctg ctc tgt gcc ttc tgg aag agt gac 1312  
 Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala Phe Trp Lys Ser Asp  
                     395                      400                      405  
 agc gac agg gga ggg cac tgg gcc acc gag ggc tgc cag gtg ctg ggc 1360  
 Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly Cys Gln Val Leu Gly  
                     410                      415                      420  
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 Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu Ser Ser Phe  
 425                      430                      435                      440  
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 Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp Trp Lys Leu Thr Leu  
                     445                      450                      455  
 atc acc agg gtg gga ctg gcg ctg tca ctc ttc tgc ctg ctg ctg tgc 1504  
 Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe Cys Leu Leu Leu Cys  
                     460                      465                      470  
 atc ctc act ttc ctg ctg gtg cgg ccc atc cag ggc tcg cgc acc acc 1552  
 Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser Arg Thr Thr  
                     475                      480                      485  
 ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc acc atc ttc 1600

Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser Thr Ile Phe  
 490 495 500  
 ctg gcc ggc atc gag aac gaa ggc ggc cag gtg ggg ctg cgc tgc cgc 1648  
 Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val Gly Leu Arg Cys Arg  
 505 510 515 520  
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 Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile Gly Tyr Gly  
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 Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr Ser Lys Gly  
 570 575 580  
 tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag ggc ttc ctc 1888  
 Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln Gly Phe Leu  
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 Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys Asn Ala Val  
 605 610 615  
 att ttc gtg act acc gtc tgg aag ctc act cag aag ttt tct gaa atc 1984  
 Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe Ser Glu Ile  
 620 625 630  
 aat cca gac atg aag aaa tta aag aag gcg agg gcg ctg acc atc acg 2032



Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu Thr Ile Thr  
 635 640 645  
 gcc atc gcg cag ctc ttc ctg ttg ggc tgc acc tgg gtc ttt ggc ctg 2080  
 Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr Trp Val Phe Gly Leu  
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 ttc atc ttc gac gat cgg agc ttg gtg ctg acc tat gtg ttt acc atc 2128  
 Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val Phe Thr Ile  
 665 670 675 680  
 ctc aac tgc ctg cag ggc gcc ttc cta tac ctg ctg cac tgc ctg ctc 2176  
 Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu Leu His Cys Leu Leu  
 685 690 695  
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 Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys Leu Val Ala  
 700 705 710  
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 His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly Ile  
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<211> 742

<212> PRT

<213> Homo sapiens

<400> 82

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20 25 30  
Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe  
35 40 45  
Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp  
50 55 60  
Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser  
65 70 75 80  
Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly  
85 90 95  
Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn  
100 105 110  
Thr Cys Gln Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp  
115 120 125  
Ser Ser Thr Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys

130	135	140	
Arg Pro Gly Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp			
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Thr Val Cys Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly			
	165	170	175
Val His Ser Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu			
	180	185	190
Gly Arg Asp Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val			
	195	200	205
Ile Lys Leu Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala			
	210	215	220
Leu Ala Pro Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn			
225	230	235	240
Leu Glu Asp Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro			
	245	250	255
Phe Thr Tyr Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln			
	260	265	270
Glu Arg Gly Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met			
	275	280	285
Lys Leu Asn Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala			
	290	295	300
Val Ala Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn			
305	310	315	320
Ala Ser Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile			
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Tyr Glu Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val			
	340	345	350

Asn Ser Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro  
 355 360 365  
 Ile Leu Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly  
 370 375 380  
 Arg Asp Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu  
 385 390 395 400  
 Leu Cys Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala  
 405 410 415  
 Thr Glu Gly Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys  
 420 425 430  
 Gln Cys Ser His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp  
 435 440 445  
 Val Glu Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu  
 450 455 460  
 Ser Leu Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg  
 465 470 475 480  
 Pro Ile Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys  
 485 490 495  
 Leu Phe Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly  
 500 505 510  
 Gly Gln Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr  
 515 520 525  
 Cys Phe Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu  
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 Tyr Phe Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg  
 545 550 555 560  
 Trp Leu Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val

565 570 575  
Ser Ala Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp  
580 585 590  
Leu Asp Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr  
595 600 605  
Phe Ile Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys  
610 615 620  
Leu Thr Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys  
625 630 635 640  
Lys Ala Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu  
645 650 655  
Gly Cys Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu  
660 665 670  
Val Leu Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe  
675 680 685  
Leu Tyr Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr  
690 695 700  
Arg Lys Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe  
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&lt;210&gt; 83

&lt;211&gt; 3156

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&lt;222&gt; (49)..(2553)

&lt;400&gt; 83

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Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro Gly Ala Glu
      5              10              15

acc cag gac tcc agg ggc tgt gcc cgg tgg tgc cct cag aac tcc tcg 153
Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser
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Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe
              40              45              50

tct gag atc atc acc acc ccg acg gag act tgt gac gac atc aac gag 249
Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp Ile Asn Glu
              55              60              65

tgt gca aca ccg tcg aaa gtg tca tgc gga aaa ttc tcg gac tgc tgg 297
Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser Asp Cys Trp
              70              75              80

aac aca gag ggg agc tac gac tgc gtg tgc agc ccg gga tat gag cct 345
Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly Tyr Glu Pro
      85              90              95
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 Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly

120 125 130  
 acc tgc gtc aac acc ctt ggc agc tat acc tgc cag tgc ctg cct ggc 489  
 Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly

135 140 145  
 ttc aag ttc ata cct gag gat ccg aag gtc tgc aca gat gtg aat gaa 537  
 Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp Val Asn Glu

150 155 160  
 tgc acc tcc gga caa aat ccg tgc cac agc tcc acc cac tgc ctc aac 585  
 Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His Cys Leu Asn

165 170 175  
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 Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp Gln Pro Ile

180 185 190 195  
 ccg ggg tcc ccc aat ggc cca aac aat acc gtc tgt gaa gat gtg gac 681  
 Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu Asp Val Asp

200 205 210  
 gag tgc agc tcc ggg cag cat cag tgt gac agc tcc acc gtc tgc ttc 729  
 Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr Val Cys Phe

215 220 225  
 aac acc gtg ggt tca tac agc tgc cgc tgc cgc cca ggc tgg aag ccc 777  
 Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly Trp Lys Pro

230	235	240	
aga cac gga atc ccg aat aac caa aag gac act gtc tgt gaa gat atg			825
Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys Glu Asp Met			
245	250	255	
act ttc tcc acc tgg acc ccg ccc cct gga gtc cac agc cag acg ctt			873
Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His Ser Gln Thr Leu			
260	265	270	275
tcc cga ttc ttc gac aaa gtc cag gac ctg ggc aga gac tcc aag aca			921
Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg Asp Ser Lys Thr			
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Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu Val Asp Glu			
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Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro Pro Val Arg			
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cac ctc ata gcc acc cag ctg ctc tca aac ctt gaa gat atc atg agg			1065
His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp Ile Met Arg			
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Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly Asp Lys Asn			
360	365	370	
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Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu Asn Trp Ala Val			



375	380	385	
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390	395	400	
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Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu Asn Leu His			
405	410	415	
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Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser Ser Ile Arg			
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440	445	450	
cac aac aac acc aag gaa ctc aac tcc ccc atc ctt ttc gcc ttc tcc			1449
His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe Ala Phe Ser			
455	460	465	
cac ctt gag tcc tcc gat ggg gag gcg gga aga gac cct cct gcc aag			1497
His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro Pro Ala Lys			
470	475	480	
gac gtg atg cct ggg cca cgg cag gag ctg ctc tgt gcc ttc tgg aag			1545
Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala Phe Trp Lys			
485	490	495	
agt gac agc gac agg gga ggg cac tgg gcc acc gag ggc tgc cag gtg			1593
Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly Cys Gln Val			
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Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser His Leu Ser			

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Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln Gly Ser Arg			
565	570	575	
acc acc ata cac ctg cac ctc tgc atc tgc ctc ttc gtg ggc tcc acc			1833
Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val Gly Ser Thr			
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Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu Ala Ala Phe			
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Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu Val Val Arg			
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gtg ttc caa ggc cag ggc ctg agt acg cgc tgg ctc tgc ctg atc ggc			2025
Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys Leu Ile Gly			
645	650	655	
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Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala Ile Tyr Ser			

660	665	670	675	
aag ggc tac ggc cgc ccc aga tac tgc tgg ttg gac ttt gag cag ggc	2121			
Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe Glu Gln Gly				
680	685	690		
ttc ctc tgg agc ttc ttg gga cct gtg acc ttc atc att ttg tgc aat	2169			
Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile Leu Cys Asn				
695	700	705		
gct gtc att ttc gtg act acc gtc tgg aag ctc act cag aag ttt tct	2217			
Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln Lys Phe Ser				
710	715	720		
gaa atc aat cca gac atg aag aaa tta aag aag gcg agg gcg ctg acc	2265			
Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg Ala Leu Thr				
725	730	735		
atc acg gcc atc gcg cag ctc ttc ctg ttg ggc tgc acc tgg gtc ttt	2313			
Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr Trp Val Phe				
740	745	750	755	
ggc ctg ttc atc ttc gac gat cgg agc ttg gtg ctg acc tat gtg ttt	2361			
Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr Tyr Val Phe				
760	765	770		
acc atc ctc aac tgc ctg cag ggc gcc ttc ctc tac ctg ctg cac tgc	2409			
Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu Leu His Cys				
775	780	785		
ctg ctc aac aag aag gtt cgg gaa gaa tac cgg aag tgg gcc tgc cta	2457			
Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp Ala Cys Leu				
790	795	800		
gtt gct ggg ggg agc aag tac tca gaa ttc acc tcc acc acg tct ggc	2505			
Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr Thr Ser Gly				

805                      810                      815  
 act ggc cac aat cag acc cgg gcc ctc agg gca tca gag tcc ggc ata 2553  
 Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu Ser Gly Ile  
 820                      825                      830                      835  
 tgaaggcgca tggttctgga cggcccagca gctcctgtgg ccacagcagc tttgtacacg 2613  
 aagaccatcc atcctccctt cgtccaccac tctactccct ccaccctccc tccctgatcc 2673  
 cgtgtgccac caggagggag tggcagctat agtctggcac caaagtccag gacacccagt 2733  
 ggggtggagt cggagccact ggtcctgctg ctggctgcct ctctgctcca ccttgtgacc 2793  
 cagggtgggg acaggggctg gcccagggt gcaatgcagc atgttgccct ggcacctgtg 2853  
 gccagtactc gggacagact aagggcgctt gtcccatcct ggacttttcc tctcatgtct 2913  
 ttgctgcaga actgaagaga ctaggcgctg gggctcagct tccctcttaa gctaagactg 2973  
 atgtcagagg ccccatggcg aggccccttg gggccactgc ctgaggctca cggtaacagag 3033  
 gcctgccctg cctggccggg caggagggtc tcaactgttg gaaggttgta gacgttgtgt 3093  
 aatgtgtttt tatctgttaa aatttttcag tgttgacact taaaattaaa cacatgcata 3153  
 cag 3156

<210> 84

<211> 835

<212> PRT

<213> Homo sapiens

<400> 84

Met Gly Gly Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro

1                      5                      10                      15

Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln

20                      25                      30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe

35                      40                      45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp  
 50 55 60  
 Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser  
 65 70 75 80  
 Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly  
 85 90 95  
 Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn  
 100 105 110  
 Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys  
 115 120 125  
 Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys  
 130 135 140  
 Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp  
 145 150 155 160  
 Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His  
 165 170 175  
 Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp  
 180 185 190  
 Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu  
 195 200 205  
 Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr  
 210 215 220  
 Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly  
 225 230 235 240  
 Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys  
 245 250 255  
 Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His Ser

260 265 270  
Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg Asp  
275 280 285  
Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu  
290 295 300  
Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro  
305 310 315 320  
Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp  
325 330 335  
Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr Tyr  
340 345 350  
Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg Gly  
355 360 365  
Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu Asn  
370 375 380  
Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala Val Ala Gly  
  
385 390 395 400  
Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser Leu  
405 410 415  
Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu Ser  
420 425 430  
Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser Ile  
435 440 445  
Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu Phe  
450 455 460  
Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp Pro

465                      470                      475                      480  
 Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys Ala  
                          485                      490                      495  
 Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu Gly  
                          500                      505                      510  
 Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys Ser  
                          515                      520                      525  
 His Leu Ser Ser Phe Ala Ile Leu Met Ala His Tyr Asp Val Glu Asp  
                          530                      535                      540  
 Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe  
 545                      550                      555                      560  
 Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln  
                          565                      570                      575  
 Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val  
                          580                      585                      590  
 Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val  
                          595                      600                      605  
 Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu  
                          610                      615                      620  
 Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu  
 625                      630                      635                      640  
 Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys  
                          645                      650                      655  
 Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala  
                          660                      665                      670  
 Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe  
                          675                      680                      685

Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile  
690 695 700  
Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln  
705 710 715 720  
Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg  
725 730 735  
Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr  
740 745 750  
Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr  
755 760 765  
Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu  
770 775 780  
Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp  
785 790 795 800  
Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr  
805 810 815  
Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu  
820 825 830  
Ser Gly Ile  
835

&lt;210&gt; 85

&lt;211&gt; 1239

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS



&lt;222&gt; (67).. (756)

&lt;400&gt; 85

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acacgttttc ctccaaggag cctcggacgt tgtcacgggt ttggggtcgg ggacagagcg 60
gtgacc atg gcc agg ctg gcg ttg tct cct gtg ccc agc cac tgg atg      108
      Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met
            1             5             10
gtg gcg ttg ctg ctg ctg ctc tca gca gct gag cca gta cca gca gcc      156
Val Ala Leu Leu Leu Leu Ser Ala Ala Glu Pro Val Pro Ala Ala
      15             20             25             30
aga tcg gag gac cgg tac cgg aat ccc aaa ggt agt gct tgt tcg cgg      204
Arg Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg
            35             40             45
atc tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg gtg      252
Ile Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val
            50             55             60
aaa atg cac tgc tac atg aac agc gcc tcc ggc aat gtg agc tgg ctc      300
Lys Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu
            65             70             75
tgg aag cag gag atg gac gag aat ccc cag cag ctg aag ctg gaa aag      348
Trp Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys
            80             85             90
ggc cgc atg gaa gag tcc cag aac gaa tct ctc gcc acc ctc acc atc      396
Gly Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile
      95             100             105             110
caa ggc atc cgg ttt gag gac aat ggc atc tac ttc tgc cag cag aag      444
Gln Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys
            115             120             125

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tgc aac aac acc tcg gag gtc tac cag ggc tgc ggc aca gag ctg cga 492  
 Cys Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg  
 130 135 140  
 gtc atg gga ttc agc acc ttg gca cag ctg aag cag agg aac acg ctg 540  
 Val Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu  
 145 150 155  
 aag gat ggt atc atc atg atc cag acg ctg ctg atc atc ctc ttc atc 588  
 Lys Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile  
 160 165 170  
 atc gtg cct atc ttc ctg ctg ctg gac aag gat gac agc aag gct ggc 636  
 Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly  
 175 180 185 190  
 atg gag gaa gat cac acc tac gag ggc ctg gac att gac cag aca gcc 684  
 Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala  
 195 200 205  
 acc tat gag gac ata gtg acg ctg cgg aca ggg gaa gtg aag tgg tct 732  
 Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser  
 210 215 220  
 gta ggt gag cac cca ggc cag gag tgagagccag gtcgccccat gacctgggtg 786  
 Val Gly Glu His Pro Gly Gln Glu  
 225 230  
 caggctccct ggcctcagtg actgcttcgg agctgcctgg ctcatggccc aacccttttc 846  
 ccggaccccc cagctggcct ctgaagctgg cccaccagag ctgccatttg tctccagccc 906  
 ctggtgtcca gctcttgcca aagggcctgg agtagaagga caacagggca gcaacttgga 966  
 gggagttctc tggggatgga cgggaccag ccttctgggg gtgctatgag gtgatccgtc 1026  
 cccacacatg ggatggggga ggcagagact ggtccagagc ccgcaaattg actcggagcc 1086  
 gagggcctcc cagcagagct tgggaagggc catggacca actgggcccc agaagagcca 1146

caggaacatc attcctctcc cgcaaccact cccaccccag ggaggccctg gcctccagtg 1206  
ccttcccccg tggaataaac ggtgtgtcct gag 1239

<210> 86

<211> 230

<212> PRT

<213> Homo sapiens

<400> 86

Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala

1 5 10 15

Leu Leu Leu Leu Leu Ser Ala Ala Glu Pro Val Pro Ala Ala Arg Ser

20 25 30

Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp

35 40 45

Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met

50 55 60

His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys

65 70 75 80

Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg

85 90 95

Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly

100 105 110

Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn

115 120 125

Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met

130 135 140

Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp

145                      150                      155                      160  
 Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val  
                          165                      170                      175  
 Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu  
                          180                      185                      190  
 Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr  
                          195                      200                      205  
 Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly  
                          210                      215                      220  
 Glu His Pro Gly Gln Glu  
 225                      230

<210> 87

<211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(753)

<400> 87

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                  Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met  
                  1                      5                      10  
 gtg gcg ttg ctg ctg ctg ctc tca gct gag cca gta cca gca gcc aga 156  
 Val Ala Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg  
                  15                      20                      25                      30

tcg gag gac cgg tac cgg aat ccc aaa ggt agt gct tgt tcg cgg atc	204
Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile	
35 40 45	
tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg gtg aaa	252
Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys	
50 55 60	
atg cac tgc tac atg aac agc gcc tcc ggc aat gtg agc tgg ctc tgg	300
Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp	
65 70 75	
aag cag gag atg gac gag aat ccc cag cag ctg aag ctg gaa aag ggc	348
Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly	
80 85 90	
cgc atg gaa gag tcc cag aac gaa tct ctc gcc acc ctc acc atc caa	396
Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln	
95 100 105 110	
ggc atc cgg ttt gag gac aat ggc atc tac ttc tgc cag cag aag tgc	444
Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys	
115 120 125	
aac aac acc tcg gag gtc tac cag ggc tgc ggc aca gag ctg cga gtc	492
Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val	
130 135 140	
atg gga ttc agc acc ttg gca cag ctg aag cag agg aac acg ctg aag	540
Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys	
145 150 155	
gat ggt atc atc atg atc cag acg ctg ctg atc atc ctc ttc atc atc	588
Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile	
160 165 170	

gtg cct atc ttc ctg ctg ctg gac aag gat gac agc aag gct ggc atg 636  
 Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met  
 175 180 185 190  
 gag gaa gat cac acc tac gag ggc ctg gac att gac cag aca gcc acc 684  
 Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr  
 195 200 205  
 tat gag gac ata gtg acg ctg cgg aca ggg gaa gtg aag tgg tct gta 732  
 Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val  
 210 215 220  
 ggt gag cac cca ggc cag gag tgagagccag gtcgccccat gacctgggtg 783  
 Gly Glu His Pro Gly Gln Glu  
 225  
 caggctccct ggcctcagt actgcttcgg agctgcctgg ctcatggccc aaccctttc 843  
 ccggaccccc cagctggcct ctgaagctgg cccaccagag ctgccatttg tctccagccc 903  
 ctggtgtcca gctcttgcca aagggcctgg agtagaagga caacagggca gcaacttgga 963  
 gggagtcttc tggggatgga cgggaccag ctttctgggg gtgctatgag gtgatccgtc 1023  
 cccacacatg ggatggggga ggcagagact ggtccagagc ccgcaaattg actcggagcc 1083  
 gagggcctcc cagcagagct tgggaagggc catggaccca actgggcccc agaagagcca 1143  
 caggaacatc attcctctcc cgcaaccact cccaccccag ggaggccctg gcctccagtg 1203  
 ccttcccccg tggaataaac ggtgtgtcct gag 1236

<210> 88

<211> 229

<212> PRT

<213> Homo sapiens

<400> 88

Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala

1	5	10	15
Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu			
20	25	30	
Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln			
35	40	45	
Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His			
50	55	60	
Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln			
65	70	75	80
Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met			
85	90	95	
Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile			
100	105	110	
Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn			
115	120	125	
Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly			
130	135	140	
Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly			
145	150	155	160
Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro			
165	170	175	
Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu			
180	185	190	
Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu			
195	200	205	
Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu			
210	215	220	

His Pro Gly Gln Glu

225

&lt;210&gt; 89

&lt;211&gt; 2137

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (147).. (1112)

&lt;400&gt; 89

acccttccag ctgccgtgt cgtctttgct tcagccgcag tcgccactgg ctgcttgagg 60  
 tgctcttaca gcctgttcca agtgtggctt aatccgtctc caccaccaga tctttctccg 120  
 tggattcctc tgctaagacc gctgcc atg cca gtg acg gta acc cgc acc acc 173

Met Pro Val Thr Val Thr Arg Thr Thr

1

5

atc aca acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc 221  
 Ile Thr Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile  
 10 15 20 25  
 gtg ggg tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg 269  
 Val Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu  
 30 35 40  
 ctg cag ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg 317  
 Leu Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val  
 45 50 55  
 ggc gcc tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc 365  
 Gly Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys



60	65	70	
ttc tgc ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg	413		
Phe Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly			
75	80	85	
ctc cag gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc	461		
Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe			
90	95	100	105
gcc tgc tat gcg gcc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc	509		
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro			
	110	115	120
acc acc tat gtc cag ttc ctg tcc cac gcc cgt tcg cgg gac cac gcc	557		
Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala			
	125	130	135
atc gcc gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc	605		
Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr			
	140	145	150
gaa gtg gcc tgg acc cgg gcc cgg ccc gcc gag atc act gcc tat atg	653		
Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met			
	155	160	165
gcc acc gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc	701		
Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys			
	170	175	180
atc atc ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg	749		
Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro			
	190	195	200
gcc ctg gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg	797		
Ala Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala			

205	210	215	
gcc atc gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc			845
Ala Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro			
220	225	230	
atc ccc ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc			893
Ile Pro Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu			
235	240	245	
ctc tat gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag			941
Leu Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu			
250	255	260	265
aag tat ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc			989
Lys Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg			
270	275	280	
agc cat gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc			1037
Ser His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala			
285	290	295	
atc ctg acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac			1085
Ile Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His			
300	305	310	
tct gcc cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct			1132
Ser Ala His Leu Val Phe Val Lys Val			
315	320		
cccgttccct ctccaacctc ttgtttcttc ttgcccagagt tttctttatg gagtacttct			1192
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 gcattaagca ccgaccctgg gtccctagc cccgcctggc actcagcctt gccagagatt 2032  
 ggctccagaa tttttgccag gcttacagaa caccactgc ctagaggcca tcttaaagga 2092  
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<210> 90

<211> 322

<212> PRT

<213> Homo sapiens

<400> 90

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Ser
1				5					10				15	
Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	Ala
			20					25					30	Leu
Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	Ser	Thr
			35					40					45	Cys
Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	Thr	Gly	Ser
			50					55					60	Met
Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	Phe	Ser	Val	Thr
														Leu

65                                      70                                      75                                      80  
Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu  
85                                      90                                      95  
Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe  
100                                      105                                      110  
Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu  
115                                      120                                      125  
Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser  
130                                      135                                      140  
Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala  
145                                      150                                      155                                      160  
Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu  
165                                      170                                      175  
Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser  
180                                      185                                      190  
Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala  
195                                      200                                      205  
Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn  
210                                      215                                      220  
Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
225                                      230                                      235                                      240  
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val  
245                                      250                                      255  
Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg  
260                                      265                                      270  
Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys  
275                                      280                                      285

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu

290

295

300

Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val

305

310

315

320

Lys Val

<210> 91

<211> 1644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (172).. (639)

<400> 91

aaacgtttct ttcctacgca gccgtcctg ccgccgtggt cgctggagct ttgcctctct 60  
aggccggcag cgcctctcct ccatggctcct gtctgtcagc gctgttttgg gageccgccg 120  
gtgaggccgg gccacgtca gacacttcca tcgtcgagtc tgtcactggg c atg gcg 177

Met Ala

1

ggt cag ttc cgc agc tac gtg tgg gac ccg ctg ctg atc ctg tcg cag 225

Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln

5

10

15

atc gtc ctc atg cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg 273

Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu

20

25

30

gcg ctg gtg gac ggg cta gtg cga agc agc ccc tcg ctg gac cag atg 321

Ala Leu Val Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met

35	40	45	50	
ttc gac gcc gag atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc	369			
Phe Asp Ala Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser				
55	60	65		
atg atg tcc ttc atc ctc aac gcc ctc acc tgt gcc ctg ggc ttg ctg	417			
Met Met Ser Phe Ile Leu Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu				
70	75	80		
tac ttc atc cgg cga gga aag cag tgt ctg gat ttc act gtc act gtc	465			
Tyr Phe Ile Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val				
85	90	95		
cat ttc ttt cac ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc	513			
His Phe Phe His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro				
100	105	110		
tcg gcg ctg acc tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg	561			
Ser Ala Leu Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met				
115	120	125	130	
gct gtc atc ggg gag tac ctg tgc atg cgg acg gag ctc aag gag ata	609			
Ala Val Ile Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile				
135	140	145		
ccc ctc aac tca gcc cct aaa tcc aat gtc tagaatcagg ccctttggac	659			
Pro Leu Asn Ser Ala Pro Lys Ser Asn Val				
150	155			
atcctgctga cacttgggcc ccttaacacc ttgggctgct cagaccctcc agatgaggtc	719			
cagcccagat ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag	779			
tgagggcctg tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg	839			
tctgttgaag ccttggtatc tgagaggtca ggaaggggac ctctttgagg gtaataacat	899			
aattggaacc atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga	959			

gaaaaaaaaat caaggatatc tgattggagc aaaccacttc tttagtcac tgtcttacct 1019  
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 tgccgaatca cagcagttct gttggagaaa cgcttggttt ccgatccag agccacagaa 1139  
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 taaaataca gtattttcca tgggtt 1644

<210> 92

<211> 156

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu

1 5 10 15

Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu

20 25 30

Trp Leu Ala Leu Val Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp

35 40 45

Gln Met Phe Asp Ala Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg

50 55 60

Leu Ser Met Met Ser Phe Ile Leu Asn Ala Leu Thr Cys Ala Leu Gly

65	70	75	80
Leu Leu Tyr Phe Ile Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val			
	85	90	95
Thr Val His Phe Phe His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg			
	100	105	110
Phe Pro Ser Ala Leu Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala			
	115	120	125
Leu Met Ala Val Ile Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys			
	130	135	140
Glu Ile Pro Leu Asn Ser Ala Pro Lys Ser Asn Val			
145	150	155	

&lt;210&gt; 93

&lt;211&gt; 2608

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (133).. (1053)

&lt;400&gt; 93

gtgcgcgcga agacgtgggg acgcaggcgg gtcgtagaga gcgttcagcc gtctgtatat 60  
 ctccccagat acctgaaact gaccacctga gtacgttttc ccattgctga gctgtttccc 120  
 tgatatctgg cc atg caa cgg aga tca aga ggg ata aat act gga ctt att 171

Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile

1

5

10

cta ctc ctt tct caa atc ttc cat gtt ggg atc aac aat att cca cct 219  
 Leu Leu Leu Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro



15	20	25	
gtc acc cta gca act ttg gcc ctc aac atc tgg ttc ttc ttg aac cct	267		
Val Thr Leu Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro			
30	35	40	45
cag aag cca ctg tat agc tcc tgc ctt agt gtg gag aag tgt tac cag	315		
Gln Lys Pro Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln			
50	55	60	
caa aaa gac tgg cag cgt tta ctg ctc tct ccc ctt cac cat gct gat	363		
Gln Lys Asp Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp			
65	70	75	
gat tgg cat ttg tat ttc aat atg gca tcc atg ctc tgg aaa gga ata	411		
Asp Trp His Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile			
80	85	90	
aat cta gaa aga aga ctg gga agt aga tgg ttt gcc tat gtt atc acc	459		
Asn Leu Glu Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr			
95	100	105	
gca ttt tct gta ctt act gga gtg gta tac ctg ctc ttg caa ttt gct	507		
Ala Phe Ser Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala			
110	115	120	125
gtt gcc gaa ttt atg gat gaa cct gac ttc aaa agg agc tgt gct gta	555		
Val Ala Glu Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val			
130	135	140	
ggt ttc tca gga gtt ttg ttt gct ttg aaa gtt ctt aac aac cat tat	603		
Gly Phe Ser Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr			
145	150	155	
tgc cct gga ggc ttt gtc aac att ttg ggc ttt cct gta ccg aac aga	651		
Cys Pro Gly Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg			

160	165	170	
ttt gct tgt tgg gtc gaa ctt gtg gct att cat tta ttc tca cca ggg	699		
Phe Ala Cys Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly			
175	180	185	
act tcc ttc gct ggg cat ctg gct ggg att ctt gtt gga cta atg tac	747		
Thr Ser Phe Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr			
190	195	200	205
act caa ggg cct ctg aag aaa atc atg gaa gca tgt gca ggc ggt ttt	795		
Thr Gln Gly Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe			
210	215	220	
tcc tcc agt gtt ggt tac cca gga cgg caa tac tac ttt aat agt tca	843		
Ser Ser Ser Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser			
225	230	235	
ggc agc tct gga tat cag gat tat tat ccg cat ggc agg cca gat cac	891		
Gly Ser Ser Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His			
240	245	250	
tat gaa gaa gca ccc agg aac tat gac acg tac aca gca gga ctg agt	939		
Tyr Glu Glu Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser			
255	260	265	
gaa gaa gaa cag ctc gag aga gca tta caa gcc agc ctc tgg gac cga	987		
Glu Glu Glu Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg			
270	275	280	285
gag tgc tgg gat tac agg cgt gag cca ccg tgc cca gcc gtt gtg atc	1035		
Glu Cys Trp Asp Tyr Arg Arg Glu Pro Pro Cys Pro Ala Val Val Ile			
290	295	300	
atc ttg aat tca gaa aac tgaaaactca gaggaaatac cagaaatagc	1083		
Ile Leu Asn Ser Glu Asn			

305

ccaccaccct acgggtttca tctctcacca gaagaaatga ggagacagcg gcttcacaga 1143  
 ttcatagacc agtgaggtag catcttgga agacatggcc tattctgtga attattgccc 1203  
 atttggtca tcccccaagc ccctaattca ttttaattca ttttaaaaaa aagcagagta 1263  
 caccggtatt gctccagatc gctcacatca cctgggacag tcccatggcc cctatgagtc 1323  
 aactcacagc ttgcggggag tgggccttct cctggccttg ttcttgctca taaacaggtc 1383  
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 gtggagccat ccccgctcc tcttggcga ttgccactgt ggctgtccag gaacaggatg 1623  
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 agtttttctt gagagattca gtattcagta aagaatagca ttcaattagt caaaaaatat 1923  
 atatataact tcttcctttc ctttcccatg aatcattgca gtcattccct aagtttcttc 1983  
 tctctttttt tcatggctgc tagtatttta ttttagaatc acagactctc agcttagaga 2043  
 gtcacagtat ctcaattatt tgctctgttc aatacttaac aatacctcct cactcaattc 2103  
 tacataactc cagcttagtc ttccaaaatt cactttcatg atgccactca gcatctcaaa 2163  
 tacctttcat tggctctctg ctgccaaagg ataaaggta aagtcattag cctcaacagt 2223  
 gggcttcaac cagcctttgg acctcagccc catttatcca tcacagagcg tggttaactag 2283  
 tctcactgct caggctgtga gtgttctga tcttgtaga ttctgtgctg tgcttctaca 2343  
 tggacagct ctttcctctc tcttgccca ttcagatcct cctcatccag ccccatctg 2403  
 aatcctgtaa cagacacaac cacatctaca cagtttccac ataccacttg gaattgctgg 2463  
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 catctgtttc tctgtctctc ctacagtgct cttgagcagt acgttgctctg gaatgtcaga 2583  
 accaataaat acttgtggat tgaaa 2608

&lt;210&gt; 94

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile Leu Leu Leu  
1 5 10 15  
Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu  
20 25 30  
Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro  
35 40 45  
Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp  
50 55 60  
Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His  
65 70 75 80  
Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu  
85 90 95  
Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser  
100 105 110  
Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu  
115 120 125  
Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser  
130 135 140  
Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly  
145 150 155 160  
Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys

165                                      170                                      175  
 Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe  
    180                                      185                                      190  
 Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly  
    195                                      200                                      205  
 Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser  
    210                                      215                                      220  
 Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser  
 225                                      230                                      235                                      240  
 Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu  
    245                                      250                                      255  
 Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu  
    260                                      265                                      270  
 Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Glu Cys Trp  
    275                                      280                                      285  
 Asp Tyr Arg Arg Glu Pro Pro Cys Pro Ala Val Val Ile Ile Leu Asn  
    290                                      295                                      300  
 Ser Glu Asn  
 305

<210> 95

<211> 2423

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (122).. (1066)

&lt;400&gt; 95

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 cctgaaactg accacctgag tacgttttcc cattgctgag ctgtttccct gatatctggc 120  
 c atg caa cgg aga tca aga ggg ata aat act gga ctt att cta ctc ctt 169  
 Met Gln Arg Arg Ser Arg Gly Ile Asn Thr Gly Leu Ile Leu Leu Leu  
 1 5 10 15  
 tct caa atc ttc cat gtt ggg atc aac aat att cca cct gtc acc cta 217  
 Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu  
 20 25 30  
 gca act ttg gcc ctc aac atc tgg ttc ttc ttg aac cct cag aag cca 265  
 Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro  
 35 40 45  
 ctg tat agc tcc tgc ctt agt gtg gag aag tgt tac cag caa aaa gac 313  
 Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp  
 50 55 60  
 tgg cag cgt tta ctg ctc tct ccc ctt cac cat gct gat gat tgg cat 361  
 Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His  
 65 70 75 80  
 ttg tat ttc aat atg gca tcc atg ctc tgg aaa gga ata aat cta gaa 409  
 Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu  
 85 90 95  
 aga aga ctg gga agt aga tgg ttt gcc tat gtt atc acc gca ttt tct 457  
 Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser  
 100 105 110  
 gta ctt act gga gtg gta tac ctg ctc ttg caa ttt gct gtt gcc gaa 505  
 Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu  
 115 120 125

ttt atg gat gaa cct gac ttc aaa agg agc tgt gct gta ggt ttc tca 553  
 Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser  
 130 135 140  
 gga gtt ttg ttt gct ttg aaa gtt ctt aac aac cat tat tgc cct gga 601  
 Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly  
 145 150 155 160  
 ggc ttt gtc aac att ttg ggc ttt cct gta ccg aac aga ttt gct tgt 649  
 Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys  
 165 170 175  
 tgg gtc gaa ctt gtg gct att cat tta ttc tca cca ggg act tcc ttc 697  
 Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe  
 180 185 190  
 gct ggg cat ctg gct ggg att ctt gtt gga cta atg tac act caa ggg 745  
 Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly  
 195 200 205  
 cct ctg aag aaa atc atg gaa gca tgt gca ggc ggt ttt tcc tcc agt 793  
 Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser  
 210 215 220  
 gtt ggt tac cca gga cgg caa tac tac ttt aat agt tca ggc agc tct 841  
 Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser  
 225 230 235 240  
 gga tat cag gat tat tat ccg cat ggc agg cca gat cac tat gaa gaa 889  
 Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu  
 245 250 255  
 gca ccc agg aac tat gac acg tac aca gca gga ctg agt gaa gaa gaa 937  
 Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu  
 260 265 270

cag ctc gag aga gca tta caa gcc agc ctc tgg gac cga gga aat acc 985  
 Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Gly Asn Thr  
 275 280 285  
 aga aat agc cca cca ccc tac ggg ttt cat ctc tca cca gaa gaa atg 1033  
 Arg Asn Ser Pro Pro Pro Tyr Gly Phe His Leu Ser Pro Glu Glu Met  
 290 295 300  
 agg aga cag cgg ctt cac aga ttc gat agc cag tgaggtggca tcttggaag 1086  
  
 Arg Arg Gln Arg Leu His Arg Phe Asp Ser Gln  
 305 310 315  
 acatggccta ttcgtgtaat tattgcccatt ttggtcatt cccaagccc ctaattcatt 1146  
 ttaattcatt ttaaacaaaa gcagagtaca ccggtattgc tccagatcgc tcacatcacc 1206  
 tgggacagtc ccatggcccc tatgagtcaa ctcacagctt gcggggagtg ggccttctcc 1266  
 tggccttggt cttgtcata aacaggtcac ttcttccatg aagagaccag tttccacgct 1326  
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 gtgttccatg aataaaagga caaagtcaga agatcactga tgtcttactg tcaacagaga 2106



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 cttcattttt ataactttat attactgtct tggaagatgt gtttatgtgt gtgtgttact 2346  
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<210> 96

<211> 315

<212> PRT

<213> Homo sapiens

<400> 96

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 Ser Gln Ile Phe His Val Gly Ile Asn Asn Ile Pro Pro Val Thr Leu  
 20 25 30  
 Ala Thr Leu Ala Leu Asn Ile Trp Phe Phe Leu Asn Pro Gln Lys Pro  
 35 40 45  
 Leu Tyr Ser Ser Cys Leu Ser Val Glu Lys Cys Tyr Gln Gln Lys Asp  
 50 55 60  
 Trp Gln Arg Leu Leu Leu Ser Pro Leu His His Ala Asp Asp Trp His  
 65 70 75 80  
 Leu Tyr Phe Asn Met Ala Ser Met Leu Trp Lys Gly Ile Asn Leu Glu  
 85 90 95  
 Arg Arg Leu Gly Ser Arg Trp Phe Ala Tyr Val Ile Thr Ala Phe Ser  
 100 105 110  
 Val Leu Thr Gly Val Val Tyr Leu Leu Leu Gln Phe Ala Val Ala Glu

115 120 125  
Phe Met Asp Glu Pro Asp Phe Lys Arg Ser Cys Ala Val Gly Phe Ser  
130 135 140  
Gly Val Leu Phe Ala Leu Lys Val Leu Asn Asn His Tyr Cys Pro Gly  
145 150 155 160  
Gly Phe Val Asn Ile Leu Gly Phe Pro Val Pro Asn Arg Phe Ala Cys  
165 170 175  
Trp Val Glu Leu Val Ala Ile His Leu Phe Ser Pro Gly Thr Ser Phe  
180 185 190  
Ala Gly His Leu Ala Gly Ile Leu Val Gly Leu Met Tyr Thr Gln Gly  
195 200 205  
Pro Leu Lys Lys Ile Met Glu Ala Cys Ala Gly Gly Phe Ser Ser Ser  
210 215 220  
Val Gly Tyr Pro Gly Arg Gln Tyr Tyr Phe Asn Ser Ser Gly Ser Ser  
225 230 235 240  
Gly Tyr Gln Asp Tyr Tyr Pro His Gly Arg Pro Asp His Tyr Glu Glu  
245 250 255  
Ala Pro Arg Asn Tyr Asp Thr Tyr Thr Ala Gly Leu Ser Glu Glu Glu  
260 265 270  
Gln Leu Glu Arg Ala Leu Gln Ala Ser Leu Trp Asp Arg Gly Asn Thr  
275 280 285  
Arg Asn Ser Pro Pro Pro Tyr Gly Phe His Leu Ser Pro Glu Glu Met  
290 295 300  
Arg Arg Gln Arg Leu His Arg Phe Asp Ser Gln  
305 310 315

&lt;210&gt; 97

&lt;211&gt; 2207

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138)..(443)

&lt;400&gt; 97

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Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro

1

5

10

gga ttc ccc atc ccc agc ttc tcg ccc tcc ccg cac cgc ccc cac ccc 218

Gly Phe Pro Ile Pro Ser Phe Ser Pro Ser Pro His Arg Pro His Pro

15

20

25

ggg att tcg acc ccc tta agg gct cca ccc cgc tcc ggg atc ccc ttc 266

Gly Ile Ser Thr Pro Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe

30

35

40

tcc cag ctc cta tcc ctt agg act gcc ccg ccc cct aga acc tcc ccg 314

Ser Gln Leu Leu Ser Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro

45

50

55

tca gga tct ccg tcc ctc agc cgc tca cag cct cct ccc agc gcc cat 362

Ser Gly Ser Pro Ser Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His

60

65

70

75

cgc ctt gag ctg ccc act acc tct aga ctg ccc tcc cgg gct ggc gtc 410

Arg Leu Glu Leu Pro Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val

80

85

90

cca cgg agt ctc agc cgc gca ccc ctt ctc cgg tagctcctac ccctgcctgt 463  
Pro Arg Ser Leu Ser Arg Ala Pro Leu Leu Arg

95

100

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 caga 2207

<210> 98

<211> 102

<212> PRT

<213> Homo sapiens

<400> 98

Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro Gly Phe Pro Ile Pro  
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 Ser Phe Ser Pro Ser Pro His Arg Pro His Pro Gly Ile Ser Thr Pro  
 20 25 30  
 Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe Ser Gln Leu Leu Ser  
 35 40 45  
 Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro Ser Gly Ser Pro Ser  
 50 55 60  
 Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His Arg Leu Glu Leu Pro  
 65 70 75 80  
 Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val Pro Arg Ser Leu Ser  
 85 90 95  
 Arg Ala Pro Leu Leu Arg  
 100

&lt;210&gt; 99

&lt;211&gt; 2246

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138)..(482)

&lt;400&gt; 99

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tctgccggtc acagcca atg tac ggc tcg gcc tgg ctg ccc cct ccc cca 170  
Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro  
1 5 10  
gga ttc ccc atc ccc agc ttc tcg ccc tcc ccg cac cgc ccc cac ccc 218  
Gly Phe Pro Ile Pro Ser Phe Ser Pro Ser Pro His Arg Pro His Pro  
15 20 25  
ggg att tcg acc ccc tta agg gct cca ccc cgc tcc ggg atc ccc ttc 266  
Gly Ile Ser Thr Pro Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe  
30 35 40  
tcc cag ctc cta tcc ctt agg act gcc ccg ccc cct aga acc tcc ccg 314  
Ser Gln Leu Leu Ser Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro  
45 50 55  
tca gga tct ccg tcc ctc agc cgc tca cag cct cct ccc agc gcc cat 362  
Ser Gly Ser Pro Ser Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His  
60 65 70 75  
cgc ctt gag ctg ccc act acc tct aga ctg ccc tcc cgg gct ggc gtc 410  
Arg Leu Glu Leu Pro Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val

80	85	90	
cca cgg agt ctc agc cgc gca ccc ctt cct cgc gtt acc ctc ctt ccg			458
Pro Arg Ser Leu Ser Arg Ala Pro Leu Pro Arg Val Thr Leu Leu Pro			
95	100	105	
gac agc acc ccc tcc ctt ctc cgg tagctcctac ccctgcctgt gcgggcctcg			512
Asp Ser Thr Pro Ser Leu Leu Arg			
110	115		
tccccgcgcc cagccctcgg tgctgcctcc gacagcgccg cgctctctca gccgcccccc			572
tgccccctcgg gccccctct ctgctgcccc tggcgccatg gcgtgcagcc tcaaggacga			632
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 gccctacccc aacccttcaa ctaccagaat ctggggccacc ccagcagtat ttttattta 2192  
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<210> 100

<211> 115

<212> PRT

<213> Homo sapiens

<400> 100

Met Tyr Gly Ser Ala Trp Leu Pro Pro Pro Pro Gly Phe Pro Ile Pro  
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 20 25 30  
 Leu Arg Ala Pro Pro Arg Ser Gly Ile Pro Phe Ser Gln Leu Leu Ser  
 35 40 45  
 Leu Arg Thr Ala Pro Pro Pro Arg Thr Ser Pro Ser Gly Ser Pro Ser  
 50 55 60  
 Leu Ser Arg Ser Gln Pro Pro Pro Ser Ala His Arg Leu Glu Leu Pro  
 65 70 75 80  
 Thr Thr Ser Arg Leu Pro Ser Arg Ala Gly Val Pro Arg Ser Leu Ser  
 85 90 95



Arg Ala Pro Leu Pro Arg Val Thr Leu Leu Pro Asp Ser Thr Pro Ser

100

105

110

Leu Leu Arg

115

<210> 101

<211> 3243

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43).. (1467)

<400> 101

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Met Ala Cys Ser

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Leu Lys Asp Glu Leu Leu Cys Ser Ile Cys Leu Ser Ile Tyr Gln Asp

5

10

15

20

ccg gtg agc ctg ggc tgc gag cac tac ttc tgc cgc cgc tgc atc acg 150

Pro Val Ser Leu Gly Cys Glu His Tyr Phe Cys Arg Arg Cys Ile Thr

25

30

35

gag cac tgg gtg cgg cag gag gcg cag ggc gcc cgc gac tgc ccc gag 198

Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg Asp Cys Pro Glu

40

45

50

tgc cgg cgc acg ttc gcc gag ccc gcg ctg gcg ccc agc ctc aag ctg 246

Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro Ser Leu Lys Leu

55	60	65	
gcc aac atc gtg gag cgc tac agc tcc ttc ccg ctg gac gcc atc ctc			294
Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu Asp Ala Ile Leu			
70	75	80	
aac gcg cgc cgc gcc gcg cga ccc tgc cag gcg cac gac aag gtc aag			342
Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His Asp Lys Val Lys			
85	90	95	100
ctc ttc tgc ctc acg gac cgc gcg ctt ctc tgc ttc ttc tgc gac gag			390
Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe Phe Cys Asp Glu			
	105	110	115
cct gca ctg cac gag cag cat cag gtc acc ggc atc gac gac gcc ttc			438
Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile Asp Asp Ala Phe			
	120	125	130
gac gag ctg cag agg gag ctg aag gac caa ctt cag gcc ctt caa gac			486
Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln Ala Leu Gln Asp			
	135	140	145
agc gag cgg gaa cac acc gaa gcg ctg cag ctg ctc aag cga caa ctg			534
Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu Lys Arg Gln Leu			
	150	155	160
gcg gag acc aag tct tcc acc aag agc ctg cgg acc act atc ggc gag			582
Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr Thr Ile Gly Glu			
165	170	175	180
gcc ttc gag cgg ctg cac cgg ctg ctg cgt gaa cgc cag aag gcc atg			630
Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg Gln Lys Ala Met			
	185	190	195
cta gag gag ctg gag gcg gac acg gcc cgc acg ctg acc gac atc gag			678
Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu Thr Asp Ile Glu			

200	205	210	
cag aaa gtc cag cgc tac agc cag cag ctg cgc aag gtc cag gag gga			726
Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys Val Gln Glu Gly			
215	220	225	
gcc cag atc ctg cag gag cgg ctg gct gaa acc gac cgg cac acc ttc			774
Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp Arg His Thr Phe			
230	235	240	
ctg gct ggg gtg gcc tca ctg tcc gag cgg ctc aag gga aaa atc cat			822
Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys Gly Lys Ile His			
245	250	255	260
gag acc aac ctc aca tat gaa gac ttc ccg acc tcc aag tac aca ggc			870
Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser Lys Tyr Thr Gly			
265	270	275	
ccc ctg cag tac acc atc tgg aag tcc ctg ttc cag gac atc cac cca			918
Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln Asp Ile His Pro			
280	285	290	
gtg cca gcc gcc cta acc ctg gac ccg ggc aca gcc cac cag cgc ctg			966
Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala His Gln Arg Leu			
295	300	305	
atc ctg tcg gac gac tgc acc att gtg gct tac ggc aac ttg cac cca			1014
Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly Asn Leu His Pro			
310	315	320	
cag cca ctg cag gac tcg cca aag cgc ttc gat gtg gag gtg tcg gtg			1062
Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val Glu Val Ser Val			
325	330	335	340
ctg ggt tct gaa gcc ttc agt agt ggc gtc cac tac tgg gag gtg gtg			1110
Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr Trp Glu Val Val			

345	350	355	
gtg gcg gag aag acc cag tgg gtg atc ggg ctg gca cac gaa gcc gca			1158
Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala His Glu Ala Ala			
360	365	370	
agc cgc aag ggc agc atc cag atc cag ccc agc cgc ggc ttc tac tgc			1206
Ser Arg Lys Gly Ser Ile Gln Ile Gln Pro Ser Arg Gly Phe Tyr Cys			
375	380	385	
atc gtg atg cac gat ggc aac cag tac agc gcc tgc acg gag ccc tgg			1254
Ile Val Met His Asp Gly Asn Gln Tyr Ser Ala Cys Thr Glu Pro Trp			
390	395	400	
acg cgg ctt aac gtc cgg gac aag ctt gac aag gtg ggt gtc ttc ctg			1302
Thr Arg Leu Asn Val Arg Asp Lys Leu Asp Lys Val Gly Val Phe Leu			
405	410	415	420
gac tat gac caa ggc ttg ctc atc ttc tac aat gct gat gac atg tcc			1350
Asp Tyr Asp Gln Gly Leu Leu Ile Phe Tyr Asn Ala Asp Asp Met Ser			
425	430	435	
tgg ctc tac acc ttc cgc gag aag ttc cct ggc aag ctc tgc tct tac			1398
Trp Leu Tyr Thr Phe Arg Glu Lys Phe Pro Gly Lys Leu Cys Ser Tyr			
440	445	450	
ttc agc cct ggc cag agc cac gcc aat ggc aag aac gtt cag ccg ctg			1446
Phe Ser Pro Gly Gln Ser His Ala Asn Gly Lys Asn Val Gln Pro Leu			
455	460	465	
cgg atc aac acc gtc cgc atc tagtccaggc agaaggagac cacaacctcc			1497
Arg Ile Asn Thr Val Arg Ile			
470	475		
tgggaccact gccacctgca agagccctgc ccaggagata gaagacctgg actccagccc			1557
accgtggcca ctggagacct caggccagtt gtttacccctc cagcctccag tctgtaaaat			1617

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aattgtcagc cctaccccaa ccttcaact accagaatct gggccacccc agcagtattt 3177  
ttatttaaaa tgttgcccat tttatgagtt atgatcaatt tgtattaaat taaagttaca 3237

gatgtc

3243

&lt;210&gt; 102

&lt;211&gt; 475

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

Met Ala Cys Ser Leu Lys Asp Glu Leu Leu Cys Ser Ile Cys Leu Ser

1 5 10 15

Ile Tyr Gln Asp Pro Val Ser Leu Gly Cys Glu His Tyr Phe Cys Arg

20 25 30

Arg Cys Ile Thr Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg

35 40 45

Asp Cys Pro Glu Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro

50 55 60

Ser Leu Lys Leu Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu

65 70 75 80

Asp Ala Ile Leu Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His

85 90 95

Asp Lys Val Lys Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe

100 105 110

Phe Cys Asp Glu Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile

115 120 125

Asp Asp Ala Phe Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln

130 135 140

Ala Leu Gln Asp Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu

145 150 155 160

Lys Arg Gln Leu Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr  
165 170 175  
Thr Ile Gly Glu Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg  
180 185 190  
Gln Lys Ala Met Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu  
195 200 205  
Thr Asp Ile Glu Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys  
210 215 220  
Val Gln Glu Gly Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp  
225 230 235 240  
Arg His Thr Phe Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys  
245 250 255  
Gly Lys Ile His Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser  
260 265 270  
Lys Tyr Thr Gly Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln  
275 280 285  
Asp Ile His Pro Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala  
290 295 300  
His Gln Arg Leu Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly  
305 310 315 320  
Asn Leu His Pro Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val  
325 330 335  
Glu Val Ser Val Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr  
340 345 350  
Trp Glu Val Val Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala  
355 360 365  
His Glu Ala Ala Ser Arg Lys Gly Ser Ile Gln Ile Gln Pro Ser Arg

370                                      375                                      380  
 Gly Phe Tyr Cys Ile Val Met His Asp Gly Asn Gln Tyr Ser Ala Cys  
 385                                      390                                      395                                      400  
 Thr Glu Pro Trp Thr Arg Leu Asn Val Arg Asp Lys Leu Asp Lys Val  
                                     405                                      410                                      415  
 Gly Val Phe Leu Asp Tyr Asp Gln Gly Leu Leu Ile Phe Tyr Asn Ala  
                                     420                                      425                                      430  
 Asp Asp Met Ser Trp Leu Tyr Thr Phe Arg Glu Lys Phe Pro Gly Lys  
                                     435                                      440                                      445  
 Leu Cys Ser Tyr Phe Ser Pro Gly Gln Ser His Ala Asn Gly Lys Asn  
                                     450                                      455                                      460  
 Val Gln Pro Leu Arg Ile Asn Thr Val Arg Ile  
 465                                      470                                      475

<210> 103

<211> 788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (126).. (431)

<400> 103

cgggcttaga aggcccggt actgacgcgc agtgccagac ctagccctc acggctctta 60  
 agtctcggtc gccctcgct cgcagcctgc caccgcgct cagctgcccg cctcctcagc 120  
 cagcc atg ctg gag cat ctg agc tcg ctg ccc acg çag atg gat tac aag 170

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys

1

5

10

15



ggc cag aag cta gct gaa cag atg ttt cag gga att att ctt ttt tct 218  
 Gly Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser  
                     20                    25                    30  
 gca ata gtt gga ttt atc tac ggg tac gtg gct gaa cag ttc ggg tgg 266  
 Ala Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp  
                     35                    40                    45  
 act gtc tat ata gtt atg gcc gga ttt gct ttt tca tgt ttg ctg aca 314  
 Thr Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr  
                     50                    55                    60  
 ctt cct cca tgg ccc atc tat cgc cgg cat cct ctc aag tgg tta cct 362  
 Leu Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro  
                     65                    70                    75  
 gtt caa gaa tca agc aca gac gac aag aaa cca ggg gaa aga aaa att 410  
 Val Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile  
                     80                    85                    90                    95  
 aag agg cat gct aaa aat aat tgaggttttc atgattcagc acctgctttt 461  
 Lys Arg His Ala Lys Asn Asn  
                     100  
 gtttctgtga gatgagctaa attgctttca taccacagat aagagctaaa accacctaatt 521  
 gctcttatgg cacagctgtg tatagattta gttctcttta tacttcattt ctagcccagt 581  
 tgggttttga tttatataag tagtttagac cttctcttca taatcttgct ctgagatggg 641  
 gaacagaaca cacaagtatg aagtttcttt caggtgtaaa taatgaaaaa taaatgcctc 701  
 ataaatgata gtacaatgta actatcaaag ttttataatt cattatgagt taaccatttt 761  
 aatgtttcca attaaacctc atagtgc 788

&lt;210&gt; 104

&lt;211&gt; 102

<212> PRT

<213> Homo sapiens

<400> 104

Met Leu Glu His Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly  
1 5 10 15  
Gln Lys Leu Ala Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala  
20 25 30  
Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr  
35 40 45  
Val Tyr Ile Val Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu  
50 55 60  
Pro Pro Trp Pro Ile Tyr Arg Arg His Pro Leu Lys Trp Leu Pro Val  
65 70 75 80  
Gln Glu Ser Ser Thr Asp Asp Lys Lys Pro Gly Glu Arg Lys Ile Lys  
85 90 95  
Arg His Ala Lys Asn Asn  
100

<210> 105

<211> 2189

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (253).. (966)

<400> 105

atcggccccg ggtctgtccg ggcgttgccg gattggggcc tgggaacgct cggcccccg 60

cagccgagaa gcccgtagact gggctgagca gcaccatccc agccctgggg cctgctgact 120  
 gccagtccc ggcttcacct gcagcgaacc cggagcgttg ctatcctcca ccgactgtc 180  
 aggctctgcg cgccccgcgg aggtcggcgg cgaccagcag cgactgcgga gcgacggcgg 240  
 gcggccccgg gc atg tac gcc ccc gga ggc gca ggg ctg ccc ggc ggg cgc 291

Met Tyr Ala Pro Gly Gly Ala Gly Leu Pro Gly Gly Arg

1

5

10

cgg cgg agg agc ccg gga ggc agc gct ctg ccc aag cag ccg gag cgt 339  
 Arg Arg Arg Ser Pro Gly Gly Ser Ala Leu Pro Lys Gln Pro Glu Arg

15

20

25

agc ctg gcc tcg gcc ctg cct ggc gcc ctg tct atc acg gcg ctg tgc 387  
 Ser Leu Ala Ser Ala Leu Pro Gly Ala Leu Ser Ile Thr Ala Leu Cys

30

35

40

45

act gcc ctc gcc gag ccc gcc tgg ttg cac atc cac gga ggc acc tgt 435  
 Thr Ala Leu Ala Glu Pro Ala Trp Leu His Ile His Gly Gly Thr Cys

50

55

60

tcg cgc cag gag ctg ggg gtc tcc gac gtg ttg ggc tat gtg cac ccg 483  
 Ser Arg Gln Glu Leu Gly Val Ser Asp Val Leu Gly Tyr Val His Pro

65

70

75

gac ctg ctg aaa gat ttc tgc atg aat ccc cag aca gtg ctg ctc ctg 531  
 Asp Leu Leu Lys Asp Phe Cys Met Asn Pro Gln Thr Val Leu Leu Leu

80

85

90

cgg gtc atc gcc gcc ttc tgt ttc ctg ggc atc ctg tgt agt ctc tcc 579  
 Arg Val Ile Ala Ala Phe Cys Phe Leu Gly Ile Leu Cys Ser Leu Ser

95

100

105

gct ttc ctt ctg gat gtc ttt ggg ccg aag cat cct gct ctg aag atc 627  
 Ala Phe Leu Leu Asp Val Phe Gly Pro Lys His Pro Ala Leu Lys Ile

110

115

120

125

act cgt cgc tat gcc ttc gcc cat atc cta acg gtt ctg cag tgt gcc 675  
 Thr Arg Arg Tyr Ala Phe Ala His Ile Leu Thr Val Leu Gln Cys Ala  
 130 135 140  
 acc gtc att ggc ttt tct tat tgg gct tct gaa ctc atc ttg gcc cag 723  
 Thr Val Ile Gly Phe Ser Tyr Trp Ala Ser Glu Leu Ile Leu Ala Gln  
 145 150 155  
 cag cag cag cat aag aag tac cat gga tcc cag gtc tat gtc acc ttc 771  
 Gln Gln Gln His Lys Lys Tyr His Gly Ser Gln Val Tyr Val Thr Phe  
 160 165 170  
 gcc gtt agc ttc tac ctg gtg gca gga gct ggt gga gcc tca atc ctg 819  
 Ala Val Ser Phe Tyr Leu Val Ala Gly Ala Gly Gly Ala Ser Ile Leu  
 175 180 185  
 gcc acg gca gcc aac ctc ctg cgc cac tac ccc aca gag gaa gag gag 867  
 Ala Thr Ala Ala Asn Leu Leu Arg His Tyr Pro Thr Glu Glu Glu Glu  
 190 195 200 205  
 cag gcg ctg gag ctg ctc tca gag atg gaa gag aac gag ccc tac ccg 915  
 Gln Ala Leu Glu Leu Leu Ser Glu Met Glu Glu Asn Glu Pro Tyr Pro  
 210 215 220  
 gcg gaa tat gag gtc atc aac cag ttc cag cca ccc cct gct tac aca 963  
 Ala Glu Tyr Glu Val Ile Asn Gln Phe Gln Pro Pro Pro Ala Tyr Thr  
 225 230 235  
 ccc taatgccagc cctgggctct cttcctcggc agcccctccc tcaactctgc 1016  
 Pro  
 agtcctcttc gcacccagag gagctccttt ccccagcagg cctcactggt aggatcctga 1076  
 gatggaacct ggcctcagtt taggaacagg ggccacaaca gggcaggaac ccaccacct 1136  
 ccacatagga atacaaccag tggggccaca tcatgtgagg catcagaccc aactgtcag 1196  
 cccagcaggc cgggctgtgt ccttcagacc cagtgtgcc ctagactctg actcgggact 1256

gcagcttgcc acgtgccctc tcccctcttg aatgtactct ggtcttgca tgtgctgctg 1316  
ggactttctt gctcagccat cactctgggc accttgtttg ctctgggtct ggctgaattt 1376  
tctgccctga gatctgggca taaagtggat gaaacttgaa agaccttcag tgtagatcca 1436  
gatggccaac ctgtccttgt taagttactt gcttcttggg aatcagtgtc ccctgctgag 1496  
ctgaaaagga aatggattcc aatctcttcc aacctttaag gtgatagata gtttgagcaa 1556  
gactggagaa tggacaacac tatgaagctg tggctagaaa gggactgtca tgtcccatcc 1616  
tttggccaga ttgactgggg atgtccggac agatgcctgc atgggtgggtg agggccacat 1676  
ctgcacacga gccagtggct gcttgcgggt cactgctgtg atgccagagt gtgttcaaag 1736  
gtgactctcc tgctcttctg gactcttctc tcaggcaaga aaggctgcag gctgcctgct 1796  
atgtgatgcc tgagcacaaa gccaaaggac tgaactaagt ctttctgtta agtcctgagt 1856  
ttgtcattgg caggtttact tgtggccagc tctctctgcc cttgggtgtc tgagcaggca 1916  
gaccagaaga ccaggcactg gacctgcatg ccaaaggac tggcatctc ctgaggacct 1976  
gtacatgacc ctgtggactg ttccgcacga tccggaaccc actttttatt cactcccat 2036  
gtctttggcc ttctcttctt ttctctttcc ctctgccatc ctgacactga tagtttgtca 2096  
tataaattcc ccgggttgtg ttttttttcc tagaaaaaaa ttaaaaggga aaacaaaacc 2156  
aaaaaaacca gaaaccacga ataagaatgg aaa 2189

<210> 106

<211> 238

<212> PRT

<213> Homo sapiens

<400> 106

Met Tyr Ala Pro Gly Gly Ala Gly Leu Pro Gly Gly Arg Arg Arg Arg

1

5

10

15

Ser Pro Gly Gly Ser Ala Leu Pro Lys Gln Pro Glu Arg Ser Leu Ala

20

25

30

Ser Ala Leu Pro Gly Ala Leu Ser Ile Thr Ala Leu Cys Thr Ala Leu

35 40 45  
Ala Glu Pro Ala Trp Leu His Ile His Gly Gly Thr Cys Ser Arg Gln  
50 55 60  
Glu Leu Gly Val Ser Asp Val Leu Gly Tyr Val His Pro Asp Leu Leu  
65 70 75 80  
Lys Asp Phe Cys Met Asn Pro Gln Thr Val Leu Leu Leu Arg Val Ile  
85 90 95  
Ala Ala Phe Cys Phe Leu Gly Ile Leu Cys Ser Leu Ser Ala Phe Leu  
100 105 110  
Leu Asp Val Phe Gly Pro Lys His Pro Ala Leu Lys Ile Thr Arg Arg  
115 120 125  
Tyr Ala Phe Ala His Ile Leu Thr Val Leu Gln Cys Ala Thr Val Ile  
130 135 140  
Gly Phe Ser Tyr Trp Ala Ser Glu Leu Ile Leu Ala Gln Gln Gln Gln  
145 150 155 160  
His Lys Lys Tyr His Gly Ser Gln Val Tyr Val Thr Phe Ala Val Ser  
165 170 175  
Phe Tyr Leu Val Ala Gly Ala Gly Gly Ala Ser Ile Leu Ala Thr Ala  
180 185 190  
Ala Asn Leu Leu Arg His Tyr Pro Thr Glu Glu Glu Glu Gln Ala Leu  
195 200 205  
Glu Leu Leu Ser Glu Met Glu Glu Asn Glu Pro Tyr Pro Ala Glu Tyr  
210 215 220  
Glu Val Ile Asn Gln Phe Gln Pro Pro Pro Ala Tyr Thr Pro  
225 230 235

&lt;210&gt; 107

&lt;211&gt; 1195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (102)..(1166)

&lt;400&gt; 107

aacttcagct gaggaacttg gcacggccag cttgggaccc aggaccctaa cgttactgca 60  
 gaggcgctgt gtttgaagt cccgctatca cggcccccca g atg ggg cct gga cga 116

Met Gly Pro Gly Arg

1

5

tgc ctc ctg acg gcc ttg ttg ctt ctg gcc ctg gcg cca ccg ccg gaa 164

Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu Ala Pro Pro Pro Glu

10

15

20

gcc tcc cag tac tgc ggc cgc ctt gaa tac tgg aac cca gac aac aag 212

Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp Asn Pro Asp Asn Lys

25

30

35

tgc tgc agc agc tgc ctg caa cgc ttc ggg ccg ccc ccc tgc ccg gac 260

Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro Pro Pro Cys Pro Asp

40

45

50

tat gag ttc cgg gaa aac tgc gga ctc aat gac cac ggc gat ttc gta 308

Tyr Glu Phe Arg Glu Asn Cys Gly Leu Asn Asp His Gly Asp Phe Val

55

60

65

acg ccc ccg ttc cga aag tgt tct tct ggg cag tgc aac ccc gac ggc 356

Thr Pro Pro Phe Arg Lys Cys Ser Ser Gly Gln Cys Asn Pro Asp Gly

70

75

80

85

gcg gag cta tgt agc ccc tgc ggc ggc gga gcc gtg acc cct act ccc 404

Ala Glu Leu Cys Ser Pro Cys Gly Gly Gly Ala Val Thr Pro Thr Pro	
90 95 100	
gcc gcg ggc ggg ggc aga acc ccg tgg cgc tgc aga gag agg ccg gtc	452
Ala Ala Gly Gly Gly Arg Thr Pro Trp Arg Cys Arg Glu Arg Pro Val	
105 110 115	
cct gcc aag ggg cac tgc ccc ctc aca cct gga aac cca ggc gcc cct	500
Pro Ala Lys Gly His Cys Pro Leu Thr Pro Gly Asn Pro Gly Ala Pro	
120 125 130	
agc tcc cag gag cgc agc tca ccg gca agt tcc att gcc tgg agg acc	548
Ser Ser Gln Glu Arg Ser Ser Pro Ala Ser Ser Ile Ala Trp Arg Thr	
135 140 145	
cct gag cct gtc cct cag cag gcc tgg ccg aat ttc ctt ccg ctc gtg	596
Pro Glu Pro Val Pro Gln Gln Ala Trp Pro Asn Phe Leu Pro Leu Val	
150 155 160 165	
gtg ctg gtc ctg ctc ctg acc ttg gcg gtg ata gcg atc ctc ctg ttt	644
Val Leu Val Leu Leu Leu Thr Leu Ala Val Ile Ala Ile Leu Leu Phe	
170 175 180	
att ctg ctc tgg cat ctc tgc tgg ccc aag gag aaa gcc gac ccc tat	692
Ile Leu Leu Trp His Leu Cys Trp Pro Lys Glu Lys Ala Asp Pro Tyr	
185 190 195	
ccc tat cct ggc ttg gtc tgc gga gtc ccc aac acc cac acc cct tcc	740
Pro Tyr Pro Gly Leu Val Cys Gly Val Pro Asn Thr His Thr Pro Ser	
200 205 210	
tcc tcg cat ctg tcc tcc cca ggc gcc ctg gag aca ggg gac aca tgg	788
Ser Ser His Leu Ser Ser Pro Gly Ala Leu Glu Thr Gly Asp Thr Trp	
215 220 225	
aag gag gcc tca cta ctt cca ctc ctg agc agg gaa ctg tcc agt ctg	836



[illegible]

<210> 108

**<211> 355**

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

Met Gly Pro Gly Arg Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu

1 5 10 15

Ala Pro Pro Pro Glu Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp

20 25 30

Asn Pro Asp Asn Lys Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro

35 40 45

Pro Pro Cys Pro Asp Tyr Glu Phe Arg Glu Asn Cys Gly Leu Asn Asp

50 55 60

His Gly Asp Phe Val Thr Pro Pro Phe Arg Lys Cys Ser Ser Gly Gln

65 70 75 80

Cys Asn Pro Asp Gly Ala Glu Leu Cys Ser Pro Cys Gly Gly Gly Ala

85 90 95

Val Thr Pro Thr Pro Ala Ala Gly Gly Gly Arg Thr Pro Trp Arg Cys

100 105 110

Arg Glu Arg Pro Val Pro Ala Lys Gly His Cys Pro Leu Thr Pro Gly

115 120 125

Asn Pro Gly Ala Pro Ser Ser Gln Glu Arg Ser Ser Pro Ala Ser Ser

130 135 140

Ile Ala Trp Arg Thr Pro Glu Pro Val Pro Gln Gln Ala Trp Pro Asn

145 150 155 160

Phe Leu Pro Leu Val Val Leu Val Leu Leu Leu Thr Leu Ala Val Ile

165 170 175

Ala Ile Leu Leu Phe Ile Leu Leu Trp His Leu Cys Trp Pro Lys Glu

180 185 190

Lys Ala Asp Pro Tyr Pro Tyr Pro Gly Leu Val Cys Gly Val Pro Asn  
 195 200 205  
 Thr His Thr Pro Ser Ser Ser His Leu Ser Ser Pro Gly Ala Leu Glu  
 210 215 220  
 Thr Gly Asp Thr Trp Lys Glu Ala Ser Leu Leu Pro Leu Leu Ser Arg  
 225 230 235 240  
 Glu Leu Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg Leu Leu Asp Glu  
 245 250 255  
 Leu Glu Val Leu Glu Glu Leu Ile Val Leu Leu Asp Pro Glu Pro Gly  
 260 265 270  
 Pro Gly Gly Gly Met Ala His Gly Thr Thr Arg His Leu Ala Ala Arg  
 275 280 285  
 Tyr Gly Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr Ser Leu Arg Pro  
 290 295 300  
 Ser Arg Ser Pro Leu Arg Ala Leu Ile Glu Met Val Val Ala Arg Glu  
 305 310 315 320  
 Pro Ser Ala Ser Leu Gly Gln Leu Gly Thr His Leu Ala Gln Leu Gly  
 325 330 335  
 Arg Ala Asp Ala Leu Arg Val Leu Ser Lys Leu Gly Ser Ser Gly Val  
 340 345 350  
 Cys Trp Ala  
 355

&lt;210&gt; 109

&lt;211&gt; 685

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (156).. (656)

&lt;400&gt; 109

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gttgggggat gagggctcgg gggtagattc ccggttccg aagaggcgtg agaattctgt 60
tccccacat caccgcgtcc tttcttctgc cggatttccc cggaaagtgt agcagaggcg 120
ctgtgtttgg aagtcccgt atcacggccc cccag atg ggg cct gga cga tgc 173
                                Met Gly Pro Gly Arg Cys
                                1             5

ctc ctg acg gcc ttg ttg ctt ctg gcc ctg gcg cca ccg ccg gaa gcc 221
Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu Ala Pro Pro Pro Glu Ala
                10             15             20

tcc cag tac tgc ggc cgc ctt gaa tac tgg aac cca gac aac aag tgc 269
Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp Asn Pro Asp Asn Lys Cys
                25             30             35

tgc agc agc tgc ctg caa cgc ttc ggg ccg ccc ccc tgc ccg gaa ctg 317
Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro Pro Pro Cys Pro Glu Leu
                40             45             50

tcc agt ctg gcg tca caa ccc ctg tct cgc ctc ctg gat gag ctg gag 365
Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg Leu Leu Asp Glu Leu Glu
                55             60             65             70

gtg ctg gaa gag ctg att gta ctg ctg gac cct gag cct ggg cca ggt 413
Val Leu Glu Glu Leu Ile Val Leu Leu Asp Pro Glu Pro Gly Pro Gly
                75             80             85

ggg ggt atg gcc cat ggc act act cga cac ctg gcc gca aga tat ggg 461
Gly Gly Met Ala His Gly Thr Thr Arg His Leu Ala Ala Arg Tyr Gly
                90             95             100

```

ctg cct gct gcc tgg tcc acc ttt gcc tat tcg ctg agg ccg agt cgc 509  
 Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr Ser Leu Arg Pro Ser Arg  
 105 110 115  
 tcg ccg ctg cgg gct ctg att gag atg gtg gtg gca agg gag ccc tct 557  
 Ser Pro Leu Arg Ala Leu Ile Glu Met Val Val Ala Arg Glu Pro Ser  
 120 125 130  
 gcc tcc ctg ggc cag ctt ggc aca cac ctc gcc cag cta ggg cgg gca 605  
 Ala Ser Leu Gly Gln Leu Gly Thr His Leu Ala Gln Leu Gly Arg Ala  
 135 140 145 150  
 gat gca ttg cgg gtg ctg tcc aag ctt ggc tca tct ggg gtt tgc tgg 653  
 Asp Ala Leu Arg Val Leu Ser Lys Leu Gly Ser Ser Gly Val Cys Trp  
 155 160 165  
 gct taacacccaa taaagaactt tgctgacta 685  
 Ala

&lt;210&gt; 110

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

Met Gly Pro Gly Arg Cys Leu Leu Thr Ala Leu Leu Leu Leu Ala Leu  
 1 5 10 15  
 Ala Pro Pro Pro Glu Ala Ser Gln Tyr Cys Gly Arg Leu Glu Tyr Trp  
 20 25 30  
 Asn Pro Asp Asn Lys Cys Cys Ser Ser Cys Leu Gln Arg Phe Gly Pro  
 35 40 45  
 Pro Pro Cys Pro Glu Leu Ser Ser Leu Ala Ser Gln Pro Leu Ser Arg

50                      55                      60  
 Leu Leu Asp Glu Leu Glu Val Leu Glu Glu Leu Ile Val Leu Leu Asp  
 65                      70                      75                      80  
 Pro Glu Pro Gly Pro Gly Gly Gly Met Ala His Gly Thr Thr Arg His  
 85                      90                      95  
 Leu Ala Ala Arg Tyr Gly Leu Pro Ala Ala Trp Ser Thr Phe Ala Tyr  
 100                      105                      110  
 Ser Leu Arg Pro Ser Arg Ser Pro Leu Arg Ala Leu Ile Glu Met Val  
 115                      120                      125  
 Val Ala Arg Glu Pro Ser Ala Ser Leu Gly Gln Leu Gly Thr His Leu  
 130                      135                      140  
 Ala Gln Leu Gly Arg Ala Asp Ala Leu Arg Val Leu Ser Lys Leu Gly  
 145                      150                      155                      160  
 Ser Ser Gly Val Cys Trp Ala  
 165

&lt;210&gt; 111

&lt;211&gt; 2887

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (175).. (1287)

&lt;400&gt; 111

acttcctgaa acctcagcta ggactgcagg gaggggtgcg aggctagcca cgcaggcggg 60  
 gccctgggtc attttaaaact ctcagagtga acgtcttgat aggaccgaca agacgcatga 120  
 catgtactta gaaagcttat cttagagcca cactgagatt ggaaccgca aaat atg 177

Met

1

cca gga aac gcc acc cca gtg acc acc act gcc ccg tgg gcc tcc ctg 225  
 Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser Leu

5                      10                      15

ggc ctc tcc gcc aag acc tgc aac aac gtg tcc ttc gaa gag agc agg 273  
 Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser Arg

20                      25                      30

ata gtc ctg gtc gtg gtg tac agc gcg gtg tgc acg ctg ggg gtg ccg 321  
 Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val Pro

35                      40                      45

gcc aac tgc ctg act gcg tgg ctg gcg ctg ctg cag gta ctg cag ggc 369  
 Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln Gly

50                      55                      60                      65

aac gtg ctg gcc gtc tac ctg ctc tgc ctg gca ctc tgc gag ctg ctg 417  
 Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu

70                      75                      80

tac aca ggc acg ctg cca ctc tgg gtc atc tat atc cgc aac cag cac 465  
 Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln His

85                      90                      95

cgc tgg acc cta ggc ctg ctg gcc tgc aag gtg acc gcc tac atc ttc 513  
 Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe

100                      105                      110

ttc tgc aac atc tac gtc agc atc ctc ttc ctg tgc tgc atc tcc tgc 561  
 Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys

115                      120                      125

gac cgc ttc gtg gcc gtg gtg tac gcg ctg gag agt cgg ggc cgc cgc 609

Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg	
130	135 140 145
cgc cgg agg acc gcc atc ctc atc tcc gcc tgc atc ttc atc ctc gtc	657
Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu Val	
150	155 160
ggg atc gtt cac tac ccg gtg ttc cag acg gaa gac aag gag acc tgc	705
Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr Cys	
165	170 175
ttt gac atg ctg cag atg gac agc agg att gcc ggg tac tat tac gcc	753
Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala	
180	185 190
agg ttc acc gtt ggc ttt gcc atc cct ctc tcc atc atc gcc ttc acc	801
Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr	
195	200 205
aac cac cgg att ttc agg agc atc aag cag agc atg ggc tta agc gct	849
Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser Ala	
210	215 220 225
gcc cag aag gcc aag gtg aag cac tcg gcc atc gcg gtg gtt gtc atc	897
Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile	
230	235 240
ttc cta gtc tgc ttc gcc ccg tac cac ctg gtt ctc ctc gtc aaa gcc	945
Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala	
245	250 255
gct gcc ttt tcc tac tac aga gga gac agg aac gcc atg tgc ggc ttg	993
Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu	
260	265 270
gag gaa agg ctg tac aca gcc tct gtg gtg ttt ctg tgc ctg tcc acg	1041



Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr  
 275 280 285  
 gtg aac ggc gtg gct gac ccc att atc tac gtg ctg gcc acg gac cat 1089  
 Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His  
 290 295 300 305  
 tcc cgc caa gaa gtg tcc aga atc cat aag ggg tgg.aaa gag tgg tcc 1137  
 Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser  
 310 315 320  
 atg aag aca gac gtc acc agg ctc acc cac agc agg gac acc gag gag 1185  
 Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu  
 325 330 335  
 ctg cag tgc ccc gtg gcc ctt gca gac cac tac acc ttc tcc agg ccc 1233  
 Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro  
 340 345 350  
 gtg cac cca cca ggg tca cca tgc cct gca aag agg ctg att gag gag 1281  
 Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu  
 355 360 365  
 tcc tgc tgagcccact gtgtggcagg gggatggcag gttgggggtc ctggggccag 1337  
 Ser Cys  
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cagcactgtg gcagcgccca ggagggcata gggcagccta ccacctcaa gggggcaggc 1817  
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 ggtggccagc tgctggctcc cagagcgag cccaggcgtc ctcaacgggg agccccc aaat 1937  
 gtccacgccc agaacaacag ttggcaggac aggtgtgaca cagccacagc agaggcaagg 1997  
 ggtgccagga gtccccagcg gcatcctcgg ggagatgctg gtgaggggtc cgtacagggt 2057  
 ggggtcccca cccctagccc ctactgagg ggggagtga gcagttggcc tgcttgtctg 2117  
 gcggagaaag ccagctccct gcaccctcgg ggctgagtca gatctgggtc tgccgcaaag 2177  
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 tttttgtttt taatatttat ttttttagag acagggcctt gctctgttgc ctgggctgga 2537  
 gaacagtggc accatcatag ctactgcag cctcaaactc ctgggctcaa gcgatacctc 2597  
 ccgctcagcc tcctgagtag ctgggactac aggtgtgcac caccacaccc agccaaaaca 2657  
 gccatcctcc ccttgagagt catcagaaaa atacattagg aaaatgtgtt tagaaataaa 2717  
 agcacaaggc agggcagtgc tcacgcctgt catcccagca ctttgggagg ccgagacggg 2777  
  
 aggatcagtt gaggtcagga gtttgagacc agcctcggca acatggcaaa atcttgtctc 2837  
 ttttttttgg tattaaaaaa atcataaaaa taaaagaaat aatgcaattt 2887

<210> 112

<211> 371

<212> PRT

<213> Homo sapiens

<400> 112

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser

1	5	10	15
Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser			
20	25	30	
Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val			
35	40	45	
Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln			
50	55	60	
Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu			
65	70	75	80
Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln			
85	90	95	
His Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile			
100	105	110	
Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser			
115	120	125	
Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg			
130	135	140	
Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu			
145	150	155	160
Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr			
165	170	175	
Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr			
180	185	190	
Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe			
195	200	205	
Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser			
210	215	220	

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
225 230 235 240  
Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
245 250 255  
Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
260 265 270  
Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
275 280 285  
Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
290 295 300  
His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
305 310 315 320  
Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335  
Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
340 345 350  
Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
355 360 365  
Glu Ser Cys  
370

&lt;210&gt; 113

&lt;211&gt; 2066

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (98).. (556)

&lt;400&gt; 113

gttacagctg ctggagcagc agcggccccc gctcccgga accgttcccg ggccgttgat 60

cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca gcg 115

Met Asn Val Gly Thr Ala

1

5

cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc atc 163

His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile

10

15

20

tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg ctg 211

Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu Leu

25

30

35

agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac ctc 259

Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn Leu

40

45

50

att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg aca 307

Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly Thr

55

60

65

70

ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac tgg 355

Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp

75

80

85

gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc ttg 403

Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe Leu

90

95

100

acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act aag 451

Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr Lys

105

110

115

tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc gtg 499  
 Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser Val  
 120 125 130  
 ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga atc 547  
 Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly Ile  
 135 140 145 150  
 aat aag tac tgagagtgcg gcccttccc ctgccaggg tggcaggga 596  
 Asn Lys Tyr  
 ggggtagggt aaaaggcatg tgctgcaaca ctgaagacag aaagaagaag cctctggaca 656  
 ctgccagaga tgggggttga gcctctggcc taatttcccc cctcgcttcc ccagtagcc 716  
 aacttggagt agctttagt ggggttggg taggccccct gggctctgac cttttctgaa 776  
 ttttttgatc ttttctttt gctttttgaa tagagactcc atggagttagg tcatggaatg 836  
 ggctgggctc ctgggctgaa catggaccac gcagttgcga caggaggcca ggggaaaaac 896  
 cctgctcac ttgtttgcc tcaggcagcc aaagcacttt aaccctgca tagggagcag 956  
 agggcggtac ggcttctgga ttgtttcact gtgattccta ggttttttcg atgccacgca 1016  
 gtgtgtgctt ttgtgtatgg aagcaagtgt gggatgggtc ttgcctttc tgggtaggga 1076  
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 gggagggagg ggtagggaca gaagctagac ccaatctcct ttgggatgtg ggcagggagg 1376  
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 gctgtgggtt taactcctgg gttggctgtt gggtagacag gtggggaaaa ggcccgtgag 1496  
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 ctggcactgg gcagggcctc tcatgtggca gccacatgtg gcgttgtgag gccaccccat 1676  
 gtggggctctg tgggtgagagt cctgtaggat ccctgctcaa gcagcacaga ggaaggggca 1736

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 gttttctccc tcctgaccct gcatctccca ccccggtgat catagggaac tttcacctta 1976  
 aaatctttct aagcaaagtg tgaataggat ttttactccc tttgtacagt attctgagaa 2036  
 acgcaaataa aagggaaca tgtttctgtt 2066

<210> 114

<211> 153

<212> PRT

<213> Homo sapiens

<400> 114

Met	Asn	Val	Gly	Thr	Ala	His	Ser	Glu	Val	Asn	Pro	Asn	Thr	Arg	Val
1				5						10				15	
Met	Asn	Ser	Arg	Gly	Ile	Trp	Leu	Ser	Tyr	Val	Leu	Ala	Ile	Gly	Leu
				20				25						30	
Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
				35				40						45	
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
				50				55						60	
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
				65				70						75	
Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Val	Gln	Phe	Thr
				85				90						95	
Ala	Ser	Arg	Lys	Phe	Leu	Thr	Ile	Thr	Pro	Ile	Val	Leu	Tyr	Phe	Leu
				100				105						110	
Thr	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Gln	Ile	His	Phe	Val	Leu	Asn	Thr

115                      120                      125  
 Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly  
 130                      135                      140  
 Val Arg Ile Phe Gly Ile Asn Lys Tyr  
 145                      150

<210> 115

<211> 2709

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148).. (2502)

<400> 115

gaaagtgcag gcagctgtgg aaggcgaagt tcaatcccag agtccgcccc ctgaattggg 60  
 gcctttccgg aggaggaagc tctgaaaaac agggggccca gtgccattcc gcagggaatt 120  
 gtcgcttgog ttcagctgtt ctacaca atg gac tca gta cct gcc act gtg cct 174

Met Asp Ser Val Pro Ala Thr Val Pro

1

5

tct atc gcc gct acc ccg ggg gac ccg gaa ctt gtg gga ccc ttg tct 222

Ser Ile Ala Ala Thr Pro Gly Asp Pro Glu Leu Val Gly Pro Leu Ser

10

15

20

25

gtg ctc tac gca gcc ttc ata gcc aag ctg ctg gag cta gtt gct aca 270

Val Leu Tyr Ala Ala Phe Ile Ala Lys Leu Leu Glu Leu Val Ala Thr

30

35

40

ttg cct gat gat gtt cag cct ggg cct gat ttt tat gga ctg cca tgg 318

Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Leu Pro Trp



45	50	55	
aaa cct gta ttt atc act gcc ttc ttg gga att gct tcg ttt gcc att			366
Lys Pro Val Phe Ile Thr Ala Phe Leu Gly Ile Ala Ser Phe Ala Ile			
60	65	70	
ttc tta tgg aga act gtc ctt gtt gtg aag gat aga gta tat caa gtc			414
Phe Leu Trp Arg Thr Val Leu Val Val Lys Asp Arg Val Tyr Gln Val			
75	80	85	
acg gaa cag caa att tct gag aag ttg aag act atc atg aaa gaa aat			462
Thr Glu Gln Gln Ile Ser Glu Lys Leu Lys Thr Ile Met Lys Glu Asn			
90	95	100	105
aca gaa ctt gta caa aaa ttg tca aat tat gaa cag aag atc aag gaa			510
Thr Glu Leu Val Gln Lys Leu Ser Asn Tyr Glu Gln Lys Ile Lys Glu			
110	115	120	
tca aag aaa cat gtt cag gaa acc agg aaa caa aat atg att ctc tct			558
Ser Lys Lys His Val Gln Glu Thr Arg Lys Gln Asn Met Ile Leu Ser			
125	130	135	
gat gaa gca att aaa tat aag gat aaa atc aag aca ctt gaa aaa aat			606
Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile Lys Thr Leu Glu Lys Asn			
140	145	150	
cag gaa att ctg gat gac aca gct aaa aat ctt cgt gtt atg cta gaa			654
Gln Glu Ile Leu Asp Asp Thr Ala Lys Asn Leu Arg Val Met Leu Glu			
155	160	165	
tct gag aga gaa cag aat gtc aag aat cag gac ttg ata tca gaa aac			702
Ser Glu Arg Glu Gln Asn Val Lys Asn Gln Asp Leu Ile Ser Glu Asn			
170	175	180	185
aag aaa tct ata gag aag tta aag gat gtt att tca atg aat gcc tca			750
Lys Lys Ser Ile Glu Lys Leu Lys Asp Val Ile Ser Met Asn Ala Ser			

190	195	200	
gaa ttt tca gag gtt cag att gca ctt aat gaa gct aag ctt agt gaa			798
Glu Phe Ser Glu Val Gln Ile Ala Leu Asn Glu Ala Lys Leu Ser Glu			
205	210	215	
gag aag gtg aag tct gaa tgc cat cgg gtt caa gaa gaa aat gct agg			846
Glu Lys Val Lys Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala Arg			
220	225	230	
ctt aag aag aaa aaa gag cag ttg cag cag gaa atc gaa gac tgg agt			894
Leu Lys Lys Lys Lys Glu Gln Leu Gln Gln Glu Ile Glu Asp Trp Ser			
235	240	245	
aaa tta cat gct gag ctc agt gag caa atc aaa tca ttt gag aag tct			942
Lys Leu His Ala Glu Leu Ser Glu Gln Ile Lys Ser Phe Glu Lys Ser			
250	255	260	265
cag aaa gat ttg gaa gta gct ctt act cac aag gat gat aat att aat			990
Gln Lys Asp Leu Glu Val Ala Leu Thr His Lys Asp Asp Asn Ile Asn			
270	275	280	
gct ttg act aac tgc att aca cag ttg aat ctg tta gag tgt gaa tct			1038
Ala Leu Thr Asn Cys Ile Thr Gln Leu Asn Leu Leu Glu Cys Glu Ser			
285	290	295	
gaa tct gag ggt caa aat aaa ggt gga aat gat tca gat gaa tta gca			1086
Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn Asp Ser Asp Glu Leu Ala			
300	305	310	
aat gga gaa gtg gga ggt gac cgg aat gag aag atg aaa aat caa att			1134
Asn Gly Glu Val Gly Gly Asp Arg Asn Glu Lys Met Lys Asn Gln Ile			
315	320	325	
aag cag atg atg gat gtc tct cgg aca cag act gca ata tcg gta gtt			1182
Lys Gln Met Met Asp Val Ser Arg Thr Gln Thr Ala Ile Ser Val Val			

330	335	340	345	
gaa gag gat cta aag ctt tta cag ctt aag cta aga gcc tcc gtg tcc				1230
Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys Leu Arg Ala Ser Val Ser				
	350	355	360	
act aaa tgt aac ctg gaa gac cag gta aag aaa ttg gaa gat gac cgc				1278
Thr Lys Cys Asn Leu Glu Asp Gln Val Lys Lys Leu Glu Asp Asp Arg				
	365	370	375	
aac tca cta caa gct gcc aaa gct gga ctg gaa gat gaa tgc aaa acc				1326
Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu Glu Asp Glu Cys Lys Thr				
	380	385	390	
ttg agg cag aaa gtg gag att ctg aat gag ctc tat cag cag aag gag				1374
Leu Arg Gln Lys Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys Glu				
	395	400	405	
atg gct ttg caa aag aaa ctg agt caa gaa gag tat gaa cgg caa gaa				1422
Met Ala Leu Gln Lys Lys Leu Ser Gln Glu Glu Tyr Glu Arg Gln Glu				
410	415	420	425	
aga gag cac agg ctg tca gct gca gat gaa aag gca gtt tcg gct gca				1470
Arg Glu His Arg Leu Ser Ala Ala Asp Glu Lys Ala Val Ser Ala Ala				
	430	435	440	
gag gaa gta aaa act tac aag cgg aga att gaa gaa atg gag gat gaa				1518
Glu Glu Val Lys Thr Tyr Lys Arg Arg Ile Glu Glu Met Glu Asp Glu				
	445	450	455	
tta cag aag aca gag cgg tca ttt aaa aac cag atc gct acc cat gag				1566
Leu Gln Lys Thr Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His Glu				
	460	465	470	
aag aaa gct cat gaa aac tgg ctc aaa gct cgt gct gca gaa aga gct				1614
Lys Lys Ala His Glu Asn Trp Leu Lys Ala Arg Ala Ala Glu Arg Ala				

475	480	485	
ata gct gaa gag aaa agg gaa gct gcc aat ttg aga cac aaa tta tta			1662
Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu Leu			
490	495	500	505
gaa tta aca caa aag atg gca atg ctg caa gaa gaa cct gtg att gta			1710
Glu Leu Thr Gln Lys Met Ala Met Leu Gln Glu Glu Pro Val Ile Val			
	510	515	520
aaa cca atg cca gga aaa cca aat aca caa aac cct cca cgg aga ggt			1758
Lys Pro Met Pro Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg Gly			
	525	530	535
cct ctg agc cag aat ggg tct ttt ggc cca tcc cct gtg agt ggt gga			1806
Pro Leu Ser Gln Asn Gly Ser Phe Gly Pro Ser Pro Val Ser Gly Gly			
	540	545	550
gaa tgc tcc cct cca ttg aca gtg gag cca ccc gtg aga cct ctc tct			1854
Glu Cys Ser Pro Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu Ser			
	555	560	565
gct act ctc aat cga aga gat atg cct aga agt gaa ttt gga tca gtg			1902
Ala Thr Leu Asn Arg Arg Asp Met Pro Arg Ser Glu Phe Gly Ser Val			
570	575	580	585
gac ggg cct cta cct cat cct cga tgg tca gct gag gca tct ggg aaa			1950
Asp Gly Pro Leu Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly Lys			
	590	595	600
ccc tct cct tct gat cca gga tct ggt aca gct acc atg atg aac agc			1998
Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr Ala Thr Met Met Asn Ser			
	605	610	615
agc tca aga ggc tct tcc cct acc agg gta ctc gat gaa ggc aag gtt			2046
Ser Ser Arg Gly Ser Ser Pro Thr Arg Val Leu Asp Glu Gly Lys Val			

620	625	630	
aat atg gct cca aaa ggg ccc cct cct ttc cca gga gtc cct ctc atg			2094
Asn Met Ala Pro Lys Gly Pro Pro Pro Phe Pro Gly Val Pro Leu Met			
635	640	645	
agc acc ccc atg gga ggc cct gta cca cca ccc att cga tat gga cca			2142
Ser Thr Pro Met Gly Gly Pro Val Pro Pro Pro Ile Arg Tyr Gly Pro			
650	655	660	665
cca cct cag ctc tgc gga cct ttt ggg cct cgg cca ctt cct cca ccc			2190
Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro Arg Pro Leu Pro Pro Pro			
670	675	680	
ttt ggc cct ggt atg cgt cca cca cta ggc tta aga gaa ttt gca cca			2238
Phe Gly Pro Gly Met Arg Pro Pro Leu Gly Leu Arg Glu Phe Ala Pro			
685	690	695	
ggc gtt cca cca gga aga cgg gac ctg cct ctc cac cct cgg gga ttt			2286
Gly Val Pro Pro Gly Arg Arg Asp Leu Pro Leu His Pro Arg Gly Phe			
700	705	710	
tta cct gga cac gca cca ttt aga cct tta ggt tca ctt ggc cca aga			2334
Leu Pro Gly His Ala Pro Phe Arg Pro Leu Gly Ser Leu Gly Pro Arg			
715	720	725	
gag tac ttt att cct ggt acc cga tta cca ccc cca acc cat ggt ccc			2382
Glu Tyr Phe Ile Pro Gly Thr Arg Leu Pro Pro Pro Thr His Gly Pro			
730	735	740	745
cag gaa tac cca cca cca cct gct gta aga gac tta ctg ccg tca ggc			2430
Gln Glu Tyr Pro Pro Pro Pro Ala Val Arg Asp Leu Leu Pro Ser Gly			
750	755	760	
tct aga gat gag cct cca cct gcc tct cag agc act agc cag gac tgt			2478
Ser Arg Asp Glu Pro Pro Pro Ala Ser Gln Ser Thr Ser Gln Asp Cys			

765 770 775  
 tca cag gct tta aaa cag agc cca taaaactatg acctctgagg tttcattgga 2532  
 Ser Gln Ala Leu Lys Gln Ser Pro

780 785  
 aagaaagtgt actgtgcatt atccattaca gtaaaggatt tcattggcctt caaaatccaa 2592  
 aagttttattt taaaaggttt gttgtagaa ctaagctgcc ttggcagtgt gcatttttga 2652  
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<210> 116

<211> 785

<212> PRT

<213> Homo sapiens

<400> 116

Met Asp Ser Val Pro Ala Thr Val Pro Ser Ile Ala Ala Thr Pro Gly  
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 Asp Pro Glu Leu Val Gly Pro Leu Ser Val Leu Tyr Ala Ala Phe Ile  
 20 25 30  
 Ala Lys Leu Leu Glu Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro  
 35 40 45  
 Gly Pro Asp Phe Tyr Gly Leu Pro Trp Lys Pro Val Phe Ile Thr Ala  
 50 55 60  
 Phe Leu Gly Ile Ala Ser Phe Ala Ile Phe Leu Trp Arg Thr Val Leu  
 65 70 75 80  
 Val Val Lys Asp Arg Val Tyr Gln Val Thr Glu Gln Gln Ile Ser Glu  
 85 90 95  
 Lys Leu Lys Thr Ile Met Lys Glu Asn Thr Glu Leu Val Gln Lys Leu  
 100 105 110

Ser Asn Tyr Glu Gln Lys Ile Lys Glu Ser Lys Lys His Val Gln Glu  
 115 120 125  
 Thr Arg Lys Gln Asn Met Ile Leu Ser Asp Glu Ala Ile Lys Tyr Lys  
 130 135 140  
 Asp Lys Ile Lys Thr Leu Glu Lys Asn Gln Glu Ile Leu Asp Asp Thr  
 145 150 155 160  
 Ala Lys Asn Leu Arg Val Met Leu Glu Ser Glu Arg Glu Gln Asn Val  
 165 170 175  
 Lys Asn Gln Asp Leu Ile Ser Glu Asn Lys Lys Ser Ile Glu Lys Leu  
 180 185 190  
 Lys Asp Val Ile Ser Met Asn Ala Ser Glu Phe Ser Glu Val Gln Ile  
 195 200 205  
 Ala Leu Asn Glu Ala Lys Leu Ser Glu Glu Lys Val Lys Ser Glu Cys  
 210 215 220  
 His Arg Val Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys Lys Glu Gln  
 225 230 235 240  
 Leu Gln Gln Glu Ile Glu Asp Trp Ser Lys Leu His Ala Glu Leu Ser  
 245 250 255  
 Glu Gln Ile Lys Ser Phe Glu Lys Ser Gln Lys Asp Leu Glu Val Ala  
 260 265 270  
 Leu Thr His Lys Asp Asp Asn Ile Asn Ala Leu Thr Asn Cys Ile Thr  
 275 280 285  
 Gln Leu Asn Leu Leu Glu Cys Glu Ser Glu Ser Glu Gly Gln Asn Lys  
 290 295 300  
 Gly Gly Asn Asp Ser Asp Glu Leu Ala Asn Gly Glu Val Gly Gly Asp  
 305 310 315 320  
 Arg Asn Glu Lys Met Lys Asn Gln Ile Lys Gln Met Met Asp Val Ser

325 330 335  
Arg Thr Gln Thr Ala Ile Ser Val Val Glu Glu Asp Leu Lys Leu Leu  
340 345 350  
Gln Leu Lys Leu Arg Ala Ser Val Ser Thr Lys Cys Asn Leu Glu Asp  
355 360 365  
Gln Val Lys Lys Leu Glu Asp Asp Arg Asn Ser Leu Gln Ala Ala Lys  
370 375 380  
Ala Gly Leu Glu Asp Glu Cys Lys Thr Leu Arg Gln Lys Val Glu Ile  
385 390 395 400  
Leu Asn Glu Leu Tyr Gln Gln Lys Glu Met Ala Leu Gln Lys Lys Leu  
405 410 415  
Ser Gln Glu Glu Tyr Glu Arg Gln Glu Arg Glu His Arg Leu Ser Ala  
420 425 430  
Ala Asp Glu Lys Ala Val Ser Ala Ala Glu Glu Val Lys Thr Tyr Lys  
435 440 445  
Arg Arg Ile Glu Glu Met Glu Asp Glu Leu Gln Lys Thr Glu Arg Ser  
450 455 460  
Phe Lys Asn Gln Ile Ala Thr His Glu Lys Lys Ala His Glu Asn Trp  
465 470 475 480  
Leu Lys Ala Arg Ala Ala Glu Arg Ala Ile Ala Glu Glu Lys Arg Glu  
485 490 495  
Ala Ala Asn Leu Arg His Lys Leu Leu Glu Leu Thr Gln Lys Met Ala  
500 505 510  
Met Leu Gln Glu Glu Pro Val Ile Val Lys Pro Met Pro Gly Lys Pro  
515 520 525  
Asn Thr Gln Asn Pro Pro Arg Arg Gly Pro Leu Ser Gln Asn Gly Ser



530	535	540
Phe Gly Pro Ser Pro Val Ser Gly Gly Glu Cys Ser Pro Pro Leu Thr		
545	550	555
Val Glu Pro Pro Val Arg Pro Leu Ser Ala Thr Leu Asn Arg Arg Asp		
565	570	575
Met Pro Arg Ser Glu Phe Gly Ser Val Asp Gly Pro Leu Pro His Pro		
580	585	590
Arg Trp Ser Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser Asp Pro Gly		
595	600	605
Ser Gly Thr Ala Thr Met Met Asn Ser Ser Ser Arg Gly Ser Ser Pro		
610	615	620
Thr Arg Val Leu Asp Glu Gly Lys Val Asn Met Ala Pro Lys Gly Pro		
625	630	635
Pro Pro Phe Pro Gly Val Pro Leu Met Ser Thr Pro Met Gly Gly Pro		
645	650	655
Val Pro Pro Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu Cys Gly Pro		
660	665	670
Phe Gly Pro Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly Met Arg Pro		
675	680	685
Pro Leu Gly Leu Arg Glu Phe Ala Pro Gly Val Pro Pro Gly Arg Arg		
690	695	700
Asp Leu Pro Leu His Pro Arg Gly Phe Leu Pro Gly His Ala Pro Phe		
705	710	715
Arg Pro Leu Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile Pro Gly Thr		
725	730	735
Arg Leu Pro Pro Pro Thr His Gly Pro Gln Glu Tyr Pro Pro Pro Pro		
740	745	750

Ala Val Arg Asp Leu Leu Pro Ser Gly Ser Arg Asp Glu Pro Pro Pro

755

760

765

Ala Ser Gln Ser Thr Ser Gln Asp Cys Ser Gln Ala Leu Lys Gln Ser

770

775

780

Pro

785

&lt;210&gt; 117

&lt;211&gt; 3621

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (39).. (3410)

&lt;400&gt; 117

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Met Ile Leu Asp Ser Glu

1

5

aaa aca agt gag act gct gcc aaa ggg gtc aac aca gga ggc agg gaa 104

Lys Thr Ser Glu Thr Ala Ala Lys Gly Val Asn Thr Gly Gly Arg Glu

10

15

20

cca aat aca atg gtg gaa aaa gaa cgc cct ctg gca gat aag aaa gca 152

Pro Asn Thr Met Val Glu Lys Glu Arg Pro Leu Ala Asp Lys Lys Ala

25

30

35

cag aga cca ttt gaa cga agt gac ttt tct gac agc ata aaa att cag 200

Gln Arg Pro Phe Glu Arg Ser Asp Phe Ser Asp Ser Ile Lys Ile Gln

40

45

50

act cca gaa tta ggt gaa gtg ttt cag aat aaa gat tct gat tat ctg 248  
 Thr Pro Glu Leu Gly Glu Val Phe Gln Asn Lys Asp Ser Asp Tyr Leu  
 55 60 65 70  
 aag aac gac aac cct gag gaa cat ctg aag acc tca ggg ctt gca ggg 296  
 Lys Asn Asp Asn Pro Glu Glu His Leu Lys Thr Ser Gly Leu Ala Gly  
 75 80 85  
 gag cct gag gga gaa ctc tca aaa gag gac cat ggg aac aca gag aag 344  
 Glu Pro Glu Gly Glu Leu Ser Lys Glu Asp His Gly Asn Thr Glu Lys  
 90 95 100  
 tac atg ggc aca gaa agc cag ggg tct gct gct gca gaa cct gaa gat 392  
 Tyr Met Gly Thr Glu Ser Gln Gly Ser Ala Ala Ala Glu Pro Glu Asp  
 105 110 115  
 gac tcg ttc cac tgg act cca cat aca agt gta gag cca ggg cat agt 440  
 Asp Ser Phe His Trp Thr Pro His Thr Ser Val Glu Pro Gly His Ser  
 120 125 130  
 gac aag agg gag gac tta ctt atc ata agc agc ttc ttt aaa gaa caa 488  
 Asp Lys Arg Glu Asp Leu Leu Ile Ile Ser Ser Phe Phe Lys Glu Gln  
 135 140 145 150  
 cag tct ttg cag cgg ttc cag aag tac ttt aat gtc cat gag ctg gaa 536  
 Gln Ser Leu Gln Arg Phe Gln Lys Tyr Phe Asn Val His Glu Leu Glu  
 155 160 165  
 gcc ttg cta caa gaa atg tca tca aaa ctg aag tca gcg cag cag gag 584  
 Ala Leu Leu Gln Glu Met Ser Ser Lys Leu Lys Ser Ala Gln Gln Glu  
 170 175 180  
 agc ctg ccc tat aat atg gaa aaa gtc cta gat aag gtc ttc cgt gct 632  
 Ser Leu Pro Tyr Asn Met Glu Lys Val Leu Asp Lys Val Phe Arg Ala  
 185 190 195

tct gag tca caa att ctg agc ata gca gaa aaa atg ctt gat act cgt 680  
 Ser Glu Ser Gln Ile Leu Ser Ile Ala Glu Lys Met Leu Asp Thr Arg  
 200 205 210  
 gtg gct gaa aat aga gat ctg gga atg aac gaa aat aac ata ttt gaa 728  
 Val Ala Glu Asn Arg Asp Leu Gly Met Asn Glu Asn Asn Ile Phe Glu  
 215 220 225 230  
 gag gct gca gtg ctt gat gac att caa gac ctc atc tat ttt gtc agg 776  
 Glu Ala Ala Val Leu Asp Asp Ile Gln Asp Leu Ile Tyr Phe Val Arg  
 235 240 245  
 tac aag cac tcc aca gca gag gag aca gcc aca ctg gtg atg gca cca 824  
 Tyr Lys His Ser Thr Ala Glu Glu Thr Ala Thr Leu Val Met Ala Pro  
 250 255 260  
 cct cta gag gaa ggc ttg ggt gga gca atg gaa gag atg caa cca ctg 872  
 Pro Leu Glu Glu Gly Leu Gly Gly Ala Met Glu Glu Met Gln Pro Leu  
 265 270 275  
 cat gaa gat aat ttc tca cga gag aag aca gca gaa ctt aat gtg cag 920  
 His Glu Asp Asn Phe Ser Arg Glu Lys Thr Ala Glu Leu Asn Val Gln  
 280 285 290  
 gtt cct gaa gaa ccc acc cac ttg gac caa cgt gtg att ggg gac act 968  
 Val Pro Glu Glu Pro Thr His Leu Asp Gln Arg Val Ile Gly Asp Thr  
 295 300 305 310  
 cat gcc tca gaa gtg tca cag aag cca aat act gag aaa gac ctg gac 1016  
 His Ala Ser Glu Val Ser Gln Lys Pro Asn Thr Glu Lys Asp Leu Asp  
 315 320 325  
 cca ggg cca gtt aca aca gaa gac act cct atg gat gct att gat gca 1064  
 Pro Gly Pro Val Thr Thr Glu Asp Thr Pro Met Asp Ala Ile Asp Ala  
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aac aag caa cca gag aca gcc gcc gaa gag ccg gca agt gtc aca cct 1112  
 Asn Lys Gln Pro Glu Thr Ala Ala Glu Glu Pro Ala Ser Val Thr Pro  
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 Lys Ser Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp  
 375 380 385 390  
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 Phe Tyr Gly Leu Pro Trp Lys Pro Val Phe Ile Thr Ala Phe Leu Gly  
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 Ile Ala Ser Phe Ala Ile Phe Leu Trp Arg Thr Val Leu Val Val Lys  
 410 415 420  
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 Asp Arg Val Tyr Gln Val Thr Glu Gln Gln Ile Ser Glu Lys Leu Lys  
 425 430 435  
 act atc atg aaa gaa aat aca gaa ctt gta caa aaa ttg tca aat tat 1400  
 Thr Ile Met Lys Glu Asn Thr Glu Leu Val Gln Lys Leu Ser Asn Tyr  
 440 445 450  
 gaa cag aag atc aag gaa tca aag aaa cat gtt cag gaa acc agg aaa 1448  
 Glu Gln Lys Ile Lys Glu Ser Lys Lys His Val Gln Glu Thr Arg Lys  
 455 460 465 470  
 caa aat atg att ctc tct gat gaa gca att aaa tat aag gat aaa atc 1496  
 Gln Asn Met Ile Leu Ser Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile  
 475 480 485

aag aca ctt gaa aaa aat cag gaa att ctg gat gac aca gct aaa aat 1544  
Lys Thr Leu Glu Lys Asn Gln Glu Ile Leu Asp Asp Thr Ala Lys Asn  
490 495 500  
ctt cgt gtt atg cta gaa tct gag aga gaa cag aat gtc aag aat cag 1592  
Leu Arg Val Met Leu Glu Ser Glu Arg Glu Gln Asn Val Lys Asn Gln  
505 510 515  
gac ttg ata tca gaa aac aag aaa tct ata gag aag tta aag gat gtt 1640  
Asp Leu Ile Ser Glu Asn Lys Lys Ser Ile Glu Lys Leu Lys Asp Val  
520 525 530  
att tca atg aat gcc tca gag ttt tca gag gtt cag att gca ctt aat 1688  
Ile Ser Met Asn Ala Ser Glu Phe Ser Glu Val Gln Ile Ala Leu Asn  
535 540 545 550  
gaa gct aag ctt agt gaa gag aag gtg aag tct gaa tgc cat cgg gtt 1736  
Glu Ala Lys Leu Ser Glu Glu Lys Val Lys Ser Glu Cys His Arg Val  
555 560 565  
caa gaa gaa aat gct agg ctt aag aag aaa aaa gag cag ttg cag cag 1784  
Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys Lys Glu Gln Leu Gln Gln  
570 575 580  
gaa atc gaa gac tgg agt aaa tta cat gct gag ctc agt gag caa atc 1832  
Glu Ile Glu Asp Trp Ser Lys Leu His Ala Glu Leu Ser Glu Gln Ile  
585 590 595  
aaa tca ttt gag aag tct cag aaa gat ttg gaa gta gct ctt act cac 1880  
Lys Ser Phe Glu Lys Ser Gln Lys Asp Leu Glu Val Ala Leu Thr His  
600 605 610  
aag gat gat aat att aat gct ttg act aac tgc att aca cag ttg aat 1928  
Lys Asp Asp Asn Ile Asn Ala Leu Thr Asn Cys Ile Thr Gln Leu Asn  
615 620 625 630

ctg tta gag tgt gaa tct gaa tct gag ggt caa aat aaa ggt gga aat	1976
Leu Leu Glu Cys Glu Ser Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn	
635 640 645	
gat tca gat gaa tta gca aat gga gaa gtg gga ggt gac cgg aat gag	2024
Asp Ser Asp Glu Leu Ala Asn Gly Glu Val Gly Gly Asp Arg Asn Glu	
650 655 660	
aag atg aaa aat caa att aag cag atg atg gat gtc tct cgg aca cag	2072
Lys Met Lys Asn Gln Ile Lys Gln Met Met Asp Val Ser Arg Thr Gln	
665 670 675	
act gca ata tcg gta gtt gaa gag gat cta aag ctt tta cag ctt aag	2120
Thr Ala Ile Ser Val Val Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys	
680 685 690	
cta aga gcc tcc gtg tcc act aaa tgt aac ctg gaa gac cag gta aag	2168
Leu Arg Ala Ser Val Ser Thr Lys Cys Asn Leu Glu Asp Gln Val Lys	
695 700 705 710	
aaa ttg gaa gat gac cgc aac tca cta caa gct gcc aaa gct gga ctg	2216
Lys Leu Glu Asp Asp Arg Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu	
715 720 725	
gaa gat gaa tgc aaa acc ttg agg cag aaa gtg gag att ctg aat gag	2264
Glu Asp Glu Cys Lys Thr Leu Arg Gln Lys Val Glu Ile Leu Asn Glu	
730 735 740	
ctc tat cag cag aag gag atg gct ttg caa aag aag ctg agt caa gaa	2312
Leu Tyr Gln Gln Lys Glu Met Ala Leu Gln Lys Lys Leu Ser Gln Glu	
745 750 755	
gag tat gaa cgg caa gaa aga gag cac agg ctg tca gct gca gat gaa	2360
Glu Tyr Glu Arg Gln Glu Arg Glu His Arg Leu Ser Ala Ala Asp Glu	
760 765 770	

aag gca gtt tcg gct gca gag gaa gta aaa act tac aag cgg aga att 2408  
Lys Ala Val Ser Ala Ala Glu Glu Val Lys Thr Tyr Lys Arg Arg Ile  
775 780 785 790  
gaa gaa atg gag gat gaa tta cag aag aca gag cgg tca ttt aaa aac 2456  
Glu Glu Met Glu Asp Glu Leu Gln Lys Thr Glu Arg Ser Phe Lys Asn  
795 800 805  
cag atc gct acc cat gag aag aaa gct cat gaa aac tgg ctc aaa gct 2504  
Gln Ile Ala Thr His Glu Lys Lys Ala His Glu Asn Trp Leu Lys Ala  
810 815 820  
cgt gct gca gaa aga gct ata gct gaa gag aaa agg gaa gct gcc aat 2552  
Arg Ala Ala Glu Arg Ala Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn  
825 830 835  
ttg aga cac aaa tta tta gaa tta aca caa aag atg gca atg ctg caa 2600  
Leu Arg His Lys Leu Leu Glu Leu Thr Gln Lys Met Ala Met Leu Gln  
840 845 850  
gaa gaa cct gtg att gta aaa cca atg cca gga aaa cca aat aca caa 2648  
Glu Glu Pro Val Ile Val Lys Pro Met Pro Gly Lys Pro Asn Thr Gln  
855 860 865 870  
aac cct cca cgg aga ggt cct ctg agc cag aat ggc tct ttt ggc cca 2696  
Asn Pro Pro Arg Arg Gly Pro Leu Ser Gln Asn Gly Ser Phe Gly Pro  
875 880 885  
tcc cct gtg agt ggt gga gaa tgc tcc cct cca ttg aca gtg gag cca 2744  
Ser Pro Val Ser Gly Gly Glu Cys Ser Pro Pro Leu Thr Val Glu Pro  
890 895 900  
ccc gtg aga cct ctc tct gct act ctc aat cga aga gat atg cct aga 2792  
Pro Val Arg Pro Leu Ser Ala Thr Leu Asn Arg Arg Asp Met Pro Arg  
905 910 915



agt gaa ttt gga tca gtg gac ggg cct cta cct cat cct cga tgg tca 2840  
 Ser Glu Phe Gly Ser Val Asp Gly Pro Leu Pro His Pro Arg Trp Ser  
 920 925 930  
 gct gag gca tct ggg aaa ccc tct cct tct gat cca gga tct ggt aca 2888  
 Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr  
 935 940 945 950  
 gct acc atg atg aac agc agc tca aga ggc tct tcc cct acc agg gta 2936  
 Ala Thr Met Met Asn Ser Ser Ser Arg Gly Ser Ser Pro Thr Arg Val  
 955 960 965  
 ctc gat gaa ggc aag gtt aat atg gct cca aaa ggg ccc cct cct ttc 2984  
 Leu Asp Glu Gly Lys Val Asn Met Ala Pro Lys Gly Pro Pro Pro Phe  
 970 975 980  
 cca gga gtc cct ctc atg agc acc ccc atg gga ggc cct gta cca cca 3032  
 Pro Gly Val Pro Leu Met Ser Thr Pro Met Gly Gly Pro Val Pro Pro  
 985 990 995  
 ccc att cga tat gga cca cca cct cag ctc tgc gga cct ttt ggg cct 3080  
 Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro  
 1000 1005 1010  
 cgg cca ctt cct cca ccc ttt ggc cct ggt atg cgt cca cca cta ggc 3128  
 Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly Met Arg Pro Pro Leu Gly  
 1015 1020 1025 1030  
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 Leu Arg Glu Phe Ala Pro Gly Val Pro Pro Gly Arg Arg Asp Leu Pro  
 1035 1040 1045  
 ctc cac cct cgg gga ttt tta cct gga cac gca cca ttt aga cct tta 3224  
 Leu His Pro Arg Gly Phe Leu Pro Gly His Ala Pro Phe Arg Pro Leu  
 1050 1055 1060

ggt tca ctt ggc cca aga gag tac ttt att cct ggt acc cga tta cca 3272  
 Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile Pro Gly Thr Arg Leu Pro  
 1065 1070 1075  
 ccc cca acc cat ggt ccc cag gaa tac cca cca cca cct gct gta aga 3320  
 Pro Pro Thr His Gly Pro Gln Glu Tyr Pro Pro Pro Pro Ala Val Arg  
 1080 1085 1090  
 gac tta ctg ccg tca ggc tct aga gat gag cct cca cct gcc tct cag 3368  
 Asp Leu Leu Pro Ser Gly Ser Arg Asp Glu Pro Pro Pro Ala Ser Gln  
 1095 1100 1105 1110  
 agc act agc cag gac tgt tca cag gct tta aaa cag agc cca 3410  
 Ser Thr Ser Gln Asp Cys Ser Gln Ala Leu Lys Gln Ser Pro  
 1115 1120  
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 ctaagctgcc ttggcagtgt gcatttttga gccaaacaat tcaaaaatgt cattttctcc 3590  
 ctaaataaaaa atcacctttt aagctaaaaa g 3621

&lt;210&gt; 118

&lt;211&gt; 1124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

Met Ile Leu Asp Ser Glu Lys Thr Ser Glu Thr Ala Ala Lys Gly Val

1

5

10

15

Asn Thr Gly Gly Arg Glu Pro Asn Thr Met Val Glu Lys Glu Arg Pro

20

25

30

Leu Ala Asp Lys Lys Ala Gln Arg Pro Phe Glu Arg Ser Asp Phe Ser

35	40	45
Asp Ser Ile Lys Ile Gln Thr Pro Glu Leu Gly Glu Val Phe Gln Asn		
50	55	60
Lys Asp Ser Asp Tyr Leu Lys Asn Asp Asn Pro Glu Glu His Leu Lys		
65	70	75
Thr Ser Gly Leu Ala Gly Glu Pro Glu Gly Glu Leu Ser Lys Glu Asp		
85	90	95
His Gly Asn Thr Glu Lys Tyr Met Gly Thr Glu Ser Gln Gly Ser Ala		
100	105	110
Ala Ala Glu Pro Glu Asp Asp Ser Phe His Trp Thr Pro His Thr Ser		
115	120	125
Val Glu Pro Gly His Ser Asp Lys Arg Glu Asp Leu Leu Ile Ile Ser		
130	135	140
Ser Phe Phe Lys Glu Gln Gln Ser Leu Gln Arg Phe Gln Lys Tyr Phe		
145	150	155
Asn Val His Glu Leu Glu Ala Leu Leu Gln Glu Met Ser Ser Lys Leu		
165	170	175
Lys Ser Ala Gln Gln Glu Ser Leu Pro Tyr Asn Met Glu Lys Val Leu		
180	185	190
Asp Lys Val Phe Arg Ala Ser Glu Ser Gln Ile Leu Ser Ile Ala Glu		
195	200	205
Lys Met Leu Asp Thr Arg Val Ala Glu Asn Arg Asp Leu Gly Met Asn		
210	215	220
Glu Asn Asn Ile Phe Glu Glu Ala Ala Val Leu Asp Asp Ile Gln Asp		
225	230	235
Leu Ile Tyr Phe Val Arg Tyr Lys His Ser Thr Ala Glu Glu Thr Ala		
245	250	255

Thr Leu Val Met Ala Pro Pro Leu Glu Glu Gly Leu Gly Gly Ala Met  
260 265 270  
Glu Glu Met Gln Pro Leu His Glu Asp Asn Phe Ser Arg Glu Lys Thr  
275 280 285  
Ala Glu Leu Asn Val Gln Val Pro Glu Glu Pro Thr His Leu Asp Gln  
290 295 300  
Arg Val Ile Gly Asp Thr His Ala Ser Glu Val Ser Gln Lys Pro Asn  
305 310 315 320  
Thr Glu Lys Asp Leu Asp Pro Gly Pro Val Thr Thr Glu Asp Thr Pro  
325 330 335  
Met Asp Ala Ile Asp Ala Asn Lys Gln Pro Glu Thr Ala Ala Glu Glu  
340 345 350  
Pro Ala Ser Val Thr Pro Leu Glu Asn Ala Ile Leu Leu Ile Tyr Ser  
355 360 365  
Phe Met Phe Tyr Leu Thr Lys Ser Leu Val Ala Thr Leu Pro Asp Asp  
370 375 380  
Val Gln Pro Gly Pro Asp Phe Tyr Gly Leu Pro Trp Lys Pro Val Phe  
385 390 395 400  
Ile Thr Ala Phe Leu Gly Ile Ala Ser Phe Ala Ile Phe Leu Trp Arg  
405 410 415  
Thr Val Leu Val Val Lys Asp Arg Val Tyr Gln Val Thr Glu Gln Gln  
420 425 430  
Ile Ser Glu Lys Leu Lys Thr Ile Met Lys Glu Asn Thr Glu Leu Val  
435 440 445  
Gln Lys Leu Ser Asn Tyr Glu Gln Lys Ile Lys Glu Ser Lys Lys His  
450 455 460  
Val Gln Glu Thr Arg Lys Gln Asn Met Ile Leu Ser Asp Glu Ala Ile

465	470	475	480
Lys Tyr Lys Asp Lys Ile Lys Thr Leu Glu Lys Asn Gln Glu Ile Leu			
	485	490	495
Asp Asp Thr Ala Lys Asn Leu Arg Val Met Leu Glu Ser Glu Arg Glu			
	500	505	510
Gln Asn Val Lys Asn Gln Asp Leu Ile Ser Glu Asn Lys Lys Ser Ile			
	515	520	525
Glu Lys Leu Lys Asp Val Ile Ser Met Asn Ala Ser Glu Phe Ser Glu			
	530	535	540
Val Gln Ile Ala Leu Asn Glu Ala Lys Leu Ser Glu Glu Lys Val Lys			
545	550	555	560
Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala Arg Leu Lys Lys Lys			
	565	570	575
Lys Glu Gln Leu Gln Gln Glu Ile Glu Asp Trp Ser Lys Leu His Ala			
	580	585	590
Glu Leu Ser Glu Gln Ile Lys Ser Phe Glu Lys Ser Gln Lys Asp Leu			
	595	600	605
Glu Val Ala Leu Thr His Lys Asp Asp Asn Ile Asn Ala Leu Thr Asn			
	610	615	620
Cys Ile Thr Gln Leu Asn Leu Leu Glu Cys Glu Ser Glu Ser Glu Gly			
625	630	635	640
Gln Asn Lys Gly Gly Asn Asp Ser Asp Glu Leu Ala Asn Gly Glu Val			
	645	650	655
Gly Gly Asp Arg Asn Glu Lys Met Lys Asn Gln Ile Lys Gln Met Met			
	660	665	670
Asp Val Ser Arg Thr Gln Thr Ala Ile Ser Val Val Glu Glu Asp Leu			
	675	680	685

Lys Leu Leu Gln Leu Lys Leu Arg Ala Ser Val Ser Thr Lys Cys Asn  
 690 695 700  
 Leu Glu Asp Gln Val Lys Lys Leu Glu Asp Asp Arg Asn Ser Leu Gln  
 705 710 715 720  
 Ala Ala Lys Ala Gly Leu Glu Asp Glu Cys Lys Thr Leu Arg Gln Lys  
 725 730 735  
 Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys Glu Met Ala Leu Gln  
 740 745 750  
 Lys Lys Leu Ser Gln Glu Glu Tyr Glu Arg Gln Glu Arg Glu His Arg  
 755 760 765  
 Leu Ser Ala Ala Asp Glu Lys Ala Val Ser Ala Ala Glu Glu Val Lys  
 770 775 780  
 Thr Tyr Lys Arg Arg Ile Glu Glu Met Glu Asp Glu Leu Gln Lys Thr  
 785 790 795 800  
 Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His Glu Lys Lys Ala His  
 805 810 815  
 Glu Asn Trp Leu Lys Ala Arg Ala Ala Glu Arg Ala Ile Ala Glu Glu  
 820 825 830  
 Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu Leu Glu Leu Thr Gln  
 835 840 845  
 Lys Met Ala Met Leu Gln Glu Glu Pro Val Ile Val Lys Pro Met Pro  
 850 855 860  
 Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg Gly Pro Leu Ser Gln  
 865 870 875 880  
 Asn Gly Ser Phe Gly Pro Ser Pro Val Ser Gly Gly Glu Cys Ser Pro  
 885 890 895  
 Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu Ser Ala Thr Leu Asn

900	905	910
Arg Arg Asp Met Pro Arg Ser Glu Phe Gly Ser Val Asp Gly Pro Leu		
915	920	925
Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly Lys Pro Ser Pro Ser		
930	935	940
Asp Pro Gly Ser Gly Thr Ala Thr Met Met Asn Ser Ser Ser Arg Gly		
945	950	955
Ser Ser Pro Thr Arg Val Leu Asp Glu Gly Lys Val Asn Met Ala Pro		
965	970	975
Lys Gly Pro Pro Pro Phe Pro Gly Val Pro Leu Met Ser Thr Pro Met		
980	985	990
Gly Gly Pro Val Pro Pro Pro Ile Arg Tyr Gly Pro Pro Pro Gln Leu		
995	1000	1005
Cys Gly Pro Phe Gly Pro Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly		
1010	1015	1020
Met Arg Pro Pro Leu Gly Leu Arg Glu Phe Ala Pro Gly Val Pro Pro		
1025	1030	1035
Gly Arg Arg Asp Leu Pro Leu His Pro Arg Gly Phe Leu Pro Gly His		
1045	1050	1055
Ala Pro Phe Arg Pro Leu Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile		
1060	1065	1070
Pro Gly Thr Arg Leu Pro Pro Pro Thr His Gly Pro Gln Glu Tyr Pro		
1075	1080	1085
Pro Pro Pro Ala Val Arg Asp Leu Leu Pro Ser Gly Ser Arg Asp Glu		
1090	1095	1100
Pro Pro Pro Ala Ser Gln Ser Thr Ser Gln Asp Cys Ser Gln Ala Leu		
1105	1110	1115
		1120

Lys Gln Ser Pro

&lt;210&gt; 119

&lt;211&gt; 1982

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51).. (680)

&lt;400&gt; 119

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                                                    Met Ala
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gcc tcc agc atc agt tca cca tgg gga aag cat gtg ttc aaa gcc att      104
Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys Ala Ile
           5                10                15
ctg atg gtc cta gtg gcc ctt atc ctc ctc cac tca gca ttg gcc cag      152
Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu Ala Gln
           20                25                30
tcc cgt cga gac ttt gca cca cca ggc caa cag aag aga gaa gcc cca      200
Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu Ala Pro
           35                40                45                50
gtt gat gtc ttg acc cag ata ggt cga tct gtg cga ggg aca ctg gat      248
Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr Leu Asp
           55                60                65
gcc tgg att ggg cca gag acc atg cac ctg gtg tca gag tct tcg tcc      296
Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser Ser Ser

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70	75	80	
caa gtg ttg tgg gcc atc tca tca gcc att tct gtg gcc ttc ttt gct			344
Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe Phe Ala			
85	90	95	
ctg tct ggg atc gcc gca cag ctg ctg aat gcc ttg gga cta gct ggt			392
Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu Ala Gly			
100	105	110	
gat tac ctc gcc cag ggg cct gaa gct cag ccc tgg cca ggt cca gac			440
Asp Tyr Leu Ala Gln Gly Pro Glu Ala Gln Pro Trp Pro Gly Pro Asp			
115	120	125	130
ctt cct gct gtg ggg agc agg ggc cct ggt cgt cta ctg gct gct gtc			488
Leu Pro Ala Val Gly Ser Arg Gly Pro Gly Arg Leu Leu Ala Ala Val			
135	140	145	
tct gct cct cgg ctt ggt ctt ggc ctt gct ggg gcg gat cct gtg ggg			536
Ser Ala Pro Arg Leu Gly Leu Gly Leu Ala Gly Ala Asp Pro Val Gly			
150	155	160	
cct gaa gct tgt cat ctt cct ggc cgg ctt cgt ggc cct gat gag gtc			584
Pro Glu Ala Cys His Leu Pro Gly Arg Leu Arg Gly Pro Asp Glu Val			
165	170	175	
ggt gcc cgg gtg gag ccg ccg cag gtg cag atc ttg gtg gta gta gca			632
Gly Ala Arg Val Glu Pro Pro Gln Val Gln Ile Leu Val Val Val Ala			
180	185	190	
aat att caa acg aga act ttg aag gcc gaa gtg gag aag ggt tcc atg			680
Asn Ile Gln Thr Arg Thr Leu Lys Ala Glu Val Glu Lys Gly Ser Met			
195	200	205	210
tgaacagcag tgtggaggag gaggagccg gatgccccac acaccgccag tgtcatacca			740

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cctgtctctg aaccttcaga acattgatcc ttgccgcagc cccactagcc aagagaaaca 860  
gagaaagacc attccccctg cctgtcctcg cggccctgtc ttctgagggt ctctgtctgg 920  
ggttggctct cttaacccctt tctctgctcc cagcctgcct caccaggga ggttggaggg 980  
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cctgtactcc caccaaacca tggctcctta aggcacgtc ctgtcctcct cattgcccag 1220  
cagtagggag gggcaggggt aaggggacct gaggataaag ggtggggaaa cagggtcccc 1280  
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gtggctgctt tgtgtcaaga aaagagcagt cactctcaga atcttgatc cccatcagcc 1460  
aaagcaaaag atggctgctg cttttagtagc atgtgcctgc aagtgggacc ttgctgggca 1520  
ttatatgccc tgtggggggt tcagagaccc tgaaagagga gggaggaccc gcctccttgt 1580  
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gctgaccagt gccaccccg gcagcccgagg aggaacacag gcagctcctt tcccttcacg 1700  
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ggtggttagg ggccactttt cctttgaggc tctagtggag gtggatgtcc ttctctgcca 1820  
ggcttggcac atgatgtgaa gaataaatgc ccaattctta ctgttcagggt ttgatgtgga 1880  
atcacagctg cagtgatata tattctttat cagtgccttg ttggttttta ataaagtgca 1940  
cgctatttta ttatcttggt ctgaataaaa tgtatttact cc 1982

<210> 120

<211> 210

<212> PRT

<213> Homo sapiens

<400> 120

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys  
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 20 25 30  
 Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu  
 35 40 45  
 Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr  
 50 55 60  
 Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser  
 65 70 75 80  
 Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe  
 85 90 95  
 Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu  
 100 105 110  
 Ala Gly Asp Tyr Leu Ala Gln Gly Pro Glu Ala Gln Pro Trp Pro Gly  
 115 120 125  
 Pro Asp Leu Pro Ala Val Gly Ser Arg Gly Pro Gly Arg Leu Leu Ala  
 130 135 140  
 Ala Val Ser Ala Pro Arg Leu Gly Leu Gly Leu Ala Gly Ala Asp Pro  
 145 150 155 160  
 Val Gly Pro Glu Ala Cys His Leu Pro Gly Arg Leu Arg Gly Pro Asp  
 165 170 175  
 Glu Val Gly Ala Arg Val Glu Pro Pro Gln Val Gln Ile Leu Val Val  
 180 185 190  
 Val Ala Asn Ile Gln Thr Arg Thr Leu Lys Ala Glu Val Glu Lys Gly  
 195 200 205  
 Ser Met

210

&lt;210&gt; 121

&lt;211&gt; 2077

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (73)..(801)

&lt;400&gt; 121

ggcgcgggtt tgggtggcgcg tttcagcgaa gtgcacgtg aaggatagca gtggcctgag 60  
aaagaccag tc atg gca gcc tcc agc atc agt tca cca tgg gga aag cat 111

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His

1

5

10

gtg ttc aaa gcc att ctg atg gtc cta gtg gcc ctt atc ctc ctc cac 159  
Val Phe Lys Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His

15

20

25

tca gca ttg gcc cag tcc cgt cga gac ttt gca cca cca ggc caa cag 207  
Ser Ala Leu Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln

30

35

40

45

aag aga gaa gcc cca gtt gat gtc ttg acc cag ata ggt cga tct gtg 255  
Lys Arg Glu Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val

50

55

60

cga ggg aca ctg gat gcc tgg att ggg cca gag acc atg cac ctg gtg 303  
Arg Gly Thr Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val

65

70

75

tca gag tct tcg tcc caa gtg ttg tgg gcc atc tca tca gcc att tct 351

Ser Glu Ser Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser  
 80 85 90  
 gtg gcc ttc ttt gct ctg tct ggg atc gcc gca cag ctg ctg aat gcc 399  
 Val Ala Phe Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala  
 95 100 105  
 ttg gga cta gct ggt gat tac ctc gcc cag ggc ctg aag ctc agc cct 447  
 Leu Gly Leu Ala Gly Asp Tyr Leu Ala Gln Gly Leu Lys Leu Ser Pro  
 110 115 120 125  
 ggc cag gtc cag acc ttc ctg ctg tgg gga gca ggg gcc ctg gtc gtc 495  
 Gly Gln Val Gln Thr Phe Leu Leu Trp Gly Ala Gly Ala Leu Val Val  
 130 135 140  
 tac tgg ctg ctg tct ctg ctc ctc ggc ttg gtc ttg gcc ttg ctg ggg 543  
 Tyr Trp Leu Leu Ser Leu Leu Leu Gly Leu Val Leu Ala Leu Leu Gly  
 145 150 155  
 cgg atc ctg tgg ggc ctg aag ctt gtc atc ttc ctg gcc ggc ttc gtg 591  
 Arg Ile Leu Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val  
 160 165 170  
 gcc ctg atg agg tcg gtg cct gac cct tcc acc cgg gcc ctg cta ctc 639  
 Ala Leu Met Arg Ser Val Pro Asp Pro Ser Thr Arg Ala Leu Leu Leu  
 175 180 185  
 ctg gcc ttg ctg atc ctc tac gcc ctg ctg agc cgg ctc act ggc tcc 687  
 Leu Ala Leu Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser  
 190 195 200 205  
 cga gcc tct ggg gcc caa ctc gag gcc aag gtg cga ggg ctg gaa cgc 735  
 Arg Ala Ser Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg  
 210 215 220  
 cag gtg gag gag ctg cgc tgg cgc cag agg cga gcg gcc aag ggg gcc 783

Gln Val Glu Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala

225

230

235

cgc agt gtg gag gag gag tgagccgat gccccacaca ccgccagtgt 831

Arg Ser Val Glu Glu Glu

240

cataccaaag agctgagctg cttcggggcc atgcagccct cctgccagcc ccctgccctt 891  
 ttcttgccct gtctctgaac cttcagaaca ttgatccttg ccgcagcccc actagccaag 951  
 agaaacagag aaagaccatt cccctgcct gtcttgcgg ccctgtcttc tgaggttctc 1011  
 tgtctggggt tggtctctt aaccctttct ctgtccag cctgcctcac cagggaaggt 1071  
 tggaggggcc tccctctggc ttctgcatct gcgccagcaa acatcactgc cgttggtctc 1131  
 tcatgactta actggcttcc ctctgtctgt gccttggctt cctcctaag ctctgtctct 1191  
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 cacgtggtct gcagagagca gggtagctg ccagctgcc ctctccacca gggtagcctg 1851  
 tcttggtggt taggggccac ttttccttg aggctctagt ggaggtggat gtccttctct 1911  
 gccaggcttg gcacatgat tgaagaataa atgccaatt cttactgttc aggtttgatg 1971  
 tggaatcaca gctgcagtga tatatatatt ttatcagtgc ttggttggt ttaaataaag 2031  
 tgcacgtat ttattatct tgttctgaat aaaatgtatt tactcc 2077

&lt;210&gt; 122

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

Met Ala Ala Ser Ser Ile Ser Ser Pro Trp Gly Lys His Val Phe Lys  
 1 5 10 15  
 Ala Ile Leu Met Val Leu Val Ala Leu Ile Leu Leu His Ser Ala Leu  
 20 25 30  
 Ala Gln Ser Arg Arg Asp Phe Ala Pro Pro Gly Gln Gln Lys Arg Glu  
 35 40 45  
 Ala Pro Val Asp Val Leu Thr Gln Ile Gly Arg Ser Val Arg Gly Thr  
 50 55 60  
 Leu Asp Ala Trp Ile Gly Pro Glu Thr Met His Leu Val Ser Glu Ser  
 65 70 75 80  
 Ser Ser Gln Val Leu Trp Ala Ile Ser Ser Ala Ile Ser Val Ala Phe  
 85 90 95  
 Phe Ala Leu Ser Gly Ile Ala Ala Gln Leu Leu Asn Ala Leu Gly Leu  
 100 105 110  
 Ala Gly Asp Tyr Leu Ala Gln Gly Leu Lys Leu Ser Pro Gly Gln Val  
 115 120 125  
 Gln Thr Phe Leu Leu Trp Gly Ala Gly Ala Leu Val Val Tyr Trp Leu  
 130 135 140  
 Leu Ser Leu Leu Leu Gly Leu Val Leu Ala Leu Leu Gly Arg Ile Leu  
 145 150 155 160  
 Trp Gly Leu Lys Leu Val Ile Phe Leu Ala Gly Phe Val Ala Leu Met  
 165 170 175

Arg Ser Val Phe Asp Pro Ser Thr Arg Ala Leu Leu Leu Leu Ala Leu  
 180 185 190  
 Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser Arg Ala Ser  
 195 200 205  
 Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg Gln Val Glu  
 210 215 220  
 Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala Arg Ser Val  
 225 230 235 240  
 Glu Glu Glu

<210> 123

<211> 1937

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (347).. (1534)

<400> 123

aagttggctg ggtgcgcgcc ggctccggct gcagttcccg ggtccctcgg ccaccgaagc 60  
 caccctgccc tggatgaaagg gctcccgcac cgcccgggtgc tccccatctg cctggcggtg 120  
 tgcgcagagc tggaaagcat ggctgttata aatgaattct gattttgggg agcagatgcc 180  
 aacttagagc ctcgtagcaa tctctctgtc tttaaaagat gaggtgactt ggtgattttc 240  
 ctggaaaatt ataggtgccc agctaagacc tgaatgccat caccctcccc agggctctgc 300  
 agttttctcg tggatgaacc ttgatggatt tgttgttgct tgagaa atg gcg atg 355  
 Met Ala Met

1

atc gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag 403



Ile	Glu	Leu	Gly	Phe	Gly	Arg	Gln	Asn	Phe	His	Pro	Leu	Lys	Arg	Lys		
5						10						15					
agt	tca	ttg	ctg	ttg	aaa	ctc	ata	gct	ggt	gtc	ttt	gct	gtg	ctt	cta	451	
Ser	Ser	Leu	Leu	Leu	Lys	Leu	Ile	Ala	Val	Val	Phe	Ala	Val	Leu	Leu		
20					25					30				35			
ttt	tgt	gaa	ttt	tta	atc	tat	tac	tta	gcg	atc	ttt	cag	tgt	aat	tgg	499	
Phe	Cys	Glu	Phe	Leu	Ile	Tyr	Tyr	Leu	Ala	Ile	Phe	Gln	Cys	Asn	Trp		
				40					45					50			
cct	gaa	gtg	aaa	acc	aca	gcc	tct	gat	ggt	gaa	cag	acc	aca	cgt	gag	547	
Pro	Glu	Val	Lys	Thr	Thr	Ala	Ser	Asp	Gly	Glu	Gln	Thr	Thr	Arg	Glu		
				55					60					65			
cct	gtg	ctc	aaa	gcc	atg	ttt	ttg	gct	gac	acc	cat	ttg	ctt	ggg	gaa	595	
Pro	Val	Leu	Lys	Ala	Met	Phe	Leu	Ala	Asp	Thr	His	Leu	Leu	Gly	Glu		
				70					75					80			
ttc	cta	ggc	cac	tgg	ctg	gac	aaa	tta	cga	agg	gaa	tgg	cag	atg	gag	643	
Phe	Leu	Gly	His	Trp	Leu	Asp	Lys	Leu	Arg	Arg	Glu	Trp	Gln	Met	Glu		
				85					90					95			
aga	gcg	ttc	cag	aca	gct	ctg	tgg	ttg	ctg	cag	ccg	gaa	gtc	gtc	ttc	691	
Arg	Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	Val	Phe		
100						105					110			115			
atc	ctg	ggg	gat	atc	ttt	gat	gaa	ggg	aag	tgg	agc	acc	cct	gag	gcc	739	
Ile	Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	Glu	Ala		
				120					125					130			
tgg	gcg	gat	gat	gtg	gag	cgg	ttt	cag	aaa	atg	ttc	aga	cac	cca	agt	787	
Trp	Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	Pro	Ser		
				135					140					145			
cat	gta	cag	ctg	aag	gta	gtt	gct	gga	aac	cat	gac	att	ggc	ttc	cat	835	

His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His  
 150 155 160  
 tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc 883  
 Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser  
 165 170 175  
 tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac 931  
 Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn  
 180 185 190 195  
 agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa 979  
 Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu  
 200 205 210  
 gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag gca 1027  
 Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala  
 215 220 225  
 cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc 1075  
 Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala  
 230 235 240  
 cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac 1123  
 Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn  
 245 250 255  
 tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt 1171  
 Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe  
 260 265 270 275  
 aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg 1219  
 Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu  
 280 285 290  
 tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc 1267

Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala  
                     295                            300                            305  
 tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct 1315  
 Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser  
                     310                            315                            320  
 ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc 1363  
 Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile  
                     325                            330                            335  
 acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat 1411  
 Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp  
 340                            345                            350                            355  
 gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc 1459  
 Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu  
                             360                            365                            370  
 aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg 1507  
 Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu  
                     375                            380                            385  
 aac ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat 1554  
 Asn Leu Leu Gly Lys Arg Lys Thr Arg  
                     390                            395  
 aaatatcaaa gccaagaaa tggaactttg ggcagagatc atgttagaat caagtggatg 1614  
 atgagaccaa ttacaggcgc tctctctgca cagcacagaa attctcaatc actgaaatga 1674  
 gtaactgcaa aataaatagt tgattgtact gttctcatgc tataaaagtg gacaggtact 1734  
 ctacaacaaa tctgttttct cattttttatc aaatatatgt atcatcaaag gttgcatctg 1794  
 tacagtatgt aaatgctatt aatgtcgtca ctcacatgca cgacagtcct tgttccccca 1854  
 ggaagggcct ggtggcccca gcacacactt gggattatgt gtatacataa ataaatattg 1914  
 ggctgtttcc ctcttctgt gaa 1937

&lt;210&gt; 124

&lt;211&gt; 396

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu  
 1 5 10 15  
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala  
 20 25 30  
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln  
 35 40 45  
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr  
 50 55 60  
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu  
 65 70 75 80  
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp  
 85 90 95  
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu  
 100 105 110  
 Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr  
 115 120 125  
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg  
 130 135 140  
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile  
 145 150 155 160  
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys

	165		170		175										
Val	Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val
	180		185		190										
Met	Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser
	195		200		205										
Glu	Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser
	210		215		220										
Arg	Glu	Ala	Arg	Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu	Pro
225			230		235									240	
Thr	Ser	Ala	Pro	Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg	Arg	Ser
	245		250		255										
Asp	Ala	Asn	Cys	Ser	Gly	Glu	Asp	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp
	260		265		270										
Ile	Pro	Phe	Lys	Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln
	275		280		285										
Lys	Leu	Leu	Trp	Trp	Leu	Gln	Pro	Arg	Leu	Val	Leu	Ser	Gly	His	Thr
	290		295		300										
His	Ser	Ala	Cys	Glu	Val	His	His	Gly	Gly	Arg	Val	Pro	Glu	Leu	Ser
305			310		315									320	
Val	Pro	Ser	Phe	Ser	Trp	Arg	Asn	Arg	Asn	Asn	Pro	Ser	Phe	Ile	Met
	325		330		335										
Gly	Ser	Ile	Thr	Pro	Thr	Asp	Tyr	Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro
	340		345		350										
Arg	Glu	Asp	Val	Val	Leu	Ile	Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu
	355		360		365										
Val	Val	Leu	Thr	Leu	Thr	His	Phe	Gly	Leu	Leu	Ala	Ser	Pro	Phe	Leu
	370		375		380										

Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

385

390

395

<210> 125

<211> 1748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (347)..(1345)

<400> 125

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 caccctgccc tgggtgaaagg gctcccgcaac cgcccgggtgc tccccatctg cctggcgttg 120  
 tgcgcagagc tggaaagcat ggctgttata aatgaattct gattttgggg agcagatgcc 180  
 aacttagagc ctcgtaacaa tctctctgtc tttaaaagat gaggtgactt ggtgattttc 240  
 ctggaaaatt ataggtgccc agctaagacc tgaatgccat caccctcccc agggctctgc 300  
 agttttctcg tgggtgaaccc ttgatggatt tgttggtgct tgagaa atg gcg atg 355

Met Ala Met

1

atc gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag 403

Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys

5

10

15

agt tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta 451

Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu

20

25

30

35

ttt tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg 499

Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp

40	45	50	
cct gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag			547
Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu			
55	60	65	
cct gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa			595
Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu			
70	75	80	
ttc cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag			643
Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu			
85	90	95	
aga gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc			691
Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe			
100	105	110	115
atc ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc			739
Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala			
120	125	130	
tgg gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt			787
Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser			
135	140	145	
cat gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat			835
His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His			
150	155	160	
tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc			883
Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser			
165	170	175	
tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac			931
Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn			

180	185	190	195	
agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa	979			
Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu				
200	205	210		
gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag ctg	1027			
Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Leu				
215	220	225		
ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc	1075			
Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser				
230	235	240		
gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca	1123			
Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro				
245	250	255		
tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc	1171			
Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser				
260	265	270	275	
atc acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag	1219			
Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu				
280	285	290		
gat gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc	1267			
Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val				
295	300	305		
ctc aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt	1315			
Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly				
310	315	320		
ttg aac ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat	1365			
Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg				



325

330

aaatatcaaa gcccaagaaa tggaactttg ggcagagatc atgttagaat caagtggatg 1425  
 atgagaccaa ttacaggccg tctctctgca cagcacagaa attctcaatc actgaaatga 1485  
 gtaactgcaa aataaatagt tgattgtact gttctcatgc tataaaagtg gacaggtact 1545  
 ctacaacaaa tctgttttct catTTTTtate aaatatatgt atcatcaaag gttgcatctg 1605  
 tacagtatgt aaatgctatt aatgtcgtca ctacatgca cgacagtcct tgttccccca 1665  
 ggaagggcct ggtggcccca gcacacactt gggattatgt gtatacataa ataaatattg 1725  
 ggctgtttcc ctcttcctgt gaa 1748

&lt;210&gt; 126

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu  
 1 5 10 15  
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala  
 20 25 30  
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln  
 35 40 45  
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr  
 50 55 60  
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu  
 65 70 75 80  
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp  
 85 90 95  
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu

100	105	110	
Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr			
115	120	125	
Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg			
130	135	140	
His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile			
145	150	155	160
Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys			
165	170	175	
Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val			
180	185	190	
Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser			
195	200	205	
Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser			
210	215	220	
Arg Glu Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His			
225	230	235	240
Thr His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu			
245	250	255	
Ser Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile			
260	265	270	
Met Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu			
275	280	285	
Pro Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe			
290	295	300	
Leu Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe			

305                      310                      315                      320  
 Leu Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg  
                          325                      330

<210> 127

<211> 2529

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (673)

<400> 127

tgttgcttga gaa atg gcg atg atc gaa ttg ggg ttt gga aga cag aat    49  
                          Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn  
                          1                      5                      10  
 ttt cat cca tta aag agg aag agt tca ttg ctg ttg aaa ctc ata gct    97  
 Phe His Pro Leu Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala  
                          15                      20                      25  
 gtt gtc ttt gct gtg ctt cta ttt tgt gaa ttt tta atc tat tac tta    145  
 Val Val Phe Ala Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu  
                          30                      35                      40  
 gcg atc ttt cag tgt aat tgg cct gaa gtg aaa acc aca gcc tct gat    193  
 Ala Ile Phe Gln Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp  
                          45                      50                      55                      60  
 ggt gaa cag acc aca cgt gag cct gtg ctc aaa gcc atg ttt ttg gct    241  
 Gly Glu Gln Thr Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala  
                          65                      70                      75

gac acc cat ttg ctt ggg gaa ttc cta ggc cac tgg ctg gac aaa tta 289  
 Asp Thr His Leu Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu  
 80 85 90  
 cga agg gaa tgg cag atg gag aga gcg ttc cag aca gct ctg tgg ttg 337  
 Arg Arg Glu Trp Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu  
 95 100 105  
 ctg cag ccg gaa gtc gtc ttc atc ctg ggg gat atc ttt gat gaa ggg 385  
 Leu Gln Pro Glu Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly  
 110 115 120  
 aag tgg agc acc cct gag gcc tgg gcg gat gat gtg gag cgg ttt cag 433  
 Lys Trp Ser Thr Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln  
 125 130 135 140  
 aaa atg ttc aga cac cca agt cat gta cag ctg aag gta gtt gct gga 481  
 Lys Met Phe Arg His Pro Ser His Val Gln Leu Lys Val Val Ala Gly  
 145 150 155  
 aac cat gac att ggc ttc cat tat gag atg aac aca tac aaa gta gaa 529  
 Asn His Asp Ile Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu  
 160 165 170  
 cgc ttt gag aaa gtg ttc agc tct gaa aga ctg ttt tct tgg aaa ggc 577  
 Arg Phe Glu Lys Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly  
 175 180 185  
 att aac ttt gtg atg gtc aac agc gtg gcg ctg aac ggg atg gct gtg 625  
 Ile Asn Phe Val Met Val Asn Ser Val Ala Leu Asn Gly Met Ala Val  
 190 195 200  
 gca tct gct ctg aaa cag aag cag agc tca ttg aag ttt ctc aca gac 673  
 Ala Ser Ala Leu Lys Gln Lys Gln Ser Ser Leu Lys Phe Leu Thr Asp  
 205 210 215 220

tgaactgctc ccgagaggta ggagagcatc tgaatgccac aggtgccttc tgtcccggtg 733  
tgctccgctt cggttgctca ctacagcccc tagcgtttct tgccctttga tgagggtcag 793  
gtgtgcggat taatggcctg acttgtagcc agcaggcacg tggctccagc cgggtgtggac 853  
ctgggcctct gctgcccacg tctgcccctg tctcctgca ggtgagctgg gggaggaaag 913  
ggctcatggc agacagcagg cagcctgtgg ttacacgata gccgcctgaa ctctctctc 973  
caccocggac agcattatcc tctgtatcgg agaagtgatg ctaactgttc tggggaagac 1033  
gctgctcctg cagaggaaag ggacatccca ttaaggaga actatgacgt gctttcacgg 1093  
gaggcatcac aaaaggtttg ccagggtgtc gtgatgctaa ttcattgtac agtgtgactc 1153  
tcatcacctt gcatgtcaac aagcagagtg ccagggttag agcagggtgtt tgctgaaacg 1213  
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agtcagtaat agtctcagct attctttgta ttcagagttt ttcaccaact taaatgtatt 1393  
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attttcttat atagatttat ataatacata ttacattata cataatatat aaatataaga 1513  
aatattttata agataaatgt ataaaatatt tataaagata aaataccgta aaaagtatat 1573  
aaaatctggg atgagaacaa agggctgacc ttacctttga tttagtgtaa ataaaccaa 1633  
ggatttttaa ggaaaaaat aaaccagtcc ttcaaaataa ggatttagta tgtaatttaa 1693  
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taacagcctg ctttgctgtc ttctcgcca ctgtcagctg ctgtggtggc tccagccgag 1813  
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cgagctcagc gtcccatctt tcagttggag gaacagaaac aacccagtt tcatcatggg 1933  
aacagatgct tagttgagca tcaaggggca ggaagacacc tttccctcct tgttcctcgc 1993  
tgaccgatga ccctggaact ccacggtgcc tctctgaatc tctgttatgg atccccact 2053  
atatttgatg ggaaccaggt gagccagggg ccagttttga cagggttagca tcacgccac 2113  
agactacacc ctctccaagt gctacctccc acgtgaggat gtggttttga tcatctactg 2173  
tgagtggtg ggcttccttg tggctctcac actcactcac tttgggcttc tagcctcacc 2233  
ttttctttct ggtttgaact tgctcgaaa gcgtaagaca agatgaagag caggcgccat 2293

tataaatatc aaagcccaag aagtggaact ttgggcagag atcatgtag aatcaagtgg 2353  
 atgatgagac caattacagg ccgctctctct gcacagcaca gaaattctca atcactgaaa 2413  
 tgagtaactg caaaataaat agttgattgt actgttctca tgctataaaa gtggacaggt 2473  
 actctacaac aaatctgttt tctcattttt atcaaataa tgtatcatca aagggt 2529

<210> 128

<211> 220

<212> PRT

<213> Homo sapiens

<400> 128

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu  
 1 5 10 15  
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala  
 20 25 30  
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln  
 35 40 45  
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr  
 50 55 60  
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu  
 65 70 75 80  
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp  
 85 90 95  
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu  
 100 105 110  
 Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr  
 115 120 125  
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg

130 135 140  
His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile  
145 150 155 160  
Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys  
165 170 175  
Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val  
180 185 190  
Met Val Asn Ser Val Ala Leu Asn Gly Met Ala Val Ala Ser Ala Leu  
195 200 205  
Lys Gln Lys Gln Ser Ser Leu Lys Phe Leu Thr Asp  
210 215 220

<210> 129

<211> 1910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (454).. (1182)

<400> 129

accgaagcca ccctgccctg gtgaaagggc tccgcacccg cccggtgctc cccatctgcc 60  
tggcggttg tgagagagctg gagagcatgg ctgttataaa tgaattctga ttttggggag 120  
cagatgccaa cttagagcct cgtaccaatc tctctgtctt taaaagatga ggtgacttgg 180  
tgattttcct ggaaaattat agcgatcttt cagtgttaatt ggcctgaagt gaaaaccaca 240  
gcctctgatg gtgaacagac cacacgtgag cctgtgctca aagccatggt tttggctgac 300  
accatttgc ttagggaatt cctaggccac tggctggaca aattacgaag agatggagtt 360  
ttgctgtgtt gcccatgctg gttttgaact cctggcctca agtgatcctc cctccttggc 420

ctcccaaagc attgaaatta cagggaatgg cag atg gag aga gcg ttc cag aca	474		
Met Glu Arg Ala Phe Gln Thr			
1	5		
gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc ctg ggg gat atc	522		
Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile Leu Gly Asp Ile			
10	15	20	
ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg gcg gat gat gtg	570		
Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp Ala Asp Asp Val			
25	30	35	
gag cgg ttt cag aaa atg ttc aga cac cca agt cat gta cag ctg aag	618		
Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His Val Gln Leu Lys			
40	45	50	55
gta gtt gct gga aac cat gac att ggc ttc cat tat gag atg aac aca	666		
Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr Glu Met Asn Thr			
60	65	70	
tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct gaa aga ctg ttt	714		
Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser Glu Arg Leu Phe			
75	80	85	
tct tgg aaa ggc att aac ttt gtg atg gtc aac agc gtg gcg ctg aac	762		
Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser Val Ala Leu Asn			
90	95	100	
ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca gag ctc att gaa	810		
Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala Glu Leu Ile Glu			
105	110	115	
gtt tct cac aga ctg aac tgc tcc cga gag gca cgt ggc tcc agc cgg	858		
Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg Gly Ser Ser Arg			
120	125	130	135



tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct gtc ctc ctg cag 906  
 Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro Val Leu Leu Gln  
 140 145 150  
 cat tat cct ctg tat cgg aga agt gat gct aac tgt tct ggg gaa gac 954  
 His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys Ser Gly Glu Asp  
 155 160 165  
 gct gct cct gca gag gaa agg gac atc cca ttt aag gag aac tat gac 1002  
 Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys Glu Asn Tyr Asp  
 170 175 180  
 gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg tgg ctc cag ccg 1050  
 Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp Trp Leu Gln Pro  
 185 190 195  
 cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc gag gtg cac cac 1098  
 Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys Glu Val His His  
 200 205 210 215  
 ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc agt tgg agg aac 1146  
 Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe Ser Trp Arg Asn  
 220 225 230  
 aga aac aac ccc agt ttc atc atg gga aca gat gct tagttgagca 1192  
 Arg Asn Asn Pro Ser Phe Ile Met Gly Thr Asp Ala  
 235 240  
 tcaaggggca ggaagacacc tttccctcct tggttcctgc tgaccgatga ccttggaact 1252  
 ccacggtgcc tctctgaatc tctgttatgg atcccccaact atatttgatg ggaaccagct 1312  
 gagccagggg ccagttttga cagggttagca tcacgccac agactacacc ctctccaagt 1372  
 gctacctccc acgtgaggat gtggttttga tcatctactg tggagtggcg ggcttccttg 1432  
 tggctctcac actcactcac tttgggcttc tagcctcacc ttttctttct ggtttgaaact 1492  
 tgctcggaag gcgtaagaca agatgaagag caggcgccat tataaatatc aaagcccaag 1552

aaatggaact ttgggcagag atcatgttag aatcaagtgg atgatgagac caattacagg 1612  
 ccgtctctct gcacagcaca gaaattctca atcactgaaa tgagtaactg caaaataaat 1672  
 agttgattgt gctgttctca tgctataaaa gtggacaggt actctacaac aaatctgttt 1732  
 tctcattttt atcaaataata tgtatcatca aaggttgcac ctgtacagta tgtaaagtct 1792  
 attaatgtcg tcaactcacat gcacgacagc ccttgttccc ccaggaaggg cctgggtggcc 1852  
 ccagcacaca cttgggatta tgtgtataca taaataaata ttgggctgtt tccctctt 1910

<210> 130

<211> 243

<212> PRT

<213> Homo sapiens

<400> 130

Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val
1				5					10					15	
Val	Phe	Ile	Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro
			20						25					30	
Glu	Ala	Trp	Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His
			35						40					45	
Pro	Ser	His	Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly
			50						55					60	
Phe	His	Tyr	Glu	Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val
			65						70					75	
Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met
			85						90					95	
Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu
			100						105					110	
Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg

115                      120                      125  
 Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr  
 130                      135                      140  
 Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp  
 145                      150                      155                      160  
 Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile  
 165                      170                      175  
 Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys  
 180                      185                      190  
 Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His  
 195                      200                      205  
 Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val  
 210                      215                      220  
 Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly  
 225                      230                      235                      240  
 Thr Asp Ala

<210> 131

<211> 539

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (471)

<400> 131

gcttcccgag ctggcggggt ccgtggtgcg ggatcgagat tgcgggct atg gcg ccg 57

Met Ala Pro

1

aag gtt ttt cgt cag tac tgg gat atc ccc gat ggc acc gat tgc cac 105  
Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr Asp Cys His  
5 10 15  
cgc aaa gcc tac agc acc acc agt att gcc agc gtc gct ggc ctg acc 153  
Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala Gly Leu Thr  
20 25 30 35  
gcc gct gcc tac aga gtc aca ctc aat cct ccg ggc acc ttc ctt gaa 201  
Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr Phe Leu Glu  
40 45 50  
gga gtg gct aag gtt gga caa tac acg ttc act gca gct gct gtc ggg 249  
Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala Ala Val Gly  
55 60 65  
gcc gtg ttt ggc ctc acc acc tgc atc agc gcc cat gtc cgc gag aag 297  
Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val Arg Glu Lys  
70 75 80  
ccc gac gac ccc ctg aac tac ttc ctc ggt ggc tgc gcc gga ggc ctg 345  
Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala Gly Gly Leu  
85 90 95  
act ctg gga gca cgc acg cac aac tac ggg att ggc gcc gcc gcc tgc 393  
Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala Ala Ala Cys  
100 105 110 115  
gtg tac ttt ggc ata gcg gcc tcc ctg gtc aag atg ggc cgg ctg gag 441  
Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly Arg Leu Glu  
120 125 130  
ggc tgg gag gtg ttt gca aaa ccc aag gtg tgagccctgt gcctgccggg 491  
Gly Trp Glu Val Phe Ala Lys Pro Lys Val

135

140

acctccagcc tgcagaatgc gtccagaaat aaattctgtg tctgtgtg

539

&lt;210&gt; 132

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr

1

5

10

15

Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala

20

25

30

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr

35

40

45

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala

50

55

60

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val

65

70

75

80

Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala

85

90

95

Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala

100

105

110

Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly

115

120

125

Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val

130

135

140

&lt;210&gt; 133

&lt;211&gt; 2091

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (168).. (596)

&lt;400&gt; 133

ttcgttgggg attcaacatg gcggcgggag tgtccgcggt ggtggcgggtg caagagagct 60  
 gagggaggcg cagagcctga tcgaggagtc ggctcgccgg cccaagcccc tcgtcgaccc 120  
 cgctgcctc acctccatcc agcccggggc cccaagggg gagcctc atg acg tgg 176

Met Thr Trp

1

ccc cta acg ggc cat cag cgg ggg gcc tgg cca tcc ccc agt cct cct 224  
 Pro Leu Thr Gly His Gln Arg Gly Ala Trp Pro Ser Pro Ser Pro Pro

5

10

15

cct cct cct ccc ggc ctc cca ccc gag ccc gag gtg ccc cca gcc ctg 272  
 Pro Pro Pro Pro Gly Leu Pro Pro Glu Pro Glu Val Pro Pro Ala Leu

20

25

30

35

gag tgc tgg gac ccc acg cct cag agc ccc agc tgg ccc ctc cag cct 320  
 Glu Cys Trp Asp Pro Thr Pro Gln Ser Pro Ser Trp Pro Leu Gln Pro

40

45

50

gca ccc ccg ccg ccc ctg ctg ttc ctg ggc ccc ctg gcc ccc gct cac 368  
 Ala Pro Pro Pro Pro Leu Leu Phe Leu Gly Pro Leu Ala Pro Ala His

55

60

65

cac agc ggg agc cac agc gag tat ccc atg agc agt tcc ggg ctg ccc 416  
 His Ser Gly Ser His Ser Glu Tyr Pro Met Ser Ser Ser Gly Leu Pro

70	75	80	
tgc agc tgg tgg tgg acc cag gcg acc ccc gct cct acc tgg aca act			464
Cys Ser Trp Trp Trp Thr Gln Ala Thr Pro Ala Pro Thr Trp Thr Thr			
85	90	95	
tca tca aga ttg gcg agg gct cca cgg gca tcg tgt gca tcg cca ccg			512
Ser Ser Arg Leu Ala Arg Ala Pro Arg Ala Ser Cys Ala Ser Pro Pro			
100	105	110	115
tgc gca gct cgg gca agc tgg tgg ccg tca aga aga tgg acc tgc gca			560
Cys Ala Ala Arg Ala Ser Trp Trp Pro Ser Arg Arg Trp Thr Cys Ala			
120	125	130	
agc agc aga ggc gcg agc tgc tct tca acg agg tgg taatcatgag			606
Ser Ser Arg Gly Ala Ser Cys Ser Ser Thr Arg Trp			
135	140		
ggactaccag caccgagaatg tgggtggagat gtacaacagc tacctggtgg gggacgagct			666
ctgggtggtc atggagttcc tggaaggagg cgccctcacc gacatcgtca cccacaccag			726
gatgaacgag gagcagatcg cggccgtgtg ccttgcaagt ctgcaggccc tgtcgggtgct			786
ccacgcccag ggcgtcatcc accgggacat caagagcgac tcgatcctgc tgacccatga			846
tggcagggtg aagctgtcag actttgggtt ctgcgcccag gtgagcaagg aagtgccccg			906
aaggaagtgc ctggtcggca cgccctactg gatggcccca gagctcatct cccgccttcc			966
ctacgggcca gaggtagaca tctggtcgct ggggataatg gtgattgaga tgggtggacgg			1026
agagcccccc tacttcaacg agccaccctc caaagccatg aagatgattc gggacaacct			1086
gccaccccga ctgaagaacc tgcacaaggt gtcgccatcc ctgaagggtc tcttgaccg			1146
cctgctggtg cgagaccctg cccagcgggc caccggcagc gagctgctga agcaccatt			1206
cctggccaag gcagggccgc ctgccagcat cgtgcccctc atgcgccaga accgcaccag			1266
atgaggccca gcgcccttcc cctcaaccaa agagcccccc gggtcacccc cgccccactg			1326
aggccagtag ggggccaggc ctcccactcc tcccagcccg ggagatgctc cgcgtggcac			1386
caccctcctt gctgggggta gatgagaccc tactactgaa ctccagtttt gatctcgtga			1446

cttttagaaa aacacaggga ctctgtgggag caagcgaggc tcccaggacc cccaccctct 1506  
 gggacaggcc ctcccccatg ttctttctgtc tccaggaagg gcagcggccc tcccatcact 1566  
 ggaagtctgc agtgggggtc gctgggggtg gagagaacac taagaggatga acatgtatga 1626  
 gtgtgtgcac gcgtgtgagt gtgcatgtgt gtgtgtgcaa aggtccagcc acccgtcct 1686  
 ccagcctgca aggggtgtct ggcgcttgc ctgacacca gccccctctc cccctgagcc 1746  
 attgtggggg tcgatcatga atgtccgaag agtggccttt tcccgtagcc ctgcgcccc 1806  
 tttctgtggc tggatgggga gacaggtcag ggccccccac cctctccagc cctgcagca 1866  
 aatgactact gcacctggac agcctcctct tttctagaag tctatttata ttgtcatttt 1926  
 ataacactct agccccctgcc cttattgggg gacagatggt cctgtcctg cggggtggcc 1986  
 ctggcagaac cactgcctga agaaccaggt tcctgcccgg tcagcgcagc cccagcccg 2046  
 ccaccctgc ctgagttag tttacaatt aaaacattgt cttgt 2091

<210> 134

<211> 143

<212> PRT

<213> Homo sapiens

<400> 134

Met	Thr	Trp	Pro	Leu	Thr	Gly	His	Gln	Arg	Gly	Ala	Trp	Pro	Ser	Pro
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Ser	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Leu	Pro	Pro	Glu	Pro	Glu	Val	Pro
				20					25					30	
Pro	Ala	Leu	Glu	Cys	Trp	Asp	Pro	Thr	Pro	Gln	Ser	Pro	Ser	Trp	Pro
				35					40					45	
Leu	Gln	Pro	Ala	Pro	Pro	Pro	Pro	Leu	Leu	Phe	Leu	Gly	Pro	Leu	Ala
				50					55					60	
Pro	Ala	His	His	Ser	Gly	Ser	His	Ser	Glu	Tyr	Pro	Met	Ser	Ser	Ser
65							70					75			80



Gly Leu Pro Cys Ser Trp Trp Trp Thr Gln Ala Thr Pro Ala Pro Thr  
                             85                            90                            95  
 Trp Thr Thr Ser Ser Arg Leu Ala Arg Ala Pro Arg Ala Ser Cys Ala  
                             100                            105                            110  
 Ser Pro Pro Cys Ala Ala Arg Ala Ser Trp Trp Pro Ser Arg Arg Trp  
                             115                            120                            125  
 Thr Cys Ala Ser Ser Arg Gly Ala Ser Cys Ser Ser Thr Arg Trp  
                             130                            135                            140

<210> 135

<211> 2091

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (548).. (1267)

<400> 135

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 gagggaggcg cagagcctga tcgaggagtc ggctcgccgg cccaagcccc tcgtcgaccc 120  
 cgcctgcatc acctccatcc agcccggggc cccaagggg gagcctcatg acgtggcccc 180  
 taacggggcca tcagcggggg gcctggccat ccccagttcc tcctcctcct cctcccggcc 240  
 tcccacccga gcccgagggtg ccccagccc tggagtgtgt ggacccccacg cctcagagcc 300  
 ccagctggcc cctccagcct gcacccccgc cgcccctgtt gttcctgggc cccttgcccc 360  
 ccgctcacca cagcgggagc cacagcgagt atcccatgag cagttccggg ctgccctgca 420  
 gctgggtggtg gaccagggcg acccccgtc ctacctggac aacttcatca agattggcga 480  
 gggctccacg ggcatcgtgt gcatcgccac cgtgcgcagc tcgggcaagc tgggtggccgt 540  
 caagaag atg gac ctg cgc aag cag cag agg cgc gag ctg etc ttc aac 589

Met	Asp	Leu	Arg	Lys	Gln	Gln	Arg	Arg	Glu	Leu	Leu	Phe	Asn	
1				5					10					
gag gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg														637
Glu	Val	Val	Ile	Met	Arg	Asp	Tyr	Gln	His	Glu	Asn	Val	Val	Glu Met
15				20					25					30
tac aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc														685
Tyr	Asn	Ser	Tyr	Leu	Val	Gly	Asp	Glu	Leu	Trp	Val	Val	Met	Glu Phe
				35					40					45
ctg gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac														733
Leu	Glu	Gly	Gly	Ala	Leu	Thr	Asp	Ile	Val	Thr	His	Thr	Arg	Met Asn
				50					55					60
gag gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg														781
Glu	Glu	Gln	Ile	Ala	Ala	Val	Cys	Leu	Ala	Val	Leu	Gln	Ala	Leu Ser
				65					70					75
gtg ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg														829
Val	Leu	His	Ala	Gln	Gly	Val	Ile	His	Arg	Asp	Ile	Lys	Ser	Asp Ser
				80					85					90
atc ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc														877
Ile	Leu	Leu	Thr	His	Asp	Gly	Arg	Val	Lys	Leu	Ser	Asp	Phe	Gly Phe
				95					100					110
tgc gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc														925
Cys	Ala	Gln	Val	Ser	Lys	Glu	Val	Pro	Arg	Arg	Lys	Ser	Leu	Val Gly
				115					120					125
acg ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg														973
Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Leu	Ile	Ser	Arg	Leu	Pro	Tyr Gly
				130					135					140
cca gag gta gac atc tgg tcg ctg ggg ata atg gtg att gag atg gtg														1021

Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val  
 145 150 155  
 gac gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag 1069  
 Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys  
 160 165 170  
 atg att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg 1117  
 Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val  
 175 180 185 190  
 tcg cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct 1165  
 Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro  
 195 200 205  
 gcc cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc 1213  
 Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala  
 210 215 220  
 aag gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc 1261  
 Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg  
 225 230 235  
 acc aga tgaggcccag cgcccttccc ctcaaccaa gagccccccg ggtcaccccc 1317  
 Thr Arg  
 240  
 gcccactga ggccagtagg gggccaggcc tccactcct ccagcccgg gagatgctcc 1377  
 gcgtggcacc accctccttg ctgggggtag atgagaccct actactgaac tccagttttg 1437  
 atctcgtgac ttttagaaaa acacagggac tcgtgggagc aagcgaggct ccaggacccc 1497  
 ccaccctctg ggacaggccc tccccatgt tcttctgtct ccaggaaggg cagcggccct 1557  
 cccatcactg gaagtctgca gtgggggtcg ctgggggtgg agagaacact aagaggtgaa 1617  
 catgtatgag tgtgtgcacg cgtgtgagtg tgcattgtgtg tgtgtgcaaa ggtccagcca 1677  
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ccctgagcca ttgtgggggt cgatcatgaa tgtccgaaga gtggcctttt cccgtagccc 1797  
 tgcgccccct ttctgtggct ggatggggag acaggtcagg gccccccacc ctctccagcc 1857  
 cctgcagcaa atgactactg cacctggaca gcctcctctt ttctagaagt ctatttatat 1917  
 tgtcatttta taacactcta gccctgccc ttattggggg acagatgggc cctgtcctgc 1977  
 ggggtggccc tggcagaacc actgcctgaa gaaccaggtt cctgcccggc cagcgcagcc 2037  
 ccagcccgcc caccctgcc tcgagttagt ttacaatta aaacattgtc ttgt 2091

<210> 136

<211> 240

<212> PRT

<213> Homo sapiens

<400> 136

Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val

1 5 10 15

Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr Asn

20 25 30

Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu

35 40 45

Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu

50 55 60

Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val Leu

65 70 75 80

His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu

85 90 95

Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys Ala

100 105 110

Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr Pro  
 115 120 125  
 Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu  
 130 135 140  
 Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp Gly  
 145 150 155 160  
 Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met Ile  
 165 170 175  
 Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser Pro  
 180 185 190  
 Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala Gln  
 195 200 205  
 Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys Ala  
 210 215 220  
 Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr Arg  
 225 230 235 240

<210> 137

<211> 2278

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (137).. (1450)

<400> 137

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 gcgcggagtt ccaggtcgag cagttaggcc gcgagcgact gcggcgccga gccggccgca 120

ccgagtcgcc ggcacc atg ttt ggg aag agg aag aag cgg gtg gag atc tcc 172  
 Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser  
 1 5 10  
 gcg ccg tcc aac ttc gag cac cgc gtg cac acg ggc ttc gac cag cac 220  
 Ala Pro Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Gln His  
 15 20 25  
 gag cag aag ttc acg ggg ctg ccc cgc cag tgg cag agc ctg atc gag 268  
 Glu Gln Lys Phe Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu  
 30 35 40  
 gag tcg gct cgc cgg ccc aag ccc ctc gtc gac ccc gcc tgc atc acc 316  
 Glu Ser Ala Arg Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr  
 45 50 55 60  
 tcc atc cag ccc ggg gcc ccc aag ggg gag cct cat gac gtg gcc cct 364  
 Ser Ile Gln Pro Gly Ala Pro Lys Gly Glu Pro His Asp Val Ala Pro  
 65 70 75  
 aac ggg cca tca gcg ggg ggc ctg gcc atc ccc cag tcc tcc tcc tcc 412  
 Asn Gly Pro Ser Ala Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser  
 80 85 90  
 tcc tcc cgg cct ccc acc cga gcc cga ggt gcc ccc agc cct gga gtg 460  
 Ser Ser Arg Pro Pro Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val  
 95 100 105  
 ctg gga ccc cac gcc tca gag ccc cag ctg gcc cct cca gcc tgc acc 508  
 Leu Gly Pro His Ala Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr  
 110 115 120  
 ccc gcc gcc cct gct gtt cct ggg ccc cct ggc ccc cgc tca cca cag 556  
 Pro Ala Ala Pro Ala Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln  
 125 130 135 140

cgg gag cca cag cga gta tcc cat gag cag ttc cgg gct gcc ctg cag	604
Arg Glu Pro Gln Arg Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln	
145 150 155	
ctg gtg gtg gac cca ggc gac ccc cgc tcc tac ctg gac aac ttc atc	652
Leu Val Val Asp Pro Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile	
160 165 170	
aag att ggc gag ggc tcc acg ggc atc gtg tgc atc gcc acc gtg cgc	700
Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg	
175 180 185	
agc tcg ggc aag ctg gtg gcc gtc aag aag atg gac ctg cgc aag cag	748
Ser Ser Gly Lys Leu Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln	
190 195 200	
cag agg cgc gag ctg ctc ttc aac gag gtg gta atc atg agg gac tac	796
Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr	
205 210 215 220	
cag cac gag aat gtg gtg gag atg tac aac agc tac ctg gtg ggg gac	844
Gln His Glu Asn Val Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp	
225 230 235	
gag ctc tgg gtg gtc atg gag ttc ctg gaa gga ggc gcc ctc acc gac	892
Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp	
240 245 250	
atc gtc acc cac acc agg atg aac gag gag cag atc gcg gcc gtg tgc	940
Ile Val Thr His Thr Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys	
255 260 265	
ctt gca gtg ctg cag gcc ctg tcg gtg ctc cac gcc cag ggc gtc atc	988
Leu Ala Val Leu Gln Ala Leu Ser Val Leu His Ala Gln Gly Val Ile	
270 275 280	

cac cgg gac atc aag agc gac tcg atc ctg ctg acc cat gat ggc agg 1036  
 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg  
 285 290 295 300  
 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg 1084  
 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val  
 305 310 315  
 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag 1132  
 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu  
 320 325 330  
 ctc atc tcc cgc ctt ccc tac ggg cca gag gta gac atc tgg tcg ctg 1180  
 Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu  
 335 340 345  
 ggg ata atg gtg att gag atg gtg gac gga gag ccc ccc tac ttc aac 1228  
 Gly Ile Met Val Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn  
 350 355 360  
 gag cca ccc ctc aaa gcc atg aag atg att cgg gac aac ctg cca ccc 1276  
 Glu Pro Pro Leu Lys Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro  
 365 370 375 380  
 cga ctg aag aac ctg cac aag gtg tcg cca tcc ctg aag ggc ttc ctg 1324  
 Arg Leu Lys Asn Leu His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu  
 385 390 395  
 gac cgc ctg ctg gtg cga gac cct gcc cag cgg gcc acg gca gcc gag 1372  
 Asp Arg Leu Leu Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu  
 400 405 410  
 ctg ctg aag cac cca ttc ctg gcc aag gca ggg ccg cct gcc agc atc 1420  
 Leu Leu Lys His Pro Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile  
 415 420 425



gtg ccc ctc atg cgc cag aac cgc acc aga tgaggcccag cgcccttccc 1470

Val Pro Leu Met Arg Gln Asn Arg Thr Arg

430

435

ctcaacaaaa gagcccccg ggtcaccccc gccccactga ggccagtagg gggccaggcc 1530  
 tcccactcct cccagcccgg gagatgctcc gcgtggcacc accctccttg ctgggggtag 1590  
 atgagaccct actactgaac tccagttttg atctcgtgac ttttagaaaa acacagggac 1650  
 tcgtgggagc aagcgaggct cccaggaccc ccaccctctg ggacaggccc tcccccatgt 1710  
 tcttctgtct ccaggaaggg cagcggccct cccatcactg gaagtctgca gtgggggtcg 1770  
 ctgggggttg agagaacact aagaggtgaa catgtatgag tgtgtgcacg cgtgtgagtg 1830  
 tgcatgtgtg tgtgtgcaaa ggtccagcca cccgctcctc cagcctgcaa ggggtgtctg 1890  
 gcgccttgcc tgacaccag cccctctcc cctgagcca ttgtgggggt cgatcatgaa 1950  
 tgtccgaaga gtggcctttt cccgtagccc tgcccccct ttctgtggct ggatggggag 2010  
 acaggtcagg gccccacc ctctccagcc cctgcagcaa atgactactg cacctggaca 2070  
 gcctcctctt ttctagaagt ctatttatat tgtcatttta taacactcta gccctgccc 2130  
 ttattggggg acagatggtc cctgtcctgc ggggtggccc tggcagaacc actgcctgaa 2190  
 gaaccaggtt cctgcccggg cagcgcagcc ccagcccgcc caccctgcc tcgagttagt 2250  
 ttacaatta aaacattgtc ttgttttg 2278

<210> 138

<211> 438

<212> PRT

<213> Homo sapiens

<400> 138

Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn

1

5

10

15

Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe

20

25

30

Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg  
 35 40 45  
 Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro  
 50 55 60  
 Gly Ala Pro Lys Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser  
 65 70 75 80  
 Ala Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro  
 85 90 95  
 Pro Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His  
 100 105 110  
 Ala Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro  
 115 120 125  
 Ala Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln  
 130 135 140  
 Arg Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp  
 145 150 155 160  
 Pro Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu  
 165 170 175  
 Gly Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys  
 180 185 190  
 Leu Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu  
 195 200 205  
 Leu Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn  
 210 215 220  
 Val Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val  
 225 230 235 240  
 Val Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His

245 250 255  
 Thr Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu  
 260 265 270  
 Gln Ala Leu Ser Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile  
 275 280 285  
 Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser  
 290 295 300  
 Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys  
 305 310 315 320  
 Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg  
 325 330 335  
 Leu Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val  
 340 345 350  
 Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu  
 355 360 365  
 Lys Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn  
 370 375 380  
 Leu His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu  
 385 390 395 400  
 Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His  
 405 410 415  
 Pro Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met  
 420 425 430  
 Arg Gln Asn Arg Thr Arg  
 435

&lt;210&gt; 139

434/861

&lt;211&gt; 3025

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (428).. (2200)

&lt;400&gt; 139

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gccctagag gagtgggtcac ctgcctgagg gcacttctgt cccaccagca tcagaccagg 180
tgtgtgcagg ctctctatgg gatgccgcca tcagaatgtc tcttcctcag cccctttgtt 240
ttttaaagtg gctttggtcg accatttgct ctgtgcttgg tactgtgtca agggcccgat 300
tgaagaccac agatcctaaa gataggggag tgtcgcgaca aggctgcctg ggggtgccctc 360
ttaaccagg ggatcagtaa cctgtgtctg agtcaatata caaaggccgc accgagtccc 420
cggcacc atg ttt ggg aag agg aag aag cgg gtg gag atc tcc gcg ccg 469
      Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro
          1              5              10
tcc aac ttc gag cac cgc gtg cac acg ggc ttc gac cag cac gag cag 517
Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln
    15              20              25              30
aag ttc acg ggg ctg ccc cgc cag tgg cag agc ctg atc gag gag tcg 565
Lys Phe Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser
          35              40              45
gct cgc cgg ccc aag ccc ctc gtc gac ccc gcc tgc atc acc tcc atc 613
Ala Arg Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile
          50              55              60
cag ccc ggg gcc ccc aag acc atc gtg cgg ggc agc aaa ggt gcc aaa 661

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Gln Pro Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys  
           65                          70                          75  
 gat ggg gcc ctc acg ctg ctg ctg gac gag ttt gag aac atg tcg gtg 709  
 Asp Gly Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val  
           80                          85                          90  
 aca cgc tcc aac tcc ctg cgg aga gac agc ccg ccg ccg ccc gcc cgt 757  
 Thr Arg Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg  
           95                          100                          105                          110  
 gcc cgc cag gaa aat ggg atg cca gag gag ccg gcc acc acg gcc aga 805  
 Ala Arg Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg  
                           115                          120                          125  
 ggg ggc cca ggg aag gca ggc agc cga ggc cgg ttc gcc ggt cac agc 853  
  
 Gly Gly Pro Gly Lys Ala Gly Ser Arg Gly Arg Phe Ala Gly His Ser  
           130                          135                          140  
 gag gcg ggt ggc ggc agt ggt gac agg cga cgg gcg ggg cca gag aag 901  
 Glu Ala Gly Gly Gly Ser Gly Asp Arg Arg Arg Ala Gly Pro Glu Lys  
           145                          150                          155  
 agg ccc aag tct tcc agg gag ggc tca ggg ggt ccc cag gag tcc tcc 949  
 Arg Pro Lys Ser Ser Arg Glu Gly Ser Gly Gly Pro Gln Glu Ser Ser  
           160                          165                          170  
 cgg gac aaa cgc ccc ctc tcc ggg cct gat gtc ggc acc ccc cag cct 997  
 Arg Asp Lys Arg Pro Leu Ser Gly Pro Asp Val Gly Thr Pro Gln Pro  
           175                          180                          185                          190  
 gct ggt ctg gcc agt ggg gcg aaa ctg gca gct ggc cgg ccc ttt aac 1045  
 Ala Gly Leu Ala Ser Gly Ala Lys Leu Ala Ala Gly Arg Pro Phe Asn  
                           195                          200                          205

acc tac ccg agg gct gac acg gac cac cca tcc cgg ggt gcc cag ggg 1093  
 Thr Tyr Pro Arg Ala Asp Thr Asp His Pro Ser Arg Gly Ala Gln Gly  
                   210                                  215                                  220  
 gag cct cat gac gtg gcc cct aac ggg cca tca gcg ggg ggc ctg gcc 1141  
 Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu Ala  
                   225                                  230                                  235  
 atc ccc cag tcc tcc tcc tcc tcc tcc cgg cct ccc acc cga gcc cga 1189  
 Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala Arg  
                   240                                  245                                  250  
 ggt gcc ccc agc cct gga gtg ctg gga ccc cac gcc tca gag ccc cag 1237  
 Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro Gln  
 255                                  260                                  265                                  270  
 ctg gcc cct cca gcc tgc acc ccc gcc gcc cct gct gtt cct ggg ccc 1285  
 Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly Pro  
                   275                                  280                                  285  
 cct ggc ccc cgc tca cca cag cgg gag cca cag cga gta tcc cat gag 1333  
 Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His Glu  
                   290                                  295                                  300  
 cag ttc cgg gct gcc ctg cag ctg gtg gtg gac cca ggc gac ccc cgc 1381  
 Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro Arg  
                   305                                  310                                  315  
 tcc tac ctg gac aac ttc atc aag att ggc gag ggc tcc acg ggc atc 1429  
 Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile  
                   320                                  325                                  330  
 gtg tgc atc gcc acc gtg cgc agc tcg ggc aag ctg gtg gcc gtc aag 1477  
 Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val Lys  
 335                                  340                                  345                                  350

aag atg gac ctg cgc aag cag cag agg cgc gag ctg ctc ttc aac gag	1525
Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
355 360 365	
gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg tac	1573
Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr	
370 375 380	
aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc ctg	1621
Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu	
385 390 395	
gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac gag	1669
Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu	
400 405 410	
gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg gtg	1717
Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val	
415 420 425 430	
ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg atc	1765
Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile	
435 440 445	
ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc tgc	1813
Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys	
450 455 460	
gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc acg	1861
Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr	
465 470 475	
ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg cca	1909
Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro	
480 485 490	

gag gta gac atc tgg tgc ctg ggg ata atg gtg att gag atg gtg gac 1957  
 Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp  
 495 500 505 510  
 gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag atg 2005  
 Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met  
 515 520 525  
 att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg tgc 2053  
 Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser  
 530 535 540  
 cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct gcc 2101  
 Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala  
 545 550 555  
 cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc aag 2149  
 Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys  
 560 565 570  
 gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc acc 2197  
 Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr  
 575 580 585 590  
 aga tgaggcccag cgcccttccc ctcaaccaa gagcccccg ggtaaccccc 2250  
 Arg  
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 cccatcactg gaagtctgca gtgggggtcg ctgggggtgg agagaacact aagaggtgaa 2550  
 catgtatgag tgtgtgcacg cgtgtgagtg tgcatgtgtg tgtgtgcaaa ggtccagcca 2610  
 cccgctctc cagcctgcaa ggggtgtctg ggccttgcc tgacaccag cccctctctc 2670



ccctgagcca ttgtgggggt cgatcatgaa tgtccgaaga gtggcctttt cccgtagccc 2730  
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 cctgcagcaa atgactactg cacctggaca gcctcctctt ttctagaagt ctatttatat 2850  
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 ggggtggccc tggcagaacc actgcctgaa gaaccaggtt cctgcccggg cagcgcagcc 2970  
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<210> 140

<211> 591

<212> PRT

<213> Homo sapiens

<400> 140

Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn

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Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe

20 25 30

Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg

35 40 45

Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro

50 55 60

Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly

65 70 75 80

Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg

85 90 95

Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg

100 105 110

Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly

115 120 125  
Pro Gly Lys Ala Gly Ser Arg Gly Arg Phe Ala Gly His Ser Glu Ala  
130 135 140  
Gly Gly Gly Ser Gly Asp Arg Arg Arg Ala Gly Pro Glu Lys Arg Pro  
145 150 155 160  
Lys Ser Ser Arg Glu Gly Ser Gly Gly Pro Gln Glu Ser Ser Arg Asp  
165 170 175  
Lys Arg Pro Leu Ser Gly Pro Asp Val Gly Thr Pro Gln Pro Ala Gly  
180 185 190  
Leu Ala Ser Gly Ala Lys Leu Ala Ala Gly Arg Pro Phe Asn Thr Tyr  
195 200 205  
Pro Arg Ala Asp Thr Asp His Pro Ser Arg Gly Ala Gln Gly Glu Pro  
210 215 220  
His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu Ala Ile Pro  
225 230 235 240  
Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala Arg Gly Ala  
245 250 255  
Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro Gln Leu Ala  
260 265 270  
Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly Pro Pro Gly  
275 280 285  
Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His Glu Gln Phe  
290 295 300  
Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro Arg Ser Tyr  
305 310 315 320  
Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys  
325 330 335

Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val Lys Lys Met  
340 345 350  
Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val  
355 360 365  
Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met Tyr Asn Ser  
370 375 380  
Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly  
385 390 395 400  
Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu Gln  
405 410 415  
Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val Leu His  
420 425 430  
Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu  
435 440 445  
Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln  
450 455 460  
Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr  
465 470 475 480  
Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly Pro Glu Val  
485 490 495  
Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp Gly Glu  
500 505 510  
Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys Met Ile Arg  
515 520 525  
Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val Ser Pro Ser  
530 535 540  
Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro Ala Gln Arg

545	550	555	560
Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala Lys Ala Gly			
	565	570	575
Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg Thr Arg			
	580	585	590

&lt;210&gt; 141

&lt;211&gt; 2556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (227).. (1729)

&lt;400&gt; 141

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cgcgagggcg cggagttcca ggccgagcag ttaggcgcgc agcgactgcg gcgccgagcc 120
gatgagtaac ccgaagcccc tagaggagtg gtcacctgcc tgagggcact tctgtccac 180
cagcatcaga ccaggtgtgt gcaggccgca ccgagtcgcc ggcacc atg ttt ggg      235
                                     Met Phe Gly

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1

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aag agg aag aag cgg gtg gag atc tcc gcg cgc tcc aac ttc gag cac      283
Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn Phe Glu His
      5              10              15
cgc gtg cac acg ggc ttc gac cag cac gag cag aag ttc acg ggg ctg      331
Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe Thr Gly Leu
      20              25              30              35
ccc cgc cag tgg cag agc ctg atc gag gag tcg gct cgc cgg ccc aag      379

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Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg Arg Pro Lys  
 40 45 50  
 ccc ctc gtc gac ccc gcc tgc atc acc tcc atc cag ccc ggg gcc ccc 427  
 Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro Gly Ala Pro  
 55 60 65  
 aag acc atc gtg cgg ggc agc aaa ggt gcc aaa gat ggg gcc ctc acg 475  
 Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly Ala Leu Thr  
 70 75 80  
 ctg ctg ctg gac gag ttt gag aac atg tcg gtg aca cgc tcc aac tcc 523  
 Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg Ser Asn Ser  
 85 90 95  
 ctg cgg aga gac agc ccg ccg ccg ccc gcc cgt gcc cgc cag gaa aat 571  
 Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg Gln Glu Asn  
 100 105 110 115  
 ggg atg cca gag gag ccg gcc acc acg gcc aga ggg ggc cca ggg aag 619  
 Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly Pro Gly Lys  
 120 125 130  
 ggg gag cct cat gac gtg gcc cct aac ggg cca tca gcg ggg ggc ctg 667  
 Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala Gly Gly Leu  
 135 140 145  
 gcc atc ccc cag tcc tcc tcc tcc tcc tcc cgg cct ccc acc cga gcc 715  
 Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro Thr Arg Ala  
 150 155 160  
 cga ggt gcc ccc agc cct gga gtg ctg gga ccc cac gcc tca gag ccc 763  
 Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala Ser Glu Pro  
 165 170 175  
 cag ctg gcc cct cca gcc tgc acc ccc gcc gcc cct gct gtt cct ggg 811

Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala Val Pro Gly  
 180 185 190 195  
 ccc cct ggc ccc cgc tca cca cag cgg gag cca cag cga gta tcc cat 859  
 Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg Val Ser His  
 200 205 210  
 gag cag ttc cgg gct gcc ctg cag ctg gtg gtg gac cca ggc gac ccc 907  
 Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro Gly Asp Pro  
 215 220 225  
 cgc tcc tac ctg gac aac ttc atc aag att ggc gag ggc tcc acg ggc 955  
 Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly  
 230 235 240  
 atc gtg tgc atc gcc acc gtg cgc agc tcg ggc aag ctg gtg gcc gtc 1003  
 Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu Val Ala Val  
 245 250 255  
 aag aag atg gac ctg cgc aag cag cag agg cgc gag ctg ctc ttc aac 1051  
 Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn  
 260 265 270 275  
 gag gtg gta atc atg agg gac tac cag cac gag aat gtg gtg gag atg 1099  
 Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val Val Glu Met  
 280 285 290  
 tac aac agc tac ctg gtg ggg gac gag ctc tgg gtg gtc atg gag ttc 1147  
 Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe  
 295 300 305  
 ctg gaa gga ggc gcc ctc acc gac atc gtc acc cac acc agg atg aac 1195  
 Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn  
 310 315 320  
 gag gag cag atc gcg gcc gtg tgc ctt gca gtg ctg cag gcc ctg tcg 1243

Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser  
 325 330 335  
 gtg ctc cac gcc cag ggc gtc atc cac cgg gac atc aag agc gac tcg 1291  
 Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser  
 340 345 350 355  
 atc ctg ctg acc cat gat ggc agg gtg aag ctg tca gac ttt ggg ttc 1339  
 Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe  
 360 365 370  
 tgc gcc cag gtg agc aag gaa gtg ccc cga agg aag tcg ctg gtc ggc 1387  
 Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly  
 375 380 385  
 acg ccc tac tgg atg gcc cca gag ctc atc tcc cgc ctt ccc tac ggg 1435  
 Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly  
 390 395 400  
 cca gag gta gac atc tgg tcg ctg ggg ata atg gtg att gag atg gtg 1483  
 Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val  
 405 410 415  
 gac gga gag ccc ccc tac ttc aac gag cca ccc ctc aaa gcc atg aag 1531  
 Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala Met Lys  
 420 425 430 435  
 atg att cgg gac aac ctg cca ccc cga ctg aag aac ctg cac aag gtg 1579  
 Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu His Lys Val  
 440 445 450  
 tcg cca tcc ctg aag ggc ttc ctg gac cgc ctg ctg gtg cga gac cct 1627  
 Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val Arg Asp Pro  
 455 460 465  
 gcc cag cgg gcc acg gca gcc gag ctg ctg aag cac cca ttc ctg gcc 1675

Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro Phe Leu Ala

470

475

480

aag gca ggg ccg cct gcc agc atc gtg ccc ctc atg cgc cag aac cgc 1723

Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg Gln Asn Arg

485

490

495

acc aga tgaggcccag cgcccttccc ctcaaccaa gagccccccg ggtcaccccc 1779

Thr Arg

500

gccccactga ggccagtagg gggccaggcc tcccactcct cccagcccgg gagatgctcc 1839

gcgtggcacc accctccttg ctgggggtag atgagaccct actactgaac tccagttttg 1899

atctcgtgac ttttagaaaa acacagggaac tcgtgggagc aagcgaggct cccaggaccc 1959

ccaccctctg ggacaggccc tccccatgt tcttctgtct ccaggaaggg cagcggccct 2019

cccatcactg gaagtctgca gtgggggtcg ctgggggtgg agagaacact aagaggtgaa 2079

catgtatgag tgtgtgcacg cgtgtgagtg tgcattgttg tgtgtgtgca aaggtccagc 2139

caccccgctc tccagcccgc aagggtgtgc tggcgcttg cctgacaccc agccccctct 2199

ccccctgagc cattgtgggg gtcgatcatg aatgtccgaa gagggtgctt ttccgtagc 2259

cctgcgcccc ctttctgttg ctggatgggg agacaggta gggccccca ccctctccag 2319

ccccctgcagc aaatgactac tgcacctgga cagcctcctc ttttctagaa gtctatttat 2379

attgtcattt tataacactc tagccctgc cttattggg ggacagatgg tccctgtcct 2439

gcgggggtggc cctggcagaa ccaactgcctg aagaaccagg ttctgcccg gtcagcgcag 2499

ccccagcccg cccaccctg cctcgagtta gttttacaat taaaacattg tcttggtt 2556

<210> 142

<211> 501

<212> PRT

<213> Homo sapiens

<400> 142



Met Phe Gly Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn  
 1 5 10 15  
 Phe Glu His Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe  
 20 25 30  
 Thr Gly Leu Pro Arg Gln Trp Gln Ser Leu Ile Glu Glu Ser Ala Arg  
 35 40 45  
 Arg Pro Lys Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro  
 50 55 60  
 Gly Ala Pro Lys Thr Ile Val Arg Gly Ser Lys Gly Ala Lys Asp Gly  
 65 70 75 80  
 Ala Leu Thr Leu Leu Leu Asp Glu Phe Glu Asn Met Ser Val Thr Arg  
 85 90 95  
 Ser Asn Ser Leu Arg Arg Asp Ser Pro Pro Pro Pro Ala Arg Ala Arg  
 100 105 110  
 Gln Glu Asn Gly Met Pro Glu Glu Pro Ala Thr Thr Ala Arg Gly Gly  
 115 120 125  
 Pro Gly Lys Gly Glu Pro His Asp Val Ala Pro Asn Gly Pro Ser Ala  
 130 135 140  
 Gly Gly Leu Ala Ile Pro Gln Ser Ser Ser Ser Ser Ser Arg Pro Pro  
 145 150 155 160  
 Thr Arg Ala Arg Gly Ala Pro Ser Pro Gly Val Leu Gly Pro His Ala  
 165 170 175  
 Ser Glu Pro Gln Leu Ala Pro Pro Ala Cys Thr Pro Ala Ala Pro Ala  
 180 185 190  
 Val Pro Gly Pro Pro Gly Pro Arg Ser Pro Gln Arg Glu Pro Gln Arg  
 195 200 205  
 Val Ser His Glu Gln Phe Arg Ala Ala Leu Gln Leu Val Val Asp Pro

210 215 220  
Gly Asp Pro Arg Ser Tyr Leu Asp Asn Phe Ile Lys Ile Gly Glu Gly  
225 230 235 240  
Ser Thr Gly Ile Val Cys Ile Ala Thr Val Arg Ser Ser Gly Lys Leu  
245 250 255  
Val Ala Val Lys Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu  
260 265 270  
Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr Gln His Glu Asn Val  
275 280 285  
Val Glu Met Tyr Asn Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val  
290 295 300  
Met Glu Phe Leu Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr  
305 310 315 320  
Arg Met Asn Glu Glu Gln Ile Ala Ala Val Cys Leu Ala Val Leu Gln  
325 330 335  
Ala Leu Ser Val Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys  
340 345 350  
Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg Val Lys Leu Ser Asp  
355 360 365  
Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser  
370 375 380  
Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu  
385 390 395 400  
Pro Tyr Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile  
405 410 415  
Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys  
420 425 430

Ala Met Lys Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu  
 435 440 445  
 His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu Val  
 450 455 460  
 Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys His Pro  
 465 470 475 480  
 Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile Val Pro Leu Met Arg  
 485 490 495  
 Gln Asn Arg Thr Arg  
 500

<210> 143

<211> 2030

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (169).. (1086)

<400> 143

agttttctgca aagtccaacc ctgcagggcc cttctccgc gccgcgtgt ctgctgctt 60  
 cctggagggg caatttgcatt atttctcaa agaaccatcc agaacctgag cagcctgtct 120  
 tcagacagag agaggccac ggctgtttct tgaaatctgg cgctggga atg gcc atg 177  
 Met Ala Met

1

tgg aac agg cca tgc cag agg ctg cct cag cag cct ctg gta gct gag 225  
 Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu

5

10

15

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ccc act gca gag ggg gag cca cac ctg ccc acg ggc cgg gag ctg act 273
Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr
    20                25                30                35
gag gcc aac cgc ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc 321
Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser
                40                45                50
cag tta ttt cct gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg 369
Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met
                55                60                65
gca ggc ctg gtg cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc 417
Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr
                70                75                80
atg act gct ttt gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt 465
Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe
                85                90                95
gtt caa att tta ctg aag gac ccc atc ttg aag gac gac ccg acg gtg 513
Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val
100                105                110                115
atc act cag gac ctt ctg agc ttc tca ctc aag gat ggg cac tat gac 561
Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp
                120                125                130
gcc cgg gcc aga gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg 609
Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val
                135                140                145
ccc ttg gag gag ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg 657
Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu
                150                155                160

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aag gaa atc aaa gaa gag gaa tct gaa atg gcc gag gca tcc cga aag 705  
Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys  
165 170 175  
aag aaa gaa aac cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg 753  
Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu  
180 185 190 195  
gcg act gtc gga ggc gga acg gtg atc ggt gtg act gga ggt cta gct 801  
Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala  
200 205 210  
gca ccc ctt gtt gcc gct gga gca gcg acg att att ggc agc gcc ggg 849  
Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly  
215 220 225  
gca gcg gct ctg ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg 897  
Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu  
230 235 240  
ttt ggt gca gct gga gct ggc ctg aca gga tac aag atg aag aag cga 945  
Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg  
245 250 255  
gtg gga gcc att gaa gag ttc acg ttt ctg ccg cct cat cag gcg aga 993  
Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Pro His Gln Ala Arg  
260 265 270 275  
ccc ccc acc agg ttg ggc aaa ccc agg gtc cca tat ctg gag aca cct 1041  
Pro Pro Thr Arg Leu Gly Lys Pro Arg Val Pro Tyr Leu Glu Thr Pro  
280 285 290  
cca aat tgg cca tgt cca cag acc cca gcc aag ccc agg tgc cag 1086  
Pro Asn Trp Pro Cys Pro Gln Thr Pro Ala Lys Pro Arg Cys Gln  
295 300 305

tagggctgga ccagtctgaa ggggcctccc ttctgctgc tgccagccct gaaaggcccc 1146  
 ccatctgcag ccatggcatg gacccaacc cactgggctg ccccgattgt gcctgcaaga 1206  
 cccagggccc cagcacgggg ctggactgac cacagcaggg gacctgagcc gtcttcccca 1266  
 gtctccatat gcagctctct cttataccct cgggttcctc ccaggagctc tggaggtaca 1326  
 ggatttccac aggcctcttt cctaaatgga aggaattgga actgaaaggg aaaggaaatg 1386  
 gaaggaaggg gaatttggag gagagaacac gccaccctt gggaagctgc ctgtccccag 1446  
 aggagcccca ccaggagca gctgccccct catcagagac ctgcagagtc aaccaagcac 1506  
 aggttagagt cccaggaccg gaaaccaact gtgggcttct tgtacttctc atagctttgg 1566  
 agtctggctg tccatcagga ggtcccgagg gctctctggg gcctgaggct cccacaccag 1626  
 ctctcccctg gcctcaataa aaccagggtgc atgcctgttc ttccatccac actccagggc 1686  
 tgcccaccag ctgacaggca ccatcaactg gcagcaacag agcaggcgca ggtacaaaga 1746  
 aggcagctca ctctgctct taggagatcc aatcagatct gccctgtaca gccatgtagg 1806  
 ctgtgcgctg cataactcca gggacatgag tcacacagac acaatgtgag tgtgctcccc 1866  
 cgtcatgcaa catctggaca caactaacag agcatggtga atacatgctg aattgcattc 1926  
 agtatggctg tgaactaggc ctggggacaa gaatgaattt tacatggaaa gaatttcctg 1986  
 tagcaggaac agaggggata acaacagcaa taaataataa taag 2030

<210> 144

<211> 306

<212> PRT

<213> Homo sapiens

<400> 144

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

1

5

10

15

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg

20

25

30

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile

35	40	45
Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr		
50	55	60
Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val		
65	70	75
80		
Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala		
85	90	95
Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp		
100	105	110
Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly		
115	120	125
His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu		
130	135	140
Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu		
145	150	155
160		
Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala		
165	170	175
Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu		
180	185	190
Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly		
195	200	205
Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly		
210	215	220
Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met		
225	230	235
240		
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met		
245	250	255

Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Pro His

260

265

270

Gln Ala Arg Pro Pro Thr Arg Leu Gly Lys Pro Arg Val Pro Tyr Leu

275

280

285

Glu Thr Pro Pro Asn Trp Pro Cys Pro Gln Thr Pro Ala Lys Pro Arg

290

295

300

Cys Gln

305

&lt;210&gt; 145

&lt;211&gt; 2401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (272).. (2011)

&lt;400&gt; 145

caaacagaga attccaggag ggcttgggga gcctctggag aaaaaccagg ctctcatgt 60  
 tacaaggagg ccatgtcttc tgggtgccat gcctgaagtt acaggaggga agaattactg 120  
 ctgctgactt ttgagtggat ttacagctg ggtaaactga ggctcagaga gggcaatttg 180  
 catatttctc caaagaacca tccagaacct gagcagcctg tcttcagaca gagagaggcc 240  
 cacggctgtt tcttgaaatc tggcgctggg a atg gcc atg tgg aac agg cca 292

Met Ala Met Trp Asn Arg Pro

1

5

tgc cag agg ctg cct cag cag cct ctg gta gct gag ccc act gca gag 340

Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu

10

15

20



ggg gag cca cac ctg ccc acg ggc cgg gag ctg act gag gcc aac cgc 388  
 Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg  
 25 30 35  
 ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc cag tta ttt cct 436  
 Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser Gln Leu Phe Pro  
 40 45 50 55  
 gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg gca ggc ctg gtg 484  
 Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met Ala Gly Leu Val  
 60 65 70  
 cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc atg act gct ttt 532  
 Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr Met Thr Ala Phe  
 75 80 85  
 gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt gtt caa att tta 580  
 Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe Val Gln Ile Leu  
 90 95 100  
 ctg aag gac ccc atc ttg aag gac gac ccg acg gtg atc act cag gac 628  
 Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val Ile Thr Gln Asp  
 105 110 115  
 ctt ctg agc ttc tca ctc aag gat ggg cac tat gac gcc cgg gcc aga 676  
 Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp Ala Arg Ala Arg  
 120 125 130 135  
 gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg ccc ttg gag gag 724  
 Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val Pro Leu Glu Glu  
 140 145 150  
 ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg aag gaa atc aaa 772  
 Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu Lys Glu Ile Lys  
 155 160 165

gaa gag gaa tct gaa atg gcc gag gca tcc cga aag aag aaa gaa aac 820  
 Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys Lys Lys Glu Asn  
 170 175 180  
 cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg gcg act gtc gga 868  
 Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu Ala Thr Val Gly  
 185 190 195  
 ggc gga acg gtg atc ggt gtg act gga ggt cta gct gca ccc ctt gtt 916  
 Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala Ala Pro Leu Val  
 200 205 210 215  
 gcc gct gga gca gcg acg att att ggc agc gcc ggg gca gcg gct ctg 964  
 Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly Ala Ala Ala Leu  
 220 225 230  
 ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg ttt ggt gca gct 1012  
 Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu Phe Gly Ala Ala  
 235 240 245  
 gga gct ggc ctg aca gga tac aag atg aag aag cga gtg gga gcc att 1060  
 Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg Val Gly Ala Ile  
 250 255 260  
 gaa gag ttc acg ttt ctg cct ctg acg gag ggc agg cag ctg cac atc 1108  
 Glu Glu Phe Thr Phe Leu Pro Leu Thr Glu Gly Arg Gln Leu His Ile  
 265 270 275  
 acc atc gcc gtc acg ggg tgg ctc gct tct ggc aaa tac cgc acc ttc 1156  
 Thr Ile Ala Val Thr Gly Trp Leu Ala Ser Gly Lys Tyr Arg Thr Phe  
 280 285 290 295  
 agt gcc ccg tgg gct gcc ctg gcc cac agc cgt gag cag tac tgc ctg 1204  
 Ser Ala Pro Trp Ala Ala Leu Ala His Ser Arg Glu Gln Tyr Cys Leu  
 300 305 310

gcc tgg gaa gcc aag tac ctg atg gag ctc ggc aat gcc ctg gag acc 1252  
 Ala Trp Glu Ala Lys Tyr Leu Met Glu Leu Gly Asn Ala Leu Glu Thr  
                   315                                  320                                  325  
 atc ctc agt ggt ctc gcc aac atg gtg gcc cag gag gcc cta aag tac 1300  
 Ile Leu Ser Gly Leu Ala Asn Met Val Ala Gln Glu Ala Leu Lys Tyr  
                   330                                  335                                  340  
 aca gtg ttg tct ggc att gtg gct gcc ctg acc tgg cca gcc tca ctc 1348  
 Thr Val Leu Ser Gly Ile Val Ala Ala Leu Thr Trp Pro Ala Ser Leu  
                   345                                  350                                  355  
 ctc agt gtc gcc aat gtc atc gac aac ccc tgg ggg gtg tgt ctc cat. 1396  
 Leu Ser Val Ala Asn Val Ile Asp Asn Pro Trp Gly Val Cys Leu His  
 360                                  365                                  370                                  375  
 cga tca gca gag gtt ggc aag cac ctg gcc cac atc ctg ctc tcc cgg 1444  
 Arg Ser Ala Glu Val Gly Lys His Leu Ala His Ile Leu Leu Ser Arg  
                   380                                  385                                  390  
 cag cag ggg cga cga cct gtc acc ttg att ggc ttc agc ctg gga gcc 1492  
 Gln Gln Gly Arg Arg Pro Val Thr Leu Ile Gly Phe Ser Leu Gly Ala  
                   395                                  400                                  405  
 aga gtc atc tac ttc tgt ctg cag gag atg gct caa gag aaa gat tgc 1540  
 Arg Val Ile Tyr Phe Cys Leu Gln Glu Met Ala Gln Glu Lys Asp Cys  
                   410                                  415                                  420  
 caa gga atc atc gag gac gtc atc ctg ctg ggt gcg cct gtg gag gga 1588  
 Gln Gly Ile Ile Glu Asp Val Ile Leu Leu Gly Ala Pro Val Glu Gly  
                   425                                  430                                  435  
 gaa gcc aag cat tgg gag cct ttc cgg aag gtg gtg tcc ggg agg atc 1636  
 Glu Ala Lys His Trp Glu Pro Phe Arg Lys Val Val Ser Gly Arg Ile  
 440                                  445                                  450                                  455

atc aac ggc tac tgc agg gga gac tgg ctg ctg agt ttc gtg tac cgc 1684  
 Ile Asn Gly Tyr Cys Arg Gly Asp Trp Leu Leu Ser Phe Val Tyr Arg  
 460 465 470  
 aca tcc tcg gtg cag ctc cac gtc gcc ggc cta cag ccc gtg ctg ctg 1732  
 Thr Ser Ser Val Gln Leu His Val Ala Gly Leu Gln Pro Val Leu Leu  
 475 480 485  
 cag gac agg agg gtg gag aac gtg gac ctg acc tct gtg gtc agc ggc 1780  
 Gln Asp Arg Arg Val Glu Asn Val Asp Leu Thr Ser Val Val Ser Gly  
 490 495 500  
 cac ctg gac tat gcc aag cag atg gat gcc atc ctg aag gcc gtg ggc 1828  
 His Leu Asp Tyr Ala Lys Gln Met Asp Ala Ile Leu Lys Ala Val Gly  
 505 510 515  
 atc cgc acc aag cca ggc tgg gac gag aag ggg ctc ttg ctg gcc cca 1876  
 Ile Arg Thr Lys Pro Gly Trp Asp Glu Lys Gly Leu Leu Leu Ala Pro  
 520 525 530 535  
 ggc tgc ctg ccc tcc gag gag cct cgc cag gca gca gct gcc gcc tca 1924  
 Gly Cys Leu Pro Ser Glu Glu Pro Arg Gln Ala Ala Ala Ala Ala Ser  
 540 545 550  
 tca gct ttg gag tct ggc tgt cca tca gga ggt ccc gag ggc tct ctg 1972  
 Ser Ala Leu Glu Ser Gly Cys Pro Ser Gly Gly Pro Glu Gly Ser Leu  
 555 560 565  
 ggg cct gag gct ccc aca cca gct ttc ccc tgg cct caa taaaaccagg 2021  
 Gly Pro Glu Ala Pro Thr Pro Ala Phe Pro Trp Pro Gln  
 570 575 580  
 tgc atg cctg ttcttccatc cacactccag ggctgccac cagctgacag gcaccatcaa 2081  
 ctggcagcaa cagagcaggc gcaggtacaa agaaggcagc tcaactcctgc tcttaggaga 2141  
 tccaatcaga tctgccctgt acagccatgt aggctgtgcg ctgcataact ccaggacat 2201

gagtcacaca gacacaatgt gagtgtgctc ccccgatcatg caacatctgg acacaactaa 2261  
 cagagcatgg tgaatacatg ctgaattgca ttcagtatgg ctgtgaacta ggcctgggga 2321  
 caagaatgaa ttttcatgg aaagaatttc ctgtagcagg aacagagggg ataacaacag 2381  
 caataaataa taataagaag 2401

<210> 146

<211> 580

<212> PRT

<213> Homo sapiens

<400> 146

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu  
 1 5 10 15  
 Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg  
 20 25 30  
 Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile  
 35 40 45  
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr  
 50 55 60  
 Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val  
 65 70 75 80  
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala  
 85 90 95  
 Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp  
 100 105 110  
 Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly  
 115 120 125  
 His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu

130 135 140  
Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu  
145 150 155 160  
Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala  
165 170 175  
Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu  
180 185 190  
Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly  
195 200 205  
Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly  
210 215 220  
Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met  
225 230 235 240  
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met  
245 250 255  
Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Pro Leu Thr  
260 265 270  
Glu Gly Arg Gln Leu His Ile Thr Ile Ala Val Thr Gly Trp Leu Ala  
275 280 285  
Ser Gly Lys Tyr Arg Thr Phe Ser Ala Pro Trp Ala Ala Leu Ala His  
290 295 300  
Ser Arg Glu Gln Tyr Cys Leu Ala Trp Glu Ala Lys Tyr Leu Met Glu  
305 310 315 320  
Leu Gly Asn Ala Leu Glu Thr Ile Leu Ser Gly Leu Ala Asn Met Val  
325 330 335  
Ala Gln Glu Ala Leu Lys Tyr Thr Val Leu Ser Gly Ile Val Ala Ala  
340 345 350

Leu Thr Trp Pro Ala Ser Leu Leu Ser Val Ala Asn Val Ile Asp Asn  
 355 360 365  
 Pro Trp Gly Val Cys Leu His Arg Ser Ala Glu Val Gly Lys His Leu  
 370 375 380  
 Ala His Ile Leu Leu Ser Arg Gln Gln Gly Arg Arg Pro Val Thr Leu  
 385 390 395 400  
 Ile Gly Phe Ser Leu Gly Ala Arg Val Ile Tyr Phe Cys Leu Gln Glu  
 405 410 415  
 Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu  
 420 425 430  
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg  
 435 440 445  
 Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp  
 450 455 460  
 Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala  
 465 470 475 480  
 Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp  
 485 490 495  
 Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp  
 500 505 510  
 Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu  
 515 520 525  
 Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg  
 530 535 540  
 Gln Ala Ala Ala Ala Ala Ser Ser Ala Leu Glu Ser Gly Cys Pro Ser  
 545 550 555 560  
 Gly Gly Pro Glu Gly Ser Leu Gly Pro Glu Ala Pro Thr Pro Ala Phe

565

570

575

Pro Trp Pro Gln

580

&lt;210&gt; 147

&lt;211&gt; 2281

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (272).. (1891)

&lt;400&gt; 147

caaacagaga attccaggag ggcttgggga gcctctggag aaaaaccagg ctctcatgt 60  
 tacaaggagg ccatgtcttc tgggtgccat gcctgaagtt acaggaggga agaattactg 120  
 ctgctgactt ttgagtggat ttacagctg ggtaaactga ggctcagaga gggcaatttg 180  
 catatttctc caaagaacca tccagaacct gagcagctg tcttcagaca gagagaggcc 240  
 cacggctggt tcttgaaatc tggcgctggg a atg gcc atg tgg aac agg cca 292

Met Ala Met Trp Asn Arg Pro

1

5

tgc cag agg ctg cct cag cag cct ctg gta gct gag ccc act gca gag 340  
 Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu

10

15

20

ggg gag cca cac ctg ccc acg ggc cgg gag ctg act gag gcc aac cgc 388  
 Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg

25

30

35

ttc gcc tat gct gcc ctg tgt ggc atc tcc ctg tcc cag tta ttt cct 436  
 Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser Gln Leu Phe Pro



40	45	50	55	
gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg gca ggc ctg gtg				484
Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met Ala Gly Leu Val				
	60	65	70	
cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc atg act gct ttt				532
Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr Met Thr Ala Phe				
	75	80	85	
gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt gtt caa att tta				580
Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe Val Gln Ile Leu				
	90	95	100	
ctg aag gac ccc atc ttg aag gac gac ccg acg gtg atc act cag gac				628
Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val Ile Thr Gln Asp				
	105	110	115	
ctt ctg agc ttc tca ctc aag gat ggg cac tat gac gcc cgg gcc aga				676
Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp Ala Arg Ala Arg				
	120	125	130	135
gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg ccc ttg gag gag				724
Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val Pro Leu Glu Glu				
	140	145	150	
ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg aag gaa atc aaa				772
Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu Lys Glu Ile Lys				
	155	160	165	
gaa gag gaa tct gaa atg gcc gag gca tcc cga aag aag aaa gaa aac				820
Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys Lys Lys Glu Asn				
	170	175	180	
cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg gcg act gtc gga				868
Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu Ala Thr Val Gly				

185	190	195	
ggc gga acg gtg atc ggt gtg act gga ggt cta gct gca ccc ctt gtt	916		
Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala Ala Pro Leu Val			
200	205	210	215
gcc gct gga gca gcg acg att att ggc agc gcc ggg gca gcg gct ctg	964		
Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly Ala Ala Ala Leu			
	220	225	230
ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg ttt ggt gca gct	1012		
Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu Phe Gly Ala Ala			
	235	240	245
gga gct ggc ctg aca ggc acc ttc agt gcc ccg tgg gct gcc ctg gcc	1060		
Gly Ala Gly Leu Thr Gly Thr Phe Ser Ala Pro Trp Ala Ala Leu Ala			
	250	255	260
cac agc cgt gag cag tac tgc ctg gcc tgg gaa gcc aag tac ctg atg	1108		
His Ser Arg Glu Gln Tyr Cys Leu Ala Trp Glu Ala Lys Tyr Leu Met			
	265	270	275
gag ctc ggc aat gcc ctg gag acc atc ctc agt ggt ctc gcc aac atg	1156		
Glu Leu Gly Asn Ala Leu Glu Thr Ile Leu Ser Gly Leu Ala Asn Met			
280	285	290	295
gtg gcc cag gag gcc cta aag tac aca gtg ttg tct ggc att gtg gct	1204		
Val Ala Gln Glu Ala Leu Lys Tyr Thr Val Leu Ser Gly Ile Val Ala			
	300	305	310
gcc ctg acc tgg cca gcc tca ctc ctc agt gtc gcc aat gtc atc gac	1252		
Ala Leu Thr Trp Pro Ala Ser Leu Leu Ser Val Ala Asn Val Ile Asp			
	315	320	325
aac ccc tgg ggg gtg tgt ctc cat cga tca gca gag gtt ggc aag cac	1300		
Asn Pro Trp Gly Val Cys Leu His Arg Ser Ala Glu Val Gly Lys His			

330	335	340	
ctg gcc cac atc ctg ctc tcc cgg cag cag ggg cga cga cct gtc acc			1348
Leu Ala His Ile Leu Leu Ser Arg Gln Gln Gly Arg Arg Pro Val Thr			
345	350	355	
ttg att ggc ttc agc ctg gga gcc aga gtc atc tac ttc tgt ctg cag			1396
Leu Ile Gly Phe Ser Leu Gly Ala Arg Val Ile Tyr Phe Cys Leu Gln			
360	365	370	375
gag atg gct caa gag aaa gat tgc caa gga atc atc gag gac gtc atc			1444
Glu Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile			
	380	385	390
ctg ctg ggt gcg cct gtg gag gga gaa gcc aag cat tgg gag cct ttc			1492
Leu Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe			
	395	400	405
cgg aag gtg gtg tcc ggg agg atc atc aac ggc tac tgc agg gga gac			1540
Arg Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp			
	410	415	420
tgg ctg ctg agt ttc gtg tac cgc aca tcc tcg gtg cag ctc cac gtc			1588
Trp Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val			
	425	430	435
gcc ggc cta cag ccc gtg ctg ctg cag gac agg agg gtg gag aac gtg			1636
Ala Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val			
440	445	450	455
gac ctg acc tct gtg gtc agc ggc cac ctg gac tat gcc aag cag atg			1684
Asp Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met			
	460	465	470
gat gcc atc ctg aag gcc gtg ggc atc cgc acc aag cca ggc tgg gac			1732
Asp Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp			

475 480 485  
 gag aag ggg ctc ttg ctg gcc cca ggc tgc ctg ccc tcc gag gag cct 1780  
 Glu Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro  
 490 495 500  
 cgc cag gca gca gct gcc gcc tca tca gct ttg gag tct ggc tgt cca 1828  
 Arg Gln Ala Ala Ala Ala Ala Ser Ser Ala Leu Glu Ser Gly Cys Pro  
 505 510 515  
 tca gga ggt ccc gag ggc tct ctg ggg cct gag gct ccc aca cca gct 1876  
 Ser Gly Gly Pro Glu Gly Ser Leu Gly Pro Glu Ala Pro Thr Pro Ala  
 520 525 530 535  
 ttc ccc tgg cct caa taaaaccagg tgcattgcctg ttcttccatc cacactccag 1931  
 Phe Pro Trp Pro Gln  
 540  
 ggctgcccac cagctgacag gcaccatcaa ctggcagcaa cagagcaggc gcaggtacaa 1991  
 agaaggcagc tcactcctgc tcttaggaga tccaatcaga tctgccctgt acagccatgt 2051  
 aggctgtgcg ctgcataact ccaggacat gagtcacaca gacacaatgt gagggtgtc 2111  
 ccccgctcatg caacatctgg acacaactaa cagagcatgg tgaatacatg ctgaattgca 2171  
 ttcagtatgg ctgtgaacta ggccctgggga caagaatgaa ttttacatgg aaagaatttc 2231  
 ctgtagcagg aacagagggg ataacaacag caataataa taataagaag 2281

&lt;210&gt; 148

&lt;211&gt; 540

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

1

5

10

15

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg  
                   20                                  25                                  30  
 Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile  
                   35                                  40                                  45  
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr  
                   50                                  55                                  60  
 Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val  
                   65                                  70                                  75                                  80  
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala  
                                   85                                  90                                  95  
 Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp  
                   100                                  105                                  110  
 Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly  
                   115                                  120                                  125  
 His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu  
                   130                                  135                                  140  
 Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu  
                   145                                  150                                  155                                  160  
 Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala  
                                   165                                  170                                  175  
 Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu  
                   180                                  185                                  190  
 Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly  
                   195                                  200                                  205  
 Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly  
                   210                                  215                                  220  
 Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met

225                      230                      235                      240  
Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Thr Phe Ser  
                         245                      250                      255  
Ala Pro Trp Ala Ala Leu Ala His Ser Arg Glu Gln Tyr Cys Leu Ala  
                         260                      265                      270  
Trp Glu Ala Lys Tyr Leu Met Glu Leu Gly Asn Ala Leu Glu Thr Ile  
                         275                      280                      285  
Leu Ser Gly Leu Ala Asn Met Val Ala Gln Glu Ala Leu Lys Tyr Thr  
                         290                      295                      300  
Val Leu Ser Gly Ile Val Ala Ala Leu Thr Trp Pro Ala Ser Leu Leu  
305                      310                      315                      320  
Ser Val Ala Asn Val Ile Asp Asn Pro Trp Gly Val Cys Leu His Arg  
                         325                      330                      335  
Ser Ala Glu Val Gly Lys His Leu Ala His Ile Leu Leu Ser Arg Gln  
                         340                      345                      350  
Gln Gly Arg Arg Pro Val Thr Leu Ile Gly Phe Ser Leu Gly Ala Arg  
                         355                      360                      365  
Val Ile Tyr Phe Cys Leu Gln Glu Met Ala Gln Glu Lys Asp Cys Gln  
                         370                      375                      380  
Gly Ile Ile Glu Asp Val Ile Leu Leu Gly Ala Pro Val Glu Gly Glu  
385                      390                      395                      400  
Ala Lys His Trp Glu Pro Phe Arg Lys Val Val Ser Gly Arg Ile Ile  
                         405                      410                      415  
Asn Gly Tyr Cys Arg Gly Asp Trp Leu Leu Ser Phe Val Tyr Arg Thr  
                         420                      425                      430  
Ser Ser Val Gln Leu His Val Ala Gly Leu Gln Pro Val Leu Leu Gln  
                         435                      440                      445

Asp Arg Arg Val Glu Asn Val Asp Leu Thr Ser Val Val Ser Gly His  
 450 455 460  
 Leu Asp Tyr Ala Lys Gln Met Asp Ala Ile Leu Lys Ala Val Gly Ile  
 465 470 475 480  
 Arg Thr Lys Pro Gly Trp Asp Glu Lys Gly Leu Leu Leu Ala Pro Gly  
 485 490 495  
 Cys Leu Pro Ser Glu Glu Pro Arg Gln Ala Ala Ala Ala Ala Ser Ser  
 500 505 510  
 Ala Leu Glu Ser Gly Cys Pro Ser Gly Gly Pro Glu Gly Ser Leu Gly  
 515 520 525  
 Pro Glu Ala Pro Thr Pro Ala Phe Pro Trp Pro Gln  
 530 535 540

<210> 149

<211> 2237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (169).. (1059)

<400> 149

agtttctgca aagtccaacc ctgcagggcc cttctccgc gccgcgtgt ctcgctgctt 60  
 cctggagggg caatttgcattttctccaa agaaccatcc agaacctgag cagcctgtct 120  
 tcagacagag agaggccac ggctgtttct tgaaatctgg cgctggga atg gcc atg 177  
 Met Ala Met

1

tgg aac agg cca tgc cag agg ctg cct cag cag cct ctg gta gct gag 225

Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu Val Ala Glu  
           5                          10                          15  
 ccc act gca gag ggg gag cca cac ctg ccc acg ggc cgg gag ctg act 273  
 Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg Glu Leu Thr  
           20                          25                          30                          35  
 gag gcc aac cgc ttc gcc tat gct gcc ctc tgt ggc atc tcc ctg tcc 321  
 Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile Ser Leu Ser  
                                   40                                  45                                  50  
 cag tta ttt cct gaa ccc gaa cac agc tcc ttc tgc aca gag ttc atg 369  
 Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr Glu Phe Met  
                                   55                                  60                                  65  
 gca ggc ctg gtg cag tgg ctg gag ttg tct gaa gct gtc ttg cca acc 417  
 Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val Leu Pro Thr  
                                   70                                  75                                  80  
 atg act gct ttt gcg agc ggc ctg gga ggt gaa gga gca gat gtg ttt 465  
 Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala Asp Val Phe  
                                   85                                  90                                  95  
 gtt caa att tta ctg aag gac ccc atc ttg aag gac gac ccg acg gtg 513  
 Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp Pro Thr Val  
           100                          105                          110                          115  
 atc act cag gac ctt ctg agc ttc tca ctc aag gat ggg cac tat gac 561  
 Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly His Tyr Asp  
                                   120                                  125                                  130  
 gcc cgg gcc aga gtc ctc gtt tgc cac atg acc tcc ctg ctc caa gtg 609  
 Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu Leu Gln Val  
                                   135                                  140                                  145  
 ccc ttg gag gag ctg gat gtc ctt gaa gag atg ttc ctg gag agc ctg 657



Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu Glu Ser Leu  
 150 155 160  
 aag gaa atc aaa gaa gag gaa tct gaa atg gcc gag gca tcc cga aag 705  
 Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala Ser Arg Lys  
 165 170 175  
 aag aaa gaa aac cgg agg aaa tgg aag cgt tat ctc ctg ata ggc ctg 753  
 Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu Ile Gly Leu  
 180 185 190 195  
 gcg act gtc gga ggc gga acg gtg atc ggt gtg act gga ggt cta gct 801  
 Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly Gly Leu Ala  
 200 205 210  
 gca ccc ctt gtt gcc gct gga gca gcg acg att att ggc agc gcc ggg 849  
 Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly Ser Ala Gly  
 215 220 225  
 gca gcg gct ctg ggc tca gca gcc ggc ata gcc atc atg acc tcg ctg 897  
 Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met Thr Ser Leu  
 230 235 240  
 ttt ggt gca gct gga gct ggc ctg aca gga tac aag atg aag aag cga 945  
 Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met Lys Lys Arg  
 245 250 255  
 gtg gga gcc att gaa gag ttc acg ttt ctg gca aat acc gca cct tca 993  
 Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Ala Asn Thr Ala Pro Ser  
 260 265 270 275  
 gtg ccc cgt ggg ctg ccc tgg ccc aca gcc gtg agc agt act gcc tgg 1041  
 Val Pro Arg Gly Leu Pro Trp Pro Thr Ala Val Ser Ser Thr Ala Trp  
 280 285 290  
 cct ggg aag cca agt acc tgatggagct cggcaatgcc ctggagacca 1089

Pro Gly Lys Pro Ser Thr

295

tcctcagtgg tctcgccaac atggtggccc aggaggccct aaagtacaca gtgttgtctg 1149  
 gcatttgtggc tgccctgacc tggccagcct cactcctcag tgtcgccaat gtcacgaca 1209  
 acccctgggg ggtgtgtctc catcgatcag cagaggttgg caagcacctg gccacatcc 1269  
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 gagtcatcta cttctgtctg caggagatgg ctcaagagaa agattgccaa ggaatcatcg 1389  
 aggacgtcat cctgctgggt gcgcctgtgg aggagaagc caagcattgg gaggctttcc 1449  
 ggaagggtgt gtccgggagg atcatcaacg gctactgcag gggagactgg ctgctgagtt 1509  
 tcgtgtaccg cacatcctcg gtgcagctcc acgtcgccgg cctacagccc gtgctgctgc 1569  
 aggacaggag ggtggagaac gtggacctga cctctgtggt cagcgccac ctggactatg 1629  
 ccaagcagat ggatgccatc ctgaaggccg tgggcatccg caccaagcca ggctgggacg 1689  
 agaaggggct cttgctggcc ccaggctgcc tgccctccga ggagcctcg caggcagcag 1749  
 ctgccgcctc atcagctttg gagtctggct gtccatcagg aggtcccag ggctctctgg 1809  
 ggctgaggc tcccacacca gctttcccct ggctcaata aaaccagggt catgcctgtt 1869  
 cttccatcca cactccaggg ctgccacca gctgacaggc accatcaact ggcagcaaca 1929  
 gagcaggcgc aggtacaaag aaggcagctc actcctgctc ttaggagatc caatcagatc 1989  
 tgccctgtac agccatgtag gctgtgcgct gcataactcc agggacatga gtcacacaga 2049  
 cacaatgtga gtgtgtctcc ccgtcatgca acatctggac acaactaaca gagcatgggtg 2109  
 aatacatgct gaattgcatt cagtatggct gtgaactagg cctggggaca agaatgaatt 2169  
 ttacatggaa agaatttcct gtagcaggaa cagaggggat aacaacagca ataaataata 2229  
 ataagaag 2237

&lt;210&gt; 150

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

Met Ala Met Trp Asn Arg Pro Cys Gln Arg Leu Pro Gln Gln Pro Leu

1 5 10 15

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg

20 25 30

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile

35 40 45

Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr

50 55 60

Glu Phe Met Ala Gly Leu Val Gln Trp Leu Glu Leu Ser Glu Ala Val

65 70 75 80

Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Ala

85 90 95

Asp Val Phe Val Gln Ile Leu Leu Lys Asp Pro Ile Leu Lys Asp Asp

100 105 110

Pro Thr Val Ile Thr Gln Asp Leu Leu Ser Phe Ser Leu Lys Asp Gly

115 120 125

His Tyr Asp Ala Arg Ala Arg Val Leu Val Cys His Met Thr Ser Leu

130 135 140

Leu Gln Val Pro Leu Glu Glu Leu Asp Val Leu Glu Glu Met Phe Leu

145 150 155 160

Glu Ser Leu Lys Glu Ile Lys Glu Glu Glu Ser Glu Met Ala Glu Ala

165 170 175

Ser Arg Lys Lys Lys Glu Asn Arg Arg Lys Trp Lys Arg Tyr Leu Leu

180 185 190

Ile Gly Leu Ala Thr Val Gly Gly Gly Thr Val Ile Gly Val Thr Gly

195 200 205

Gly Leu Ala Ala Pro Leu Val Ala Ala Gly Ala Ala Thr Ile Ile Gly  
 210 215 220  
 Ser Ala Gly Ala Ala Ala Leu Gly Ser Ala Ala Gly Ile Ala Ile Met  
 225 230 235 240  
 Thr Ser Leu Phe Gly Ala Ala Gly Ala Gly Leu Thr Gly Tyr Lys Met  
 245 250 255  
 Lys Lys Arg Val Gly Ala Ile Glu Glu Phe Thr Phe Leu Ala Asn Thr  
 260 265 270  
 Ala Pro Ser Val Pro Arg Gly Leu Pro Trp Pro Thr Ala Val Ser Ser  
 275 280 285  
 Thr Ala Trp Pro Gly Lys Pro Ser Thr  
 290 295

<210> 151

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (57).. (239)

<400> 151

cattctttca tctggtcggg gcagaggaat tcattcaaga ggtcgaggtg cagttc atg 59

Met

1

gcc gag gca ggg ggc gag ggc gag ggc gag gtg tgc ctg gtc atg ctg 107

Ala Glu Ala Gly Gly Glu Gly Glu Gly Glu Val Cys Leu Val Met Leu

5

10

15

tgg tgg atc acc gtc cca ggg cat tgg aga ttt ctg cat tta cgg aga 155  
 Trp Trp Ile Thr Val Pro Gly His Trp Arg Phe Leu His Leu Arg Arg  
                   20                                  25                                  30  
 gcg ata gag aag atc ttc ttc ctc att ttg cgc aat atg gtg aaa ttg 203  
 Ala Ile Glu Lys Ile Phe Phe Leu Ile Leu Arg Asn Met Val Lys Leu  
                   35                                  40                                  45  
 aag att gtc aga ttg atg att cct cac ttc atg cag taattacatt 249  
 Lys Ile Val Arg Leu Met Ile Pro His Phe Met Gln  
                   50                                  55                                  60  
 caagacaaga gcagaagctg aagcagctgc agttcatgga gctcgtttca aagggcaaga 309  
 tctaaaactg gcatggaata aaccagtaac taatatttca gctgttgaaa cagaagaagt 369  
 tgagcctgat gaagaagaat ttcaggaaga gtctttggtg gatgactcat tacttcaaga 429  
 tgatgatgaa gaagaagagg acaatgaatc tcgttcttgg agaagatgat ttgactgata 489  
 attgatctgc atatgctaga actctacctg tggttcatta gtattatcta atgtactttt 549  
 acatatttgt aaaaacaatt tttggtaaaa tgtgatgaag atggatttca caaatagaca 609  
 aaaaagaaga aaact 624

<210> 152

<211> 61

<212> PRT

<213> Homo sapiens

<400> 152

Met Ala Glu Ala Gly Gly Glu Gly Glu Gly Glu Val Cys Leu Val Met  
           1                                  5                                  10                                  15  
 Leu Trp Trp Ile Thr Val Pro Gly His Trp Arg Phe Leu His Leu Arg  
                                   20                                  25                                  30

Arg Ala Ile Glu Lys Ile Phe Phe Leu Ile Leu Arg Asn Met Val Lys

35

40

45

Leu Lys Ile Val Arg Leu Met Ile Pro His Phe Met Gln

50

55

60

&lt;210&gt; 153

&lt;211&gt; 1570

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (156).. (917)

&lt;400&gt; 153

ctgcttttgaa ggctgcacag aaaaccttac ttgtttccac ctctgcagtt gataataatg 60  
 aagcacagaa aaaaaaacag gaggcattga aacttcagca ggatgtaagg aaaaggaaac 120  
 aagaaatttt agaaaagcac attgaaacac agaag atg tta att tca aaa ctg 173

Met Leu Ile Ser Lys Leu

1

5

gag aaa aac aaa aca atg aag tct gaa gat aaa gca gaa ata atg aaa 221

Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys

10

15

20

act tta gag gtt ttg aca aaa aat att acc aag ttg aaa gat gag gtc 269

Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val

25

30

35

aaa gct gct tct cct gga cgc tgt ctt cca aaa agt ata aaa acc aag 317

Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys

40

45

50

act cag atg cag aag gaa tta ctt gac aca gaa ctg gat tta tat aag 365  
 Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys  
 55 60 65 70  
 aag atg cag gct gga gaa gaa gtc act gaa ctt agg aga aag tat aca 413  
 Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr  
 75 80 85  
 gaa tta cag ctg gaa gct gcc aaa cga ggg att ctt tca tct ggt cgg 461  
 Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg  
 90 95 100  
 ggc aga gga att cat tca aga ggt cga ggt gca gtt cat ggc cga ggc 509  
 Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg Gly  
 105 110 115  
 agg ggg cga ggg cga ggg cga ggt gtg cct ggt cat gct gtg gtg gat 557  
 Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val Asp  
 120 125 130  
 cac cgt ccc agg gca ttg gag att tct gca ttt acg gag agc gat aga 605  
 His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp Arg  
 135 140 145 150  
 gaa gat ctt ctt cct cat ttt gcg caa tat ggt gaa att gaa gat tgt 653  
 Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp Cys  
 155 160 165  
 cag att gat gat tcc tca ctt cat gca gta att aca ttc aag aca aga 701  
 Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr Arg  
 170 175 180  
 gca gaa gct gaa gca gct gca gtt cat gga gct cgt ttc aaa ggg caa 749  
 Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln  
 185 190 195

gat cta aaa ctg gca tgg aat aaa cca gta act aat att tca gct gtt 797  
Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala Val  
200 205 210  
gaa aca gaa gaa gtt gag cct gat gaa gaa gaa ttt cag gaa gag tct 845  
Glu Thr Glu Glu Val Glu Pro Asp Glu Glu Glu Phe Gln Glu Glu Ser  
215 220 225 230  
ttg gtg gat gac tca tta ctt caa gat gat gat gaa gaa gaa gag gac 893  
Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu Asp  
235 240 245  
aat gaa tct cgt tct tgg aga aga tgatttgact gatcattgat ctgcatatgc 947  
Asn Glu Ser Arg Ser Trp Arg Arg  
250  
tagaactcta cctgtgtttc attagtatta tctaattgtac ttttacaatatt ttgtaaaaac 1007  
aatttttgggt aaaatgtgat gaagatggat ttcacaaata gacaaaaaag aagaaaacta 1067  
ccttctgatc ttgtattttg aaagattgat gtttgcattt tacttcagta aacaattgct 1127  
aaagacatca cactagaaac atatgcaatg tttttattac atacttctac tggacatcac 1187  
agaattcttt gggttctttg taatttaatg aataggtctg aaaacttatg accaatactt 1247  
gttataactt agaggacttt gttttattcc aaataaggaa tgaatttgca tttaaaatct 1307  
taatgaatgt tttcaaaact gaatagataa catagtactc taactaaagt ctccaagtta 1367  
tgtattataa tattacatag tagtatgctt aggctttact atgtattagc cttttgttgg 1427  
actgtgtatg tattttacca tatgggtttt aatgataatg gtgtatgact gctttacatg 1487  
agtccttatg catccagatg ttataataaa gtggaatggt ctcttttaaaa aaaaaaaagg 1547  
aaagaaaaga gaaaagcaat gac 1570

&lt;210&gt; 154

&lt;211&gt; 254

&lt;212&gt; PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 154

Met Leu Ile Ser Lys Leu Glu Lys Asn Lys Thr Met Lys Ser Glu Asp  
 1 5 10 15  
 Lys Ala Glu Ile Met Lys Thr Leu Glu Val Leu Thr Lys Asn Ile Thr  
 20 25 30  
 Lys Leu Lys Asp Glu Val Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro  
 35 40 45  
 Lys Ser Ile Lys Thr Lys Thr Gln Met Gln Lys Glu Leu Leu Asp Thr  
 50 55 60  
 Glu Leu Asp Leu Tyr Lys Lys Met Gln Ala Gly Glu Glu Val Thr Glu  
 65 70 75 80  
 Leu Arg Arg Lys Tyr Thr Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly  
 85 90 95  
 Ile Leu Ser Ser Gly Arg Gly Arg Gly Ile His Ser Arg Gly Arg Gly  
 100 105 110  
 Ala Val His Gly Arg Gly Arg Gly Arg Gly Arg Gly Val Pro  
 115 120 125  
 Gly His Ala Val Val Asp His Arg Pro Arg Ala Leu Glu Ile Ser Ala  
 130 135 140  
 Phe Thr Glu Ser Asp Arg Glu Asp Leu Leu Pro His Phe Ala Gln Tyr  
 145 150 155 160  
 Gly Glu Ile Glu Asp Cys Gln Ile Asp Asp Ser Ser Leu His Ala Val  
 165 170 175  
 Ile Thr Phe Lys Thr Arg Ala Glu Ala Glu Ala Ala Val His Gly  
 180 185 190  
 Ala Arg Phe Lys Gly Gln Asp Leu Lys Leu Ala Trp Asn Lys Pro Val

195                      200                      205  
 Thr Asn Ile Ser Ala Val Glu Thr Glu Glu Val Glu Pro Asp Glu Glu  
 210                      215                      220  
 Glu Phe Gln Glu Glu Ser Leu Val Asp Asp Ser Leu Leu Gln Asp Asp  
 225                      230                      235                      240  
 Asp Glu Glu Glu Glu Asp Asn Glu Ser Arg Ser Trp Arg Arg  
 245                      250

<210> 155

<211> 2661

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6)..(2045)

<400> 155

tttgt atg aga gga gac atg tgt cct ttt gat cat gga agt gat cca gta 50

Met Arg Gly Asp Met Cys Pro Phe Asp His Gly Ser Asp Pro Val

1                      5                      10                      15

gtt gta gaa gat gtg aat ctt cct ggt atg ctg cct ttc cca gca cag 98

Val Val Glu Asp Val Asn Leu Pro Gly Met Leu Pro Phe Pro Ala Gln

20                      25                      30

cct cct gtt gtt gaa gga cca cct cct cct gga ctc ccc cca cct cca 146

Pro Pro Val Val Glu Gly Pro Pro Pro Pro Gly Leu Pro Pro Pro Pro

35                      40                      45

cca att ctt aca ccc cca cct gtg aat ctc agg ccc cca gta cca cag 194

Pro Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro

50	55	60	
cca ggt cca ttg cca ccc agt ctc cca cct gtt aca gga cca cca cct	242		
Pro Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro			
65	70	75	
cca ctt cct cct ttg cag cca tct ggc atg gat gct cct cca aac tct	290		
Pro Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser			
80	85	90	95
gca acc agt tct gtt cct act gta gta aca act ggc att cat cac cag	338		
Ala Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln			
100	105	110	
cct cct cct gct cca ccc tct ctt ttt act gca gat aca tat gac aca	386		
Pro Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr			
115	120	125	
gat ggc tac aat cct gaa gcc cca agc ata aca aac act tcc aga cct	434		
Asp Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro			
130	135	140	
atg tat aga cac aga gtg cat gca caa agg ccc aac ttg ata gga cta	482		
Met Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu			
145	150	155	
aca tca ggg gat atg gat ttg cca ccc aga gaa aag cct ccc aat aaa	530		
Thr Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys			
160	165	170	175
agc agt atg agg ata gta gtg gac tca gaa tca agg aaa aga acc att	578		
Ser Ser Met Arg Ile Val Val Asp Ser Glu Ser Arg Lys Arg Thr Ile			
180	185	190	
ggt tct gga gag cct gga gtt cct aca aag aag act tgg ttt gat aaa	626		
Gly Ser Gly Glu Pro Gly Val Pro Thr Lys Lys Thr Trp Phe Asp Lys			

195	200	205	
cca aat ttt aat aga aca aac agc cca ggc ttt cag aag aag gtt caa			674
Pro Asn Phe Asn Arg Thr Asn Ser Pro Gly Phe Gln Lys Lys Val Gln			
210	215	220	
ttt gga aat gaa aat acc aag ctt gaa ctt aga aaa gtt cct cca gaa			722
Phe Gly Asn Glu Asn Thr Lys Leu Glu Leu Arg Lys Val Pro Pro Glu			
225	230	235	
tta aat aat atc agc aaa ctt aat gaa cat ttt agt cga ttt gga acc			770
Leu Asn Asn Ile Ser Lys Leu Asn Glu His Phe Ser Arg Phe Gly Thr			
240	245	250	255
ttg gtt aac tta cag gtt gct tat aat ggt gat cct gaa ggt gcc cta			818
Leu Val Asn Leu Gln Val Ala Tyr Asn Gly Asp Pro Glu Gly Ala Leu			
260	265	270	
atc caa ttt gca aca tac gaa gaa gca aag aaa gca ata tca agt acg			866
Ile Gln Phe Ala Thr Tyr Glu Glu Ala Lys Lys Ala Ile Ser Ser Thr			
275	280	285	
gaa gca gta tta aac aat cgc ttt att aag gtt tat tgg cac aga gaa			914
Glu Ala Val Leu Asn Asn Arg Phe Ile Lys Val Tyr Trp His Arg Glu			
290	295	300	
gga agc acc caa cag tta caa act act tct cca aag gta atg cag cct			962
Gly Ser Thr Gln Gln Leu Gln Thr Thr Ser Pro Lys Val Met Gln Pro			
305	310	315	
tta gtc cag cag ccc att ttg cct gtt gtg aag cag tca gtc aaa gag			1010
Leu Val Gln Gln Pro Ile Leu Pro Val Val Lys Gln Ser Val Lys Glu			
320	325	330	335
cgg ctg ggt cca gta cct tca agt act att gaa cct gca gaa gcc cag			1058
Arg Leu Gly Pro Val Pro Ser Ser Thr Ile Glu Pro Ala Glu Ala Gln			

	340	345	350	
agt gcc tct tca gac ctt cct cag gtg ttg tct aca tct act ggc cta				1106
Ser Ala Ser Ser Asp Leu Pro Gln Val Leu Ser Thr Ser Thr Gly Leu				
	355	360	365	
aca aaa aca gtg tat aat cca gct gct ttg aag gct gca cag aaa acc				1154
Thr Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr				
	370	375	380	
tta ctt gtt tcc acc tct gca gtt gat aat aat gaa gca cag aaa aaa				1202
Leu Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys				
	385	390	395	
aaa cag gag gca ttg aaa ctt cag cag gat gta agg aaa agg aaa caa				1250
Lys Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln				
	400	405	410	415
gaa att tta gaa aag cac att gaa aca cag aag atg tta att tca aaa				1298
Glu Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys				
	420	425	430	
ctg gag aaa aac aaa aca atg aag tct gaa gat aaa gca gaa ata atg				1346
Leu Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met				
	435	440	445	
aaa act tta gag gtt ttg aca aaa aat att acc aag ttg aaa gat gag				1394
Lys Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu				
	450	455	460	
gtc aaa gct gct tct cct gga cgc tgt ctt cca aaa agt ata aaa acc				1442
Val Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr				
	465	470	475	
aag act cag atg cag aag gaa tta ctt gac aca gaa ctg gat tta tat				1490

Lys Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr  
 480 485 490 495  
 aag aag atg cag gct gga gaa gaa gtc act gaa ctt agg aga aag tat 1538  
 Lys Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr  
 500 505 510  
 aca gaa tta cag ctg gaa gct gcc aaa cga ggg att ctt tca tct ggt 1586  
 Thr Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly  
 515 520 525  
 cgg ggc aga gga att cat tca aga ggt cga ggt gca gtt cat ggc cga 1634  
 Arg Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg  
 530 535 540  
 ggc agg ggg cga ggg cga ggg cga ggt gtg cct ggt cat gct gtg gtg 1682  
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val  
 545 550 555  
 gat cac cgt ccc agg gca ttg gag att tct gca ttt acg gag agc gat 1730  
 Asp His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp  
 560 565 570 575  
 aga gaa gat ctt ctt cct cat ttt gcg caa tat ggt gaa att gaa gat 1778  
 Arg Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp  
 580 585 590  
 tgt cag att gat gat tcc tca ctt cat gca gta att aca ttc aag aca 1826  
 Cys Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr  
 595 600 605  
 aga gca gaa gct gaa gca gct gca gtt cat gga gct cgt ttc aaa ggg 1874  
 Arg Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly  
 610 615 620  
 caa gat cta aaa ctg gca tgg aat aaa cca gta act aat att tca gct 1922

Gln Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala  
 625 630 635  
 gtt gaa aca gaa gaa gtt ggg cct gat gaa gaa gaa ttt cag gaa gag 1970  
 Val Glu Thr Glu Glu Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu  
 640 645 650 655  
 tct ttg gtg gat gac tca tta ctt caa gat gat gat gaa gaa gaa gag 2018  
 Ser Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu  
 660 665 670  
 gac aat gaa tct cgt tct tgg aga aga tgatttgact gatcattgat 2065  
 Asp Asn Glu Ser Arg Ser Trp Arg Arg  
 675 680  
 ctgcatatgc tagaactcta cctgtgtttc attagtatta tctaattgtac ttttacatat 2125  
 ttgtaaaaac aatTTTTTggt aaaatgtgat gaagatggat ttcacaaata gacaaaaaag 2185  
 aagaaaacta ccttctgatac ttgtatTTTg aaagattgat gtttgcattt tacttcagta 2245  
 aacaattgct aaagacatca cactagaaac atatgcaatg tttttattac atacttctac 2305  
 tggacatcac agaattcttt gggttctttg taatttaatg aataggtctg aaaacttatg 2365  
 accaataactt gttataactt agaggacttt gttttattcc aaataaggaa tgaatttgca 2425  
 tttaaaatct taatgaatgt tttcaaaact gaatagataa catagtactc taactaaagt 2485  
 ctccaagtta tgtattataa tattacatag tagtatgctt aggctttact atgtattagc 2545  
 cttttgttgg actgtgtatg tattttacca taagggtttt aatgataatg gtgtatgact 2605  
 gctttacatg agtccttatg catccagatg ttataataaa gtggaatggc ctcttt 2661

<210> 156

<211> 680

<212> PRT

<213> Homo sapiens

<400> 156

Met Arg Gly Asp Met Cys Pro Phe Asp His Gly Ser Asp Pro Val Val  
 1 5 10 15  
 Val Glu Asp Val Asn Leu Pro Gly Met Leu Pro Phe Pro Ala Gln Pro  
 20 25 30  
 Pro Val Val Glu Gly Pro Pro Pro Pro Gly Leu Pro Pro Pro Pro Pro  
 35 40 45  
 Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro Pro  
 50 55 60  
 Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro Pro  
 65 70 75 80  
 Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser Ala  
 85 90 95  
 Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln Pro  
 100 105 110  
 Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr Asp  
 115 120 125  
 Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro Met  
 130 135 140  
 Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu Thr  
 145 150 155 160  
 Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys Ser  
 165 170 175  
 Ser Met Arg Ile Val Val Asp Ser Glu Ser Arg Lys Arg Thr Ile Gly  
 180 185 190  
 Ser Gly Glu Pro Gly Val Pro Thr Lys Lys Thr Trp Phe Asp Lys Pro  
 195 200 205  
 Asn Phe Asn Arg Thr Asn Ser Pro Gly Phe Gln Lys Lys Val Gln Phe



210	215	220	
Gly Asn Glu Asn Thr Lys Leu Glu Leu Arg Lys Val Pro Pro Glu Leu			
225	230	235	240
Asn Asn Ile Ser Lys Leu Asn Glu His Phe Ser Arg Phe Gly Thr Leu			
	245	250	255
Val Asn Leu Gln Val Ala Tyr Asn Gly Asp Pro Glu Gly Ala Leu Ile			
	260	265	270
Gln Phe Ala Thr Tyr Glu Glu Ala Lys Lys Ala Ile Ser Ser Thr Glu			
	275	280	285
Ala Val Leu Asn Asn Arg Phe Ile Lys Val Tyr Trp His Arg Glu Gly			
	290	295	300
Ser Thr Gln Gln Leu Gln Thr Thr Ser Pro Lys Val Met Gln Pro Leu			
305	310	315	320
Val Gln Gln Pro Ile Leu Pro Val Val Lys Gln Ser Val Lys Glu Arg			
	325	330	335
Leu Gly Pro Val Pro Ser Ser Thr Ile Glu Pro Ala Glu Ala Gln Ser			
	340	345	350
Ala Ser Ser Asp Leu Pro Gln Val Leu Ser Thr Ser Thr Gly Leu Thr			
	355	360	365
Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr Leu			
	370	375	380
Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys Lys			
385	390	395	400
Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln Glu			
	405	410	415
Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys Leu			
	420	425	430

Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys  
435 440 445  
Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val  
450 455 460  
Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys  
465 470 475 480  
Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys  
485 490 495  
Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr  
500 505 510  
Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg  
515 520 525  
Gly Arg Gly Ile His Ser Arg Gly Arg Gly Ala Val His Gly Arg Gly  
530 535 540  
Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val Asp  
545 550 555 560  
His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp Arg  
565 570 575  
Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp Cys  
580 585 590  
Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr Arg  
595 600 605  
Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln  
610 615 620  
Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala Val  
625 630 635 640  
Glu Thr Glu Glu Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu Ser

	645	650	655
Leu Val Asp Asp Ser Leu Leu Gln Asp Asp Asp Glu Glu Glu Glu Asp			
	660	665	670
Asn Glu Ser Arg Ser Trp Arg Arg			
	675	680	

&lt;210&gt; 157

&lt;211&gt; 1085

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (128).. (883)

&lt;400&gt; 157

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cacgcgagtt cccgtctttc ctggtcgtcc tccttgggtt cgggtgaaag cgcttggggg 60
ttcagtgggc catgatcccc gagctgctgg agaactgaag gcggacggtc tcctgcgaaa 120
ccaggca atg gcg gag ctg gag ttt gtt cag atc atc atc atc gtg gtg 169
      Met Ala Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val
          1             5             10
gtg atg atg gtg atg gtg gtg gtg atc acg tgc ctg ctg agc cac tac 217
Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His Tyr
    15             20             25             30
aag ctg tct gca cgg tcc ttc atc agc cgg cac agc cag ggg cgg agg 265
Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg
          35             40             45
aga gaa gat gcc ctg tcc tca gaa gga tgc ctg tgg ccc tcg gag agc 313
Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser

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50	55	60	
aca gtg tca ggc aac gga atc cca gag ccg cag gtc tac gcc ccg cct	361		
Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro			
65	70	75	
cgg ccc acc gac cgc ctg gcc gtg ccg ccc ttc gcc cag cgg gag cgc	409		
Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg			
80	85	90	
ttc cac cgc ttc cag ccc acc tat ccg tac ctg cag cac gag atc gac	457		
Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp			
95	100	105	110
ctg ccg ccc acc atc tcg ctg tca gac ggg gag gag ccc cca ccc tac	505		
Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr			
115	120	125	
cag ggc ccc tgc acc ctc cag ctt cgg gac ccc gag cag cag ctg gaa	553		
Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu			
130	135	140	
ctg aac cgg gag tcg gtg cgc gca ccc cca aac aga acc atc ttc gac	601		
Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp			
145	150	155	
agt gac ctg atg gat agt gcc agg ctg ggc ggc ccc tgc ccc ccc agc	649		
Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser			
160	165	170	
agt aac tcg ggc atc agc gcc acg tgc tac ggc agc ggc ggg cgc atg	697		
Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met			
175	180	185	190
gag ggg ccg ccg ccc acc tac agc gag gtc atc ggc cac tac ccg ggg	745		
Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly			

195	200	205	
tcc tcc ttc cag cac cag cag agc agt ggg ccg ccc tcc ttg ctg gag			793
Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu			
210	215	220	
ggg acc cgg ctc cac cac aca cac atc gcg ccc cta gag agc gca gcc			841
Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala			
225	230	235	
atc tgg agc aaa gag aag gat aaa cag aaa gga cac cct ctc			883
Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu			
240	245	250	
taggggtcccc agggggggccg ggctggggct gcgtaggtga aaaggcagaa cactccgcgc			943
ttcttagaag aggagtgaga ggaaggcggg gggcgcagca acgcacgtg tggccctccc			1003
ctccacctc cctgtgtata aatatttaca tgtgatgtct ggtctgaatg cacaagctaa			1063
gagagcttgc aaaaaaaaaa ag			1085

&lt;210&gt; 158

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

Met	Ala	Glu	Leu	Glu	Phe	Val	Gln	Ile	Ile	Ile	Ile	Val	Val	Val	Met
1					5				10				15		
Met	Val	Met	Val	Val	Val	Ile	Thr	Cys	Leu	Leu	Ser	His	Tyr	Lys	Leu
				20				25				30			
Ser	Ala	Arg	Ser	Phe	Ile	Ser	Arg	His	Ser	Gln	Gly	Arg	Arg	Arg	Glu
				35				40				45			
Asp	Ala	Leu	Ser	Ser	Glu	Gly	Cys	Leu	Trp	Pro	Ser	Glu	Ser	Thr	Val

50	55	60	
Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro			
65	70	75	80
Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe His			
	85	90	95
Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu Pro			
100	105	110	
Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly			
115	120	125	
Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn			
130	135	140	
Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp			
145	150	155	160
Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn			
	165	170	175
Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly			
180	185	190	
Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser			
195	200	205	
Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr			
210	215	220	
Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp			
225	230	235	240
Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu			
	245	250	

&lt;210&gt; 159

&lt;211&gt; 1383

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (321).. (1181)

&lt;400&gt; 159

ggaaagctag cggcagaggc tcagccccgg cggcagcgcg cgccccgctg ccagcccatt 60  
 ttccggacgc caccgcggg cactgccgac gccccgggg ctgccgaggg gaggcgggg 120  
 gggcgcgagcg gagcgcggtc ccgcgcactg agccccgcgg cgccccggga acttggcggc 180  
 gacccgagcc cggcgagccg gggcgcgctt cccccgccgc gcgcctcctg catgcggggc 240  
 cccagctccg ggcgccggcc ggagcccccc ccggccgccc ccgagcccc cgcgccccgc 300  
 gccgcgccgc cgcgccgtcc atg cac cgc ttg atg ggg gtc aac agc acc gcc 353

Met His Arg Leu Met Gly Val Asn Ser Thr Ala

1

5

10

gcc gcc gcc gcc ggg cag ccc aat gtc tcc tgc acg tgc aac tgc aaa 401

Ala Ala Ala Ala Gly Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys

15

20

25

cgc tct ttg ttc cag agc atg gag atc acg gag ctg gag ttt gtt cag 449

Arg Ser Leu Phe Gln Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln

30

35

40

atc atc atc atc gtg gtg gtg atg atg gtg atg gtg gtg atc acg 497

Ile Ile Ile Ile Val Val Val Met Met Val Met Val Val Val Ile Thr

45

50

55

tgc ctg ctg agc cac tac aag ctg tct gca cgg tcc ttc atc agc cgg 545

Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg

60

65

70

75

cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa gga tgc	593
His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys	
80 85 90	
ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca gag ccg	641
Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro	
95 100 105	
cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg ccg ccc	689
Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro	
110 115 120	
ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat ccg tac	737
Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr	
125 130 135	
ctg cag cac gag atc gac ctg ccg ccc acc atc tcg ctg tca gac ggg	785
Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly	
140 145 150 155	
gag gag ccc cca ccc tac cag ggc ccc tgc acc ctc cag ctt cgg gac	833
Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp	
160 165 170	
ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca ccc cca	881
Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro	
175 180 185	
aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg ctg ggc	929
Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly	
190 195 200	
ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg tgc tac	977
Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr	
205 210 215	



ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc gag gtc 1025  
 Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val  
 220 225 230 235  
 atc ggc cac tac ccg ggg tcc tcc ttc cag cac cag cag agc agt ggg 1073  
 Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly  
 240 245 250  
 ccg ccc tcc ttg ctg gag ggg acc cgg ctc cac cac aca cac atc gcg 1121  
 Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His Ile Ala  
 255 260 265  
 ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa cag aaa 1169  
 Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys  
 270 275 280  
 gga cac cct ctc taggggtcccc agggggggccg ggctgggggt gcgtaggtga 1221  
 Gly His Pro Leu  
 285  
 aaaggcagaa cactccgcgc ttcttagaag aggagtgaga ggaaggcggg gggcgcagca 1281  
 acgcctcgtg tggccctccc ctccacctc cctgtgtata aatatttaca tgtgatgtct 1341  
 ggtctgaatg cacaagctaa gagagcttgc aaaaaaaaaa ag 1383

&lt;210&gt; 160

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 160

Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly  
 1 5 10 15  
 Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln

	20	25	30
Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val			
	35	40	45
Val Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His			
	50	55	60
Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg			
	65	70	75
Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu			
	85	90	95
Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro			
	100	105	110
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu			
	115	120	125
Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile			
	130	135	140
Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro			
	145	150	155
Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu			
	165	170	175
Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe			
	180	185	190
Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro			
	195	200	205
Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg			
	210	215	220
Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro			
	225	230	235
			240

Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu  
                             245                            250                            255  
 Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala  
                             260                            265                            270  
 Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu  
                             275                            280                            285

<210> 161

<211> 761

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (138).. (623)

<400> 161

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 agagcttttt tctgggaccc aagcaaaggc atccacgctg ctgctaagct gaaattgaag 120  
 ctcacacatc ctggaaa atg cta gca ccc ata cca gaa ccc aag cct gga 170  
                             Met Leu Ala Pro Ile Pro Glu Pro Lys Pro Gly  
                             1                            5                            10  
 gac ctg att gag att ttc cgc cct atg tac aga cac tgg gcc atc tat 218  
 Asp Leu Ile Glu Ile Phe Arg Pro Met Tyr Arg His Trp Ala Ile Tyr  
                             15                            20                            25  
 gtt ggt gat gga tac gtg atc cac ctg gct cct cca agt gaa atc gca 266  
 Val Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu Ile Ala  
                             30                            35                            40  
 gga gct ggg gca gcc agc atc atg tct gct ttg act gac aag gcc ata 314

Gly Ala Gly Ala Ala Ser Ile Met Ser Ala Leu Thr Asp Lys Ala Ile  
           45                          50                          55  
 gtg aag aaa gaa ctg ctg tgc cat gtg gcc ggg aag gac aag tac cag 362  
 Val Lys Lys Glu Leu Leu Cys His Val Ala Gly Lys Asp Lys Tyr Gln  
           60                          65                          70                          75  
 gtc aat aac aaa cat gac gag gag tac acc cca ctg cct ctg agc aag 410  
 Val Asn Asn Lys His Asp Glu Glu Tyr Thr Pro Leu Pro Leu Ser Lys  
                           80                          85                          90  
 atc atc cag cgg gct gag aga ctg gtg ggg cag gag gtg ctc tac agg 458  
 Ile Ile Gln Arg Ala Glu Arg Leu Val Gly Gln Glu Val Leu Tyr Arg  
                           95                          100                          105  
 ctg acc agc gag aac tgt gag cac ttt gtg aat gaa cta cgc tat gga 506  
 Leu Thr Ser Glu Asn Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly  
                           110                          115                          120  
 gtt cct cgg agt gat cag gtc aga gat gcg gtc aag gcg gta ggc atc 554  
 Val Pro Arg Ser Asp Gln Val Arg Asp Ala Val Lys Ala Val Gly Ile  
                           125                          130                          135  
 gct gga gtg ggc ttg gcg gcc ttg ggc ctc gtt gga gtc atg ctc tcc 602  
 Ala Gly Val Gly Leu Ala Ala Leu Gly Leu Val Gly Val Met Leu Ser  
                           140                          145                          150                          155  
 aga aac aag aaa cag aag caa tgagctgaat gactgccag tttttgggct 653  
 Arg Asn Lys Lys Gln Lys Gln  
                           160  
 cttcttttgc tagagggttt ggagtttgat ttatagattc tattgcttta taattagggtt 713  
 tattttcaca acatacaata aaccacaaga aaggaatttt tgtgagga 761

&lt;210&gt; 162

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 162

Met Leu Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
 1 5 10 15  
 Phe Arg Pro Met Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr  
 20 25 30  
 Val Ile His Leu Ala Pro Pro Ser Glu Ile Ala Gly Ala Gly Ala Ala  
 35 40 45  
 Ser Ile Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
 50 55 60  
 Leu Cys His Val Ala Gly Lys Asp Lys Tyr Gln Val Asn Asn Lys His  
 65 70 75 80  
 Asp Glu Glu Tyr Thr Pro Leu Pro Leu Ser Lys Ile Ile Gln Arg Ala  
 85 90 95  
 Glu Arg Leu Val Gly Gln Glu Val Leu Tyr Arg Leu Thr Ser Glu Asn  
 100 105 110  
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Pro Arg Ser Asp  
 115 120 125  
 Gln Val Arg Asp Ala Val Lys Ala Val Gly Ile Ala Gly Val Gly Leu  
 130 135 140  
 Ala Ala Leu Gly Leu Val Gly Val Met Leu Ser Arg Asn Lys Lys Gln  
 145 150 155 160  
 Lys Gln

&lt;210&gt; 163

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55).. (540)

&lt;400&gt; 163

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acatctacgc agcgaaatcg agcctggcct tgagggtcca caccgcgagg gaag atg 57
                                                    Met
                                                    1

cgt gcg ccc att cca gag cct aag cct gga gac ctg att gag att ttt 105
Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile Phe
           5                10                15

cgc cct ttc tac aga cac tgg gcc atc tat gtt ggc gat gga tat gtg 153
Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr Val
           20                25                30

gtt cat ctg gcc cct cca agt gag gtc gca gga gct ggt gca gcc agt 201
Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala Ser
           35                40                45

gtc atg tcc gcc ctg act gac aag gcc atc gtg aag aag gaa ttg ctg 249
Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu Leu
           50                55                60                65

tat gat gtg gcc ggg agt gac aag tac cag gtc aac aac aaa cat gat 297
Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His Asp
           70                75                80

gac aag tac tcg ccg ctg ccc tgc agc aaa atc atc cag cgg gcg gag 345
Asp Lys Tyr Ser Pro Leu Pro Cys Ser Lys Ile Ile Gln Arg Ala Glu

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85	90	95	
gag ctg gtg ggg cag gag gtg ctc tac aag ctg acc agt gag aac tgc			393
Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn Cys			
100	105	110	
gag cac ttt gtg aat gag ctg cgc tat gga gtc gcc cgc agt gac cag			441
Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp Gln			
115	120	125	
gtc aga gat gtc atc atc gct gca agc gtt gca gga atg ggc ttg gca			489
Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu Ala			
130	135	140	145
gcc atg agc ctt att gga gtc atg ttc tca aga aac aag cga caa aag			537
Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln Lys			
150	155	160	
caa taactgaaaa agactgtcct gtcagc gatg actttataca tcaagggggt			590
Gln			
cttgttttgc tagagagttt ggggtttggt ttgtggattt cattgtgatt tataataagg			650
cttattttca cagaataaaa taaagc			676

&lt;210&gt; 164

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile

1

5

10

15

Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr

20

25

30

Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala  
                   35                                  40                                  45  
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
                   50                                  55                                  60  
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His  
                   65                                  70                                  75                                  80  
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Ser Lys Ile Ile Gln Arg Ala  
                                   85                                  90                                  95  
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn  
                                   100                                  105                                  110  
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp  
                                   115                                  120                                  125  
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu  
                                   130                                  135                                  140  
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln  
                   145                                  150                                  155                                  160  
 Lys Gln

<210> 165

<211> 2126

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (37)..(1743)

<400> 165

agaggctgtg ttctggggggc agtcgcagcc ccagag atg gca gtg agc gag agg 54



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																1						5
agg	ggg	ctc	agc	ggc	gag	agc	cca	acg	cag	tgc	cga	tgg	gga	tac	ttg	102						
Arg	Gly	Leu	Ser	Gly	Glu	Ser	Pro	Thr	Gln	Cys	Arg	Trp	Gly	Tyr	Leu							
				10					15					20								
tcg	ctg	ctg	gtg	ctg	acg	ctg	agc	ggc	tgc	tca	ggc	cgt	atc	cac	cgg	150						
Ser	Leu	Leu	Val	Leu	Thr	Leu	Ser	Gly	Cys	Ser	Gly	Arg	Ile	His	Arg							
				25					30					35								
ctg	act	ctc	aca	ggg	gag	aag	cga	gct	gac	atc	caa	ctg	aac	agc	ttc	198						
Leu	Thr	Leu	Thr	Gly	Glu	Lys	Arg	Ala	Asp	Ile	Gln	Leu	Asn	Ser	Phe							
				40					45					50								
gga	ttc	tac	acc	aat	ggt	tcc	ctg	gaa	gta	gag	ctg	agc	tta	ctg	cga	246						
Gly	Phe	Tyr	Thr	Asn	Gly	Ser	Leu	Glu	Val	Glu	Leu	Ser	Leu	Leu	Arg							
				55					60					65				70				
ctc	agc	ctc	cag	gag	aca	gaa	aag	aag	ttg	cca	aag	gtg	ggg	ttc	agc	294						
Leu	Ser	Leu	Gln	Glu	Thr	Glu	Lys	Lys	Leu	Pro	Lys	Val	Gly	Phe	Ser							
				75					80					85								
ttg	agc	aga	gtt	cgg	tct	ggc	agt	gtc	cgc	tcc	tac	tcg	aga	cgg	aac	342						
Leu	Ser	Arg	Val	Arg	Ser	Gly	Ser	Val	Arg	Ser	Tyr	Ser	Arg	Arg	Asn							
				90					95					100								
tcc	cat	gaa	tgc	cct	ctg	gat	aga	aac	agc	agc	aac	ttc	ctg	gtc	ctg	390						
Ser	His	Glu	Cys	Pro	Leu	Asp	Arg	Asn	Ser	Ser	Asn	Phe	Leu	Val	Leu							
				105					110					115								
ttc	ctc	atc	aat	atc	aag	gac	ctg	cag	gtc	caa	gtc	cga	aaa	tat	ggg	438						
Phe	Leu	Ile	Asn	Ile	Lys	Asp	Leu	Gln	Val	Gln	Val	Arg	Lys	Tyr	Gly							
				120					125					130								
gag	cag	aag	ttg	ttc	atc	tcc	cct	ggc	ctt	ctc	cct	gaa	gct	ccc	acc	486						

Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu Leu Pro Glu Ala Pro Thr  
 135 140 145 150  
 cag tca ggt ccc ccg aaa cca gac cca gca ggc acc ccc aag gac aac 534  
 Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala Gly Thr Pro Lys Asp Asn  
 155 160 165  
 cac gtc att cac cca tct cct aca gag atg tct gca gtc aag gag aat 582  
 His Val Ile His Pro Ser Pro Thr Glu Met Ser Ala Val Lys Glu Asn  
 170 175 180  
 cag aca gcg ccc cag gtt tca ggg gat aaa act acc cca ggg gaa cac 630  
 Gln Thr Ala Pro Gln Val Ser Gly Asp Lys Thr Thr Pro Gly Glu His  
 185 190 195  
 agg cac tca tcc gag aga cag cca ccc acg cag gac ccc agt ggg aag 678  
 Arg His Ser Ser Glu Arg Gln Pro Pro Thr Gln Asp Pro Ser Gly Lys  
 200 205 210  
 gag aag gat cag gtg ttg gga ctg ggc cac ctc aat gac tcc tac aac 726  
 Glu Lys Asp Gln Val Leu Gly Leu Gly His Leu Asn Asp Ser Tyr Asn  
 215 220 225 230  
 ttc agt ttc cac att gtg atc agc tcc agg gct gag gaa ggc cag tac 774  
 Phe Ser Phe His Ile Val Ile Ser Ser Arg Ala Glu Glu Gly Gln Tyr  
 235 240 245  
 agc ctc aac ttc cac aac tgt cac aac tcc atc cca ggc cag gag cag 822  
 Ser Leu Asn Phe His Asn Cys His Asn Ser Ile Pro Gly Gln Glu Gln  
 250 255 260  
 cca ttc gac ctc act gtg atg atc cgg gag aag aat cca gaa ggc ttc 870  
 Pro Phe Asp Leu Thr Val Met Ile Arg Glu Lys Asn Pro Glu Gly Phe  
 265 270 275  
 ttg tca gca gcc gaa atc ccc ctc ttc aaa ctc tac ctg atc atg tct 918

Leu Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser  
 280 285 290  
 gcc tgc ttt ctg gcc gca gac atc ttc tgg gtg tcc gtg ctc tgc aag 966  
 Ala Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys  
 295 300 305 310  
 aac aca tac agt gtc ttc aag atc cac tgg ctc atg gca gcc ctg gcg 1014  
 Asn Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala  
 315 320 325  
 ttc acc aag agt gtc tcc cta ctc ttc cac agc atc aac tac tac ttc 1062  
 Phe Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe  
 330 335 340  
 atc aac agc cag ggc cac ccc atc gaa ggc ctc gcg gtc atg cac tat 1110  
 Ile Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr  
 345 350 355  
 atc aca cac ctg ctg aag ggc gcc ctt ctc ttc atc acc atc gcc ttg 1158  
 Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu  
 360 365 370  
 atc ggc tca ggc tgg gcc ttt gtg aag tat atg ctg tcg gac aag gag 1206  
 Ile Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu  
 375 380 385 390  
 aag aag att ttt ggc att gtg att ccc ctg cag gtc ctg gct aat gta 1254  
 Lys Lys Ile Phe Gly Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val  
 395 400 405  
 gca tac att gtc att gag tcc cgt gag gag ggt gcc agc gac tat gga 1302  
 Ala Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly  
 410 415 420  
 ctc tgg aag gag atc ttg ttc ctg gtg gat ctc atc tgc tgt ggt gcc 1350

Leu Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala  
                   425                                  430                                  435  
 atc ctt ttc ccg gtg gtc tgg tcc att cgg cat ctg cag gat gca tcc 1398  
 Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser  
                   440                                  445                                  450  
 ggc act gat ggg aag gtg gca gtg aac ctg gcc agg ctg aag ctg ttc 1446  
 Gly Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe  
                   455                                  460                                  465                                  470  
 cga cat tac tac gtc atg gtc atc tgc tat atc tac ttt aca cgt atc 1494  
 Arg His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile  
                                   475                                  480                                  485  
 atc gcc att ctg ctg caa gta gca gtg ccc ttc cag tgg cag tgg ctg 1542  
 Ile Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu  
                                   490                                  495                                  500  
 tac cag ctc ttg gtg gag agt tcc aca ctg gcc ttc ttc gtg ctc act 1590  
 Tyr Gln Leu Leu Val Glu Ser Ser Thr Leu Ala Phe Phe Val Leu Thr  
                   505                                  510                                  515  
 ggc tac aag ttc cag ccg gct ggg gac aac cca tac ctg cag ctg cca 1638  
 Gly Tyr Lys Phe Gln Pro Ala Gly Asp Asn Pro Tyr Leu Gln Leu Pro  
                   520                                  525                                  530  
 cag gag gat gag gag gac gta cag atg gag caa gtg atg aca gac tct 1686  
 Gln Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser  
                   535                                  540                                  545                                  550  
 ggg ttt cgg gaa ggc ctg tcc aaa gtt aac aag aca gcc agt ggc cgg 1734  
 Gly Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg  
                                   555                                  560                                  565  
 gag ctg ttg tgacttcct gtgtccagt agccgccctc agacctcctg 1783

Glu Leu Leu

cacctcgcac ccctacactt gtcccaagtg tgcagggagc tggaggggat gctgcggaca 1843  
 aggcattccag gatgtggatc cccaaggagc cttcagaaaa gatgccctct cctcaccagg 1903  
 gagcaagcag ttcagcctct tgtggtacaa taaggaccag tctcttgact tggagggttc 1963  
 tgagtatcta cggcaggctg catttatgat ctcagttcac ggggtggcac gtgcctgtca 2023  
 tcccattgct ctggagagcc cgggcttcac aaaaccttga ttagtaaaca aataaagaaa 2083  
 aagtggaatt cccagtgagg ggaggaccac ctgttgagct aaa 2126

&lt;210&gt; 166

&lt;211&gt; 569

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 166

Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln  
 1 5 10 15  
 Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys  
 20 25 30  
 Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp  
 35 40 45  
 Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val  
 50 55 60  
 Glu Leu Ser Leu Leu Arg Leu Ser Leu Gln Glu Thr Glu Lys Lys Leu  
 65 70 75 80  
 Pro Lys Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Ser Val Arg  
 85 90 95  
 Ser Tyr Ser Arg Arg Asn Ser His Glu Cys Pro Leu Asp Arg Asn Ser  
 100 105 110

Ser Asn Phe Leu Val Leu Phe Leu Ile Asn Ile Lys Asp Leu Gln Val  
 115 120 125  
 Gln Val Arg Lys Tyr Gly Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu  
 130 135 140  
 Leu Pro Glu Ala Pro Thr Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala  
 145 150 155 160  
 Gly Thr Pro Lys Asp Asn His Val Ile His Pro Ser Pro Thr Glu Met  
 165 170 175  
 Ser Ala Val Lys Glu Asn Gln Thr Ala Pro Gln Val Ser Gly Asp Lys  
 180 185 190  
 Thr Thr Pro Gly Glu His Arg His Ser Ser Glu Arg Gln Pro Pro Thr  
 195 200 205  
 Gln Asp Pro Ser Gly Lys Glu Lys Asp Gln Val Leu Gly Leu Gly His  
 210 215 220  
 Leu Asn Asp Ser Tyr Asn Phe Ser Phe His Ile Val Ile Ser Ser Arg  
 225 230 235 240  
 Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe His Asn Cys His Asn Ser  
 245 250 255  
 Ile Pro Gly Gln Glu Gln Pro Phe Asp Leu Thr Val Met Ile Arg Glu  
 260 265 270  
 Lys Asn Pro Glu Gly Phe Leu Ser Ala Ala Glu Ile Pro Leu Phe Lys  
 275 280 285  
 Leu Tyr Leu Ile Met Ser Ala Cys Phe Leu Ala Ala Asp Ile Phe Trp  
 290 295 300  
 Val Ser Val Leu Cys Lys Asn Thr Tyr Ser Val Phe Lys Ile His Trp  
 305 310 315 320  
 Leu Met Ala Ala Leu Ala Phe Thr Lys Ser Val Ser Leu Leu Phe His

325	330	335
Ser Ile Asn Tyr Tyr Phe Ile Asn Ser Gln Gly His Pro Ile Glu Gly		
340	345	350
Leu Ala Val Met His Tyr Ile Thr His Leu Leu Lys Gly Ala Leu Leu		
355	360	365
Phe Ile Thr Ile Ala Leu Ile Gly Ser Gly Trp Ala Phe Val Lys Tyr		
370	375	380
Met Leu Ser Asp Lys Glu Lys Lys Ile Phe Gly Ile Val Ile Pro Leu		
385	390	395
Gln Val Leu Ala Asn Val Ala Tyr Ile Val Ile Glu Ser Arg Glu Glu		
405	410	415
Gly Ala Ser Asp Tyr Gly Leu Trp Lys Glu Ile Leu Phe Leu Val Asp		
420	425	430
Leu Ile Cys Cys Gly Ala Ile Leu Phe Pro Val Val Trp Ser Ile Arg		
435	440	445
His Leu Gln Asp Ala Ser Gly Thr Asp Gly Lys Val Ala Val Asn Leu		
450	455	460
Ala Arg Leu Lys Leu Phe Arg His Tyr Tyr Val Met Val Ile Cys Tyr		
465	470	475
Ile Tyr Phe Thr Arg Ile Ile Ala Ile Leu Leu Gln Val Ala Val Pro		
485	490	495
Phe Gln Trp Gln Trp Leu Tyr Gln Leu Leu Val Glu Ser Ser Thr Leu		
500	505	510
Ala Phe Phe Val Leu Thr Gly Tyr Lys Phe Gln Pro Ala Gly Asp Asn		
515	520	525
Pro Tyr Leu Gln Leu Pro Gln Glu Asp Glu Glu Asp Val Gln Met Glu		
530	535	540

Gln Val Met Thr Asp Ser Gly Phe Arg Glu Gly Leu Ser Lys Val Asn  
545 550 555 560

Lys Thr Ala Ser Gly Arg Glu Leu Leu  
565

<210> 167

<211> 1820

## <212> DNA

<213> Mus musculus

**<220>**

&lt;221&gt; CDS

<222> (1).. (1686)

<400> 167

atg gca gtg agc gag agg agg ggg ctc agc ggc gag agc cca acg cag 48

Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln

**1                      5                      10                      15**

tgc cga tgg gga tac ttg tcg ctg ctg gtg ctg acg ctg agc ggc tgc 96

Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys

20                      25                      30

tca ggc cgt atc cac cgg ctg act ctc aca ggg gag aag cga gct gac 144

Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp

35                      40                      45

atc caa ctg aac agc ttc gga ttc tac acc aat ggt tcc ctg gaa gta 192

Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val

50                      55                      60

gag ctg agc tta ctg cga ctc agc ctc cag gag aca gaa aag aag ttg 240

Glu Leu Ser Leu Leu Arg Leu Ser Leu Gln Glu Thr Glu Lys Lys Leu



65	70	75	80	
cca aag gtg ggg ttc agc ttg agc aga gtt cgg tct ggc agt gtc cgc	288			
Pro Lys Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Ser Val Arg				
85	90	95		
tcc tac tcg aga cgg aac tcc cat gaa tgc cct ctg gat aga aac agc	336			
Ser Tyr Ser Arg Arg Asn Ser His Glu Cys Pro Leu Asp Arg Asn Ser				
100	105	110		
agc aac ttc ctg gtc ctg ttc ctc atc aat atc aag gac ctg cag gtc	384			
Ser Asn Phe Leu Val Leu Phe Leu Ile Asn Ile Lys Asp Leu Gln Val				
115	120	125		
caa gtc cga aaa tat ggg gag cag aag ttg ttc atc tcc cct ggc ctt	432			
Gln Val Arg Lys Tyr Gly Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu				
130	135	140		
ctc cct gaa gct ccc acc cag tca ggt ccc ccg aaa cca gac cca gca	480			
Leu Pro Glu Ala Pro Thr Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala				
145	150	155	160	
ggc acc ccc aag gac aac cac gag atg tct gca gtc aag gag aat cag	528			
Gly Thr Pro Lys Asp Asn His Glu Met Ser Ala Val Lys Glu Asn Gln				
165	170	175		
aca gcg ccc cag gtt tca ggg gat aaa act acc cca ggg gaa cac agg	576			
Thr Ala Pro Gln Val Ser Gly Asp Lys Thr Thr Pro Gly Glu His Arg				
180	185	190		
cac tca tcc gag aga cag cca ccc acg cag gac ccc agt ggg aag gag	624			
His Ser Ser Glu Arg Gln Pro Pro Thr Gln Asp Pro Ser Gly Lys Glu				
195	200	205		
aag gat cag gtg ttg gga ctg ggc cac ctc aat gac tcc tac aac ttc	672			
Lys Asp Gln Val Leu Gly Leu Gly His Leu Asn Asp Ser Tyr Asn Phe				

210	215	220	
agt ttc cac att gtg atc agc tcc agg gct gag gaa ggc cag tac agc			720
Ser Phe His Ile Val Ile Ser Ser Arg Ala Glu Glu Gly Gln Tyr Ser			
225	230	235	240
ctc aac ttc cac aac tgt cac aac tcc atc cca ggc cag gag cag cca			768
Leu Asn Phe His Asn Cys His Asn Ser Ile Pro Gly Gln Glu Gln Pro			
	245	250	255
ttc gac ctc act gtg atg atc cgg gag aag aat cca gaa ggc ttc ttg			816
Phe Asp Leu Thr Val Met Ile Arg Glu Lys Asn Pro Glu Gly Phe Leu			
	260	265	270
tca gca gcc gaa atc ccc ctc ttc aaa ctc tac ctg atc atg tct gcc			864
Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser Ala			
	275	280	285
tgc ttt ctg gcc gca gac atc ttc tgg gtg tcc gtg ctc tgc aag aac			912
Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys Asn			
	290	295	300
aca tac agt gtc ttc aag atc cac tgg ctc atg gca gcc ctg gcg ttc			960
Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe			
305	310	315	320
acc aag agt gtc tcc cta ctc ttc cac agc atc aac tac tac ttc atc			1008
Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile			
	325	330	335
aac agc cag ggc cac ccc atc gaa ggc ctc gcg gtc atg cac tat atc			1056
Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr Ile			
	340	345	350
aca cac ctg ctg aag ggc gcc ctt ctc ttc atc acc atc gcc ttg atc			1104
Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile			

355	360	365	
ggc tca ggc tgg gcc ttt gtg aag tat atg ctg tcg gac aag gag aag	1152		
Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu Lys			
370	375	380	
aag att ttt ggc att gtg att ccc ctg cat gtc ctg gct aat gta gca	1200		
Lys Ile Phe Gly Ile Val Ile Pro Leu His Val Leu Ala Asn Val Ala			
385	390	395	400
tac att gtt att gag tcc cgt gag gag ggt gcc agc gac tat gga ctc	1248		
Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly Leu			
	405	410	415
tgg aag gag atc ttg ttc ctg gtg gat ctc atc tgc tgt ggt gcc atc	1296		
Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile			
	420	425	430
ctt ttc ccg gtg gtc tgg tcc att cgg cat ctg cag gat gca tcc ggc	1344		
Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly			
	435	440	445
act gat ggg aag gtg gca gtg aac ctg gcc agg ctg aag ctg ttc cga	1392		
Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe Arg			
	450	455	460
cat tac tac gtc atg gtc atc tgc tat atc tac ttt aca cgt atc atc	1440		
His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile Ile			
465	470	475	480
gcc att ctg ctg caa gta gca gtg ccc ttc cag tgg cag tgg ctg tac	1488		
Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr			
	485	490	495
cag ctc ttg gtg gag agt tcc aca ctg gcc ttc ttc gtg ctc act ggc	1536		
Gln Leu Leu Val Glu Ser Ser Thr Leu Ala Phe Phe Val Leu Thr Gly			

500 505 510  
 tac aag ttc cag ccg gct ggg gac aac cca tac ctg cag ctg cca cag 1584  
 Tyr Lys Phe Gln Pro Ala Gly Asp Asn Pro Tyr Leu Gln Leu Pro Gln  
 515 520 525  
 gag gat gag gag gac gta cag atg gag caa gtg atg aca gac tct ggg 1632  
 Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly  
 530 535 540  
 ttt cgg gaa ggc ctg tcc aaa gtt aac aag aca gcc agt ggc cgg gag 1680  
 Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu  
 545 550 555 560  
 ctg ttg tgatctcagt tcacgggggtg gcacgtgcct gtcattcccat tgctctggag 1736  
 Leu Leu  
 agccccgggct tcataaaacc ttgattagta aacaaataaa gaaaaagtgg aattcccagt 1796  
 gaggggagga ccacctgttg agct 1820

&lt;210&gt; 168

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 168

Met Ala Val Ser Glu Arg Arg Gly Leu Ser Gly Glu Ser Pro Thr Gln

1 5 10 15

Cys Arg Trp Gly Tyr Leu Ser Leu Leu Val Leu Thr Leu Ser Gly Cys

20 25 30

Ser Gly Arg Ile His Arg Leu Thr Leu Thr Gly Glu Lys Arg Ala Asp

35 40 45

Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val

50	55	60
Glu Leu Ser Leu Leu Arg Leu Ser Leu Gln Glu Thr Glu Lys Lys Leu		
65	70	75
Pro Lys Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Ser Val Arg		
85	90	95
Ser Tyr Ser Arg Arg Asn Ser His Glu Cys Pro Leu Asp Arg Asn Ser		
100	105	110
Ser Asn Phe Leu Val Leu Phe Leu Ile Asn Ile Lys Asp Leu Gln Val		
115	120	125
Gln Val Arg Lys Tyr Gly Glu Gln Lys Leu Phe Ile Ser Pro Gly Leu		
130	135	140
Leu Pro Glu Ala Pro Thr Gln Ser Gly Pro Pro Lys Pro Asp Pro Ala		
145	150	155
Gly Thr Pro Lys Asp Asn His Glu Met Ser Ala Val Lys Glu Asn Gln		
165	170	175
Thr Ala Pro Gln Val Ser Gly Asp Lys Thr Thr Pro Gly Glu His Arg		
180	185	190
His Ser Ser Glu Arg Gln Pro Pro Thr Gln Asp Pro Ser Gly Lys Glu		
195	200	205
Lys Asp Gln Val Leu Gly Leu Gly His Leu Asn Asp Ser Tyr Asn Phe		
210	215	220
Ser Phe His Ile Val Ile Ser Ser Arg Ala Glu Glu Gly Gln Tyr Ser		
225	230	235
Leu Asn Phe His Asn Cys His Asn Ser Ile Pro Gly Gln Glu Gln Pro		
245	250	255
Phe Asp Leu Thr Val Met Ile Arg Glu Lys Asn Pro Glu Gly Phe Leu		
260	265	270

Ser Ala Ala Glu Ile Pro Leu Phe Lys Leu Tyr Leu Ile Met Ser Ala  
275 280 285

Cys Phe Leu Ala Ala Asp Ile Phe Trp Val Ser Val Leu Cys Lys Asn  
290 295 300

Thr Tyr Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe  
305 310 315 320

Thr Lys Ser Val Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile  
325 330 335

Asn Ser Gln Gly His Pro Ile Glu Gly Leu Ala Val Met His Tyr Ile  
340 345 350

Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile  
355 360 365

Gly Ser Gly Trp Ala Phe Val Lys Tyr Met Leu Ser Asp Lys Glu Lys  
370 375 380

Lys Ile Phe Gly Ile Val Ile Pro Leu His Val Leu Ala Asn Val Ala  
385 390 395 400

Tyr Ile Val Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Gly Leu  
405 410 415

Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile  
420 425 430

Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly  
435 440 445

Thr Asp Gly Lys Val Ala Val Asn Leu Ala Arg Leu Lys Leu Phe Arg  
450 455 460

His Tyr Tyr Val Met Val Ile Cys Tyr Ile Tyr Phe Thr Arg Ile Ile  
465 470 475 480

Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr

	485		490		495										
Gln	Leu	Leu	Val	Glu	Ser	Ser	Thr	Leu	Ala	Phe	Phe	Val	Leu	Thr	Gly
	500				505					510					
Tyr	Lys	Phe	Gln	Pro	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Gln	Leu	Pro	Gln
	515				520					525					
Glu	Asp	Glu	Glu	Asp	Val	Gln	Met	Glu	Gln	Val	Met	Thr	Asp	Ser	Gly
	530				535					540					
Phe	Arg	Glu	Gly	Leu	Ser	Lys	Val	Asn	Lys	Thr	Ala	Ser	Gly	Arg	Glu
545			550				555				560				
Leu	Leu														

&lt;210&gt; 169

&lt;211&gt; 1914

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (28)..(1656)

&lt;400&gt; 169

ggagtcgggg aggaggtggc tccagag atg gca gtg agc gag agg agg ggg ctc 54

Met Ala Val Ser Glu Arg Arg Gly Leu

1

5

ggc cgc ggg agc ccc gcg gag tgg ggg cag cgg cta ctt ctg gtg ctg 102

Gly Arg Gly Ser Pro Ala Glu Trp Gly Gln Arg Leu Leu Leu Val Leu

10

15

20

25

ctg ttg ggt ggc tgc tcc ggg cgc atc cac cgg ctg gcg ctg acg ggg 150

Leu Leu Gly Gly Cys Ser Gly Arg Ile His Arg Leu Ala Leu Thr Gly

30	35	40	
gag aag cga gcg gac atc cag ctg aac agc ttc ggt ttc tac acc aat			198
Glu Lys Arg Ala Asp Ile Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn			
45	50	55	
ggc tct ctg gag gtg gag ttg agc gtc ctg cgg ctg ggc ctc cgg gag			246
Gly Ser Leu Glu Val Glu Leu Ser Val Leu Arg Leu Gly Leu Arg Glu			
60	65	70	
gca gaa gag aag tcc ctg ctg gtg ggg ttc agt ctc agc cgg gtt cgg			294
Ala Glu Glu Lys Ser Leu Leu Val Gly Phe Ser Leu Ser Arg Val Arg			
75	80	85	
tct ggc aga gtt cgc tcc tat tca acc cgg gat ttc cag gac tgc cct			342
Ser Gly Arg Val Arg Ser Tyr Ser Thr Arg Asp Phe Gln Asp Cys Pro			
90	95	100	105
ctc cag aaa aac agt agc agt ttc ctg gtc ctg ttc ctc atc aac acc			390
Leu Gln Lys Asn Ser Ser Ser Phe Leu Val Leu Phe Leu Ile Asn Thr			
110	115	120	
aag gat ctg cag gtc cag gtg cgg aag tat gga gag cag aag acg ttg			438
Lys Asp Leu Gln Val Gln Val Arg Lys Tyr Gly Glu Gln Lys Thr Leu			
125	130	135	
ttt atc ttt ccc ggg ctc ctc ccg gaa gca ccc tcc aaa cca ggg ctc			486
Phe Ile Phe Pro Gly Leu Leu Pro Glu Ala Pro Ser Lys Pro Gly Leu			
140	145	150	
ccg aag cca cag gcc aca gtc ccc cgc aag gtg gat ggc gga ggg acc			534
Pro Lys Pro Gln Ala Thr Val Pro Arg Lys Val Asp Gly Gly Gly Thr			
155	160	165	
tct gca gcc agc aag ccc aag tca aca ccc gca gtg att cag ggt cct			582
Ser Ala Ala Ser Lys Pro Lys Ser Thr Pro Ala Val Ile Gln Gly Pro			



170	175	180	185	
agt ggg aag gac aag gac	ctg gtg ttg ggc	ctg agc cac ctc aac aac	630	
Ser Gly Lys Asp Lys Asp	Leu Val Leu Gly Leu Ser	His Leu Asn Asn		
	190	195	200	
tcc tac aac ttc agt ttc	cac gtg gtg atc ggc	tct cag gcg gaa gaa	678	
Ser Tyr Asn Phe Ser Phe	His Val Val Ile Gly Ser	Gln Ala Glu Glu		
	205	210	215	
ggc cag tac agc ctg aac	ttc cac aac tgc aac	aat tca gtg cca gga	726	
Gly Gln Tyr Ser Leu Asn	Phe His Asn Cys Asn	Asn Ser Val Pro Gly		
	220	225	230	
aag gag cat cca ttc gac	atc acg gtg atg atc	cgg gag aag aac ccc	774	
Lys Glu His Pro Phe Asp	Ile Thr Val Met Ile Arg	Glu Lys Asn Pro		
	235	240	245	
gat ggc ttc ctg tgc gca	gcg gag atg ccc ctt	ttc aag ctc tac atg	822	
Asp Gly Phe Leu Ser Ala	Ala Glu Met Pro Leu Phe	Lys Leu Tyr Met		
	250	255	260	265
gtc atg tcc gcc tgc ttc	ctg gcc gct ggc atc	ttc tgg gtg tcc atc	870	
Val Met Ser Ala Cys Phe	Leu Ala Ala Gly Ile Phe	Trp Val Ser Ile		
	270	275	280	
ctc tgc agg aac acg tac	agc gtc ttc aag atc	cac tgg ctc atg gcg	918	
Leu Cys Arg Asn Thr Tyr	Ser Val Phe Lys Ile His	Trp Leu Met Ala		
	285	290	295	
gcc ttg gcc ttc acc aag	agc atc tct ctc ctc	ttc cac agc atc aac	966	
Ala Leu Ala Phe Thr Lys	Ser Ile Ser Leu Leu Phe	His Ser Ile Asn		
	300	305	310	
tac tac ttc atc aac agc	cag ggc cac ccc atc	gaa ggc ctt gcc gtc	1014	
Tyr Tyr Phe Ile Asn Ser	Gln Gly His Pro Ile Glu	Gly Leu Ala Val		

315	320	325	
atg tac tac atc gca cac ctg ctg aag ggc gcc ctc ctc ttc atc acc			1062
Met Tyr Tyr Ile Ala His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr			
330	335	340	345
atc gcc ctg att ggc tca ggc tgg gcc ttc atc aag tac gtc ctg tcg			1110
Ile Ala Leu Ile Gly Ser Gly Trp Ala Phe Ile Lys Tyr Val Leu Ser			
350	355	360	
gat aag gag aag aag gtc ttt ggg atc gtg atc ccc atg cag gtc ctg			1158
Asp Lys Glu Lys Lys Val Phe Gly Ile Val Ile Pro Met Gln Val Leu			
365	370	375	
gcc aac gtg gcc tac atc atc atc gag tcc cgc gag gaa ggc gcc agc			1206
Ala Asn Val Ala Tyr Ile Ile Ile Glu Ser Arg Glu Glu Gly Ala Ser			
380	385	390	
gac tac gtg ctg tgg aag gag att ttg ttc ctg gtg gac ctc atc tgc			1254
Asp Tyr Val Leu Trp Lys Glu Ile Leu Phe Leu Val Asp Leu Ile Cys			
395	400	405	
tgt ggt gcc atc ctg ttc ccc gta gtc tgg tcc atc cgg cat ctc cag			1302
Cys Gly Ala Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln			
410	415	420	425
gat gcg tct ggc aca gac ggg aag gtg gca gtg aac ctg gcc aag ctg			1350
Asp Ala Ser Gly Thr Asp Gly Lys Val Ala Val Asn Leu Ala Lys Leu			
430	435	440	
aag ctg ttc cgg cat tac tat gtc atg gtc atc tgc tac gtc tac ttc			1398
Lys Leu Phe Arg His Tyr Tyr Val Met Val Ile Cys Tyr Val Tyr Phe			
445	450	455	
acc cgc atc atc gcc atc ctg ctg cag gtg gct gtg ccc ttt cag tgg			1446
Thr Arg Ile Ile Ala Ile Leu Leu Gln Val Ala Val Pro Phe Gln Trp			

460 465 470  
 cag tgg ctg tac cag ctc ttg gtg gag ggc tcc acc ctg gcc ttc ttc 1494  
 Gln Trp Leu Tyr Gln Leu Leu Val Glu Gly Ser Thr Leu Ala Phe Phe  
 475 480 485  
 gtg ctc acg ggc tac aag ttc cag ccc aca gga aac aac ccg tac ctg 1542  
 Val Leu Thr Gly Tyr Lys Phe Gln Pro Thr Gly Asn Asn Pro Tyr Leu  
 490 495 500 505  
 cag ctg ccc cag gag gac gag gag gat gtt cag atg gag caa gta atg 1590  
 Gln Leu Pro Gln Glu Asp Glu Glu Asp Val Gln Met Glu Gln Val Met  
 510 515 520  
 acg gac tct ggg ttc cgg gaa ggc ctc tcc aaa gtc aac aaa aca gcc 1638  
 Thr Asp Ser Gly Phe Arg Glu Gly Leu Ser Lys Val Asn Lys Thr Ala  
 525 530 535  
 agc ggg cgg gaa ctg tta tgatcacctc cacatctcag accaaagggt 1686  
 Ser Gly Arg Glu Leu Leu  
 540  
 cgtcctcccc cagcatttct cactcctgcc cttcttccac agcgtatgtg gggagggtgga 1746  
 ggggggtccat gtggaccagg cgccagetc cccggggaccc cggttcccgg acaagcccat 1806  
 ttggaagaag agtcccttcc tcccccaaaa tattgggcag ccctgtcctt accccgggac 1866  
 caccctccc ttccagctat gtgtacaata atgaccaatc tgtttggc 1914

&lt;210&gt; 170

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu

1 5 10 15  
Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly  
20 25 30  
Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln  
35 40 45  
Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu  
50 55 60  
Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu  
65 70 75 80  
Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr  
85 90 95  
Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser  
100 105 110  
Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val  
115 120 125  
Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu  
130 135 140  
Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val  
145 150 155 160  
Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys  
165 170 175  
Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu  
180 185 190  
Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His  
195 200 205  
Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe  
210 215 220

His	Asn	Cys	Asn	Asn	Ser	Val	Pro	Gly	Lys	Glu	His	Pro	Phe	Asp	Ile
225					230					235					240
Thr	Val	Met	Ile	Arg	Glu	Lys	Asn	Pro	Asp	Gly	Phe	Leu	Ser	Ala	Ala
				245					250						255
Glu	Met	Pro	Leu	Phe	Lys	Leu	Tyr	Met	Val	Met	Ser	Ala	Cys	Phe	Leu
		260						265					270		
Ala	Ala	Gly	Ile	Phe	Trp	Val	Ser	Ile	Leu	Cys	Arg	Asn	Thr	Tyr	Ser
		275					280					285			
Val	Phe	Lys	Ile	His	Trp	Leu	Met	Ala	Ala	Leu	Ala	Phe	Thr	Lys	Ser
	290					295					300				
Ile	Ser	Leu	Leu	Phe	His	Ser	Ile	Asn	Tyr	Tyr	Phe	Ile	Asn	Ser	Gln
305					310						315				320
Gly	His	Pro	Ile	Glu	Gly	Leu	Ala	Val	Met	Tyr	Tyr	Ile	Ala	His	Leu
				325						330				335	
Leu	Lys	Gly	Ala	Leu	Leu	Phe	Ile	Thr	Ile	Ala	Leu	Ile	Gly	Ser	Gly
		340						345					350		
Trp	Ala	Phe	Ile	Lys	Tyr	Val	Leu	Ser	Asp	Lys	Glu	Lys	Lys	Val	Phe
		355					360					365			
Gly	Ile	Val	Ile	Pro	Met	Gln	Val	Leu	Ala	Asn	Val	Ala	Tyr	Ile	Ile
	370					375					380				
Ile	Glu	Ser	Arg	Glu	Glu	Gly	Ala	Ser	Asp	Tyr	Val	Leu	Trp	Lys	Glu
385					390						395				400
Ile	Leu	Phe	Leu	Val	Asp	Leu	Ile	Cys	Cys	Gly	Ala	Ile	Leu	Phe	Pro
			405						410				415		
Val	Val	Trp	Ser	Ile	Arg	His	Leu	Gln	Asp	Ala	Ser	Gly	Thr	Asp	Gly
		420						425					430		
Lys	Val	Ala	Val	Asn	Leu	Ala	Lys	Leu	Lys	Leu	Phe	Arg	His	Tyr	Tyr

435                      440                      445  
 Val Met Val Ile Cys Tyr Val Tyr Phe Thr Arg Ile Ile Ala Ile Leu  
 450                      455                      460  
 Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr Gln Leu Leu  
 465                      470                      475                      480  
 Val Glu Gly Ser Thr Leu Ala Phe Phe Val Leu Thr Gly Tyr Lys Phe  
 485                      490                      495  
 Gln Pro Thr Gly Asn Asn Pro Tyr Leu Gln Leu Pro Gln Glu Asp Glu  
 500                      505                      510  
 Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly Phe Arg Glu  
 515                      520                      525  
 Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu Leu Leu  
 530                      535                      540

&lt;210&gt; 171

&lt;211&gt; 1881

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (361).. (1344)

&lt;400&gt; 171

gcactctggg gcacaagaac tgcctggtgg caggggctgc ttcgggagtc tagcttgctc 60  
 cagtttctcat ggcttgcagg cggttgctgt gtcagaggga gttttcagat aaacggtgac 120  
 tgaaagaaca tggcttccca aggtggaatt cagactgagg acgtcagtgc ttccctccgt 180  
 gagctctgcg tgtgtgtgca ctgtccacag gggtaaacta aaagccacca gagctctctg 240  
 tcctggaccc aacctgcctt gaaaacaacg aggaacacca aatctggcac ttcttcctaa 300

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aacatcttcc atcttgcatg agacagactc tccgagcata ggaaaggctg acaggcagtt 360
atg gag cag gac aat ggc acc atc cag gct cca ggc ttg ccg ccc acc 408
Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr
      1              5              10              15
acc tgc gtc tac cgt gag gat ttc aag cga ctg ctg cta acc ccg gta 456
Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
      20              25              30
tac tcg gtg gtg ctg gtg gtc ggc ctg cca ctg aac atc tgc gtc att 504
Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
      35              40              45
gcc cag atc tgc gca tcc cgc cgg acc ctg acc cgt tcc gct gtg tac 552
Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
      50              55              60
acc ctg aac ctg gca ctg gcg gac ctg atg tat gcc tgt tca cta ccc 600
Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
      65              70              75              80
cta ctt atc tat aac tac gcc aga ggg gac cac tgg ccc ttc gga gac 648
Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
      85              90              95
ctc gcc tgc cgc ttt gta cgc ttc ctc ttc tat gcc aat cta cat ggc 696
Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
      100             105             110
agc atc ctg ttc ctc acc tgc att agc ttc cag cgc tac ctg ggc atc 744
Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
      115             120             125
tgc cac ccc ctg gct tcc tgg cac aag cgt gga ggt cgc cgt gct gct 792
Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala

```

130	135	140	
tgg gta gtg tgt gga gtc gtg tgg ctg gct gtg aca gcc cag tgc ctg			840
Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu			
145	150	155	160
ccc acg gca gtc ttt gct gcc aca ggc atc cag cgc aac cgc act gtg			888
Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val			
	165	170	175
tgc tac gac ctg agc cca ccc atc ctg tct act cgc tac ctg ccc tat			936
Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr			
	180	185	190
ggc atg gcc ctc acg gtc atc ggc ttc ttg ctg ccc ttc ata gcc tta			984
Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu			
	195	200	205
ctg gct tgt tat tgt cgc atg gcc cgc cgc ctg tgt cgc cag gat ggc			1032
Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly			
	210	215	220
cca gca ggt cct gtg gcc caa gag cgg cgc agc aag gcg gct cgt atg			1080
Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met			
225	230	235	240
gct gtg gtg gtg gca gct gtc ttt gcc atc agc ttc ctg cct ttc cac			1128
Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His			
	245	250	255
atc acc aag aca gcc tac ttg gct gtg cgc tcc acg ccc ggt gtc tct			1176
Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser			
	260	265	270
tgc cct gtg ctg gag acc ttc gct gct gcc tac aaa ggc act cgg ccc			1224
Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro			



275                      280                      285  
 ttc gcc agt gtc aac agt gtt ctg gac ccc att ctc ttc tac ttc aca 1272  
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
 290                      295                      300  
 caa cag aag ttc cgg cgg caa ccc cac gat ctc tta cag agg ctc aca 1320  
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr  
 305                      310                      315                      320  
 gcc aag tgg cag agg cag aga gtc tgaggcccca gaggaggccc tggggcactg 1374  
 Ala Lys Trp Gln Arg Gln Arg Val  
 325  
 gctgcaatgt gtttgtcact ggggccatgg ttgaagcttt ctctcaatcc caaaccatac 1434  
 agagaagtaa aacttggctc aacatgcctg ggcctccaga atttccacat caaccacaaa 1494  
 actaagacac ctgtgatttg gcaactggctc aattcatgct tgttacattc agaactcagg 1554  
 atgtttgtgac gagataacaa gttctggctc agcctgggtc acacagtga accccactgt 1614  
 gaaaccccat ctcagatgat caaggatctg ctagacatct caggatgtgc taggccctgg 1674  
 aatagcaatg cagattccaa caaaggtctt ctccaccccc acccccaccc cacctttctt 1734  
 gtgttttacag ggtggagggg actgctggtg cactgtcacg tgagggaag gtccctcctg 1794  
 tccaagagcc cggaaagctc acgttcacat ccatttgcca agacttttgc ataagagaga 1854  
 aataaatgtg tttttgtggt tggtggt 1881

&lt;210&gt; 172

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 172

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr

1

5

10

15

Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val  
 20 25 30  
 Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile  
 35 40 45  
 Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr  
 50 55 60  
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro  
 65 70 75 80  
 Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp  
 85 90 95  
 Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly  
 100 105 110  
 Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile  
 115 120 125  
 Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala  
 130 135 140  
 Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu  
 145 150 155 160  
 Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val  
 165 170 175  
 Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr  
 180 185 190  
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu  
 195 200 205  
 Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly  
 210 215 220  
 Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met

225                      230                      235                      240  
 Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His  
                          245                      250                      255  
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser  
                          260                      265                      270  
 Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro  
                          275                      280                      285  
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
                          290                      295                      300  
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr  
 305                      310                      315                      320  
 Ala Lys Trp Gln Arg Gln Arg Val  
                          325

<210> 173

<211> 1829

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (543).. (1526)

<400> 173

aaggacagag gaggggccct tcctgtcagc tggctgggag cagaggtggc tttgtctttt 60  
 cggaagaact ggttctgtgg aatttgtgct tatttcccat caaggatcaa ggacctgctc 120  
 tggggctacc tcagggcccc acaggatgag gggctggttt tcagatgagt tttctgcttg 180  
 cctgtcatct ggatagtgtc taaaaatttg caaactgcct tcttgtcagt gtcttgctca 240  
 ttcttcatga cactcctgat atgtctctca gtttcctcat ctgctgcctc tccagacttc 300

tgccagaaca ttgcacgcga cagtttcagg cacagaactg actggcagca ggggctgctc 360  
 cacgagtggg aatttgctcc agcacttcac ggactgcaag cgaggcactt gctaactctt 420  
 ggataacaag acctctgccga gaagaacat ggctttggaa ggcggagttc aggctgagga 480  
 gatgggtgcg gtcctcagtg agccccctgcc tccctgaaca taggaaaccc acctgggcag 540  
 cc atg gaa tgg gac aat ggc aca ggc cag gct ctg ggc ttg cca ccc 587  
 Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro  
 1 5 10 15  
 acc acc tgt gtc tac cgc gag aac ttc aag caa ctg ctg ctg cca cct 635  
 Thr Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro  
 20 25 30  
 gtg tat tcg gcg gtg ctg gcg gct ggc ctg ccg ctg aac atc tgt gtc 683  
 Val Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val  
 35 40 45  
 att acc cag atc tgc acg tcc cgc cgg gcc ctg acc cgc acg gcc gtg 731  
 Ile Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val  
 50 55 60  
 tac acc cta aac ctt gct ctg gct gac ctg cta tat gcc tgc tcc ctg 779  
 Tyr Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu  
 65 70 75  
 ccc ctg ctc atc tac aac tat gcc caa ggt gat cac tgg ccc ttt ggc 827  
 Pro Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly  
 80 85 90 95  
 gac ttc gcc tgc cgc ctg gtc cgc ttc ctc ttc tat gcc aac ctg cac 875  
 Asp Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His  
 100 105 110  
 ggc agc atc ctc ttc ctc acc tgc atc agc ttc cag cgc tac ctg ggc 923  
 Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly

115	120	125	
atc tgc cac ccg ctg gcc ccc tgg cac aaa cgt ggg ggc cgc cgg gct	971		
Ile Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala			
130	135	140	
gcc tgg cta gtg tgt gta gcc gtg tgg ctg gcc gtg aca acc cag tgc	1019		
Ala Trp Leu Val Cys Val Ala Val Trp Leu Ala Val Thr Thr Gln Cys			
145	150	155	
ctg ccc aca gcc atc ttc gct gcc aca ggc atc cag cgt aac cgc act	1067		
Leu Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr			
160	165	170	175
gtc tgc tat gac ctc agc ccg cct gcc ctg gcc acc cac tat atg ccc	1115		
Val Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro			
180	185	190	
tat ggc atg gct ctc act gtc atc ggc ttc ctg ctg ccc ttt gct gcc	1163		
Tyr Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala			
195	200	205	
ctg ctg gcc tgc tac tgt ctc ctg gcc tgc cgc ctg tgc cgc cag gat	1211		
Leu Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp			
210	215	220	
ggc ccg gca gag cct gtg gcc cag gag cgg cgt ggc aag gcg gcc cgc	1259		
Gly Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg			
225	230	235	
atg gcc gtg gtg gtg gct gct gcc ttt gcc atc agc ttc ctg cct ttt	1307		
Met Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe			
240	245	250	255
cac atc acc aag aca gcc tac ctg gca gtg cgc tcg acg ccg ggc gtc	1355		
His Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val			

260 265 270  
 ccc tgc act gta ttg gag gcc ttt gca gcg gcc tac aaa ggc acg cgg 1403  
 Pro Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg  
 275 280 285  
 ccg ttt gcc agt gcc aac agc gtg ctg gac ccc atc ctc ttc tac ttc 1451  
 Pro Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe  
 290 295 300  
 acc cag aag aag ttc cgc cgg cga cca cat gag ctc cta cag aaa ctc 1499  
 Thr Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu  
 305 310 315  
 aca gcc aaa tgg cag agg cag ggt cgc tgagtcctcc aggtcctggg 1546  
 Thr Ala Lys Trp Gln Arg Gln Gly Arg  
 320 325  
 cagccttcat atttgccatt gtgtccgggg caccaggagc cccaccaacc ccaaaccatg 1606  
 cggagaatta gagttcagct cagctgggca tggagttaag atccctcaca ggacccagaa 1666  
 gctcaccaaaa aactatttct tcagcccctt ctctggccca gaccctgtgg gcatggagat 1726  
 ggacagacct gggcctggct cttgagaggt ccagtcagc catggagagc tggggaaacc 1786  
 acattaaggt gtcacaaaa atacagtgtg acgtgtactg tca 1829

&lt;210&gt; 174

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 174

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr

1

5

10

15

Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val

20	25	30
Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile		
35	40	45
Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr		
50	55	60
Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro		
65	70	75
Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp		
85	90	95
Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly		
100	105	110
Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile		
115	120	125
Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala		
130	135	140
Trp Leu Val Cys Val Ala Val Trp Leu Ala Val Thr Thr Gln Cys Leu		
145	150	155
Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val		
165	170	175
Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr		
180	185	190
Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu		
195	200	205
Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly		
210	215	220
Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met		
225	230	235
		240

Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe His  
 245 250 255  
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Pro  
 260 265 270  
 Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro  
 275 280 285  
 Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
 290 295 300  
 Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr  
 305 310 315 320  
 Ala Lys Trp Gln Arg Gln Gly Arg  
 325

&lt;210&gt; 175

&lt;211&gt; 1477

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (35)..(1003)

&lt;400&gt; 175

aacaattcga gctgctgtga cagaggggaa caag atg gcg gcg cca aag ggg aag 55

Met Ala Ala Pro Lys Gly Lys

1

5

ctt tgg gtc cag gcc caa ctg ggg ctc ccg ccg ctg ctg ctg ttg act 103

Leu Trp Val Gln Ala Gln Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr

10

15

20



atg gcg ctg gcc gga ggc tcg ggg act gca gcg gcc gaa gcc ttt gac 151  
 Met Ala Leu Ala Gly Gly Ser Gly Thr Ala Ala Ala Glu Ala Phe Asp  
 25 30 35  
 tcg gtc ctg gga gac aca gcg tcc tgt cac cgg gcc tgt cag ctg acc 199  
 Ser Val Leu Gly Asp Thr Ala Ser Cys His Arg Ala Cys Gln Leu Thr  
 40 45 50 55  
 tac ccc ttg cac acc tac ccg aag gaa gag gag tta tac gca tgc cag 247  
 Tyr Pro Leu His Thr Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln  
 60 65 70  
 aga ggc tgc agg ctg ttt tca att tgc cag ttt gtg gat gat ggg ctt 295  
 Arg Gly Cys Arg Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Leu  
 75 80 85  
 gat tta aat cgg acc aag ctg gaa tgt gaa tct gcg tgc aca gaa gca 343  
 Asp Leu Asn Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala  
 90 95 100  
 tat tcc caa cct gat gag cag tat gct tgt cat ctt ggc tgc cag gat 391  
 Tyr Ser Gln Pro Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asp  
 105 110 115  
 cag ttg cca ttt gct gaa ctg aga caa gaa caa ctc atg tcc ctg atg 439  
 Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met  
 120 125 130 135  
 cca aga atg cat ctc ctc ttc cct ctg act ctg gtg agg tcg ttc tgg 487  
 Pro Arg Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp  
 140 145 150  
 agt gac atg atg gac tct gca cag agc ttc ata acc tct tca tgg act 535  
 Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr  
 155 160 165

ttt tat ctt caa gcc gat gac gga aaa ata gtt ata ttc cag tct aag 583  
 Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe Gln Ser Lys  
 170 175 180  
 cca gaa att cag tat gca ccg cag ttg gag cag gag cct aca aac ttg 631  
 Pro Glu Ile Gln Tyr Ala Pro Gln Leu Glu Gln Glu Pro Thr Asn Leu  
 185 190 195  
 aga gaa tca tct tta agc aaa atg tcc tat ctg cag atg aga aac tca 679  
 Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln Met Arg Asn Ser  
 200 205 210 215  
 caa gca cac agg aac tac ctt gaa gag gaa gaa agc gat ggc ttt tta 727  
 Gln Ala His Arg Asn Tyr Leu Glu Glu Glu Glu Ser Asp Gly Phe Leu  
 220 225 230  
 aga tgt cta tct ctt aac tct gga tgg att tta acc aca acc ctt gtc 775  
 Arg Cys Leu Ser Leu Asn Ser Gly Trp Ile Leu Thr Thr Thr Leu Val  
 235 240 245  
 ctc tcg gtg atg gtg ttg ctc tgg atc tgt tgt gca gct gtt gct aca 823  
 Leu Ser Val Met Val Leu Leu Trp Ile Cys Cys Ala Ala Val Ala Thr  
 250 255 260  
 gct gta gaa cag tat gtt ccc cct gag aag ctg agt atc tat ggt gac 871  
 Ala Val Glu Gln Tyr Val Pro Pro Glu Lys Leu Ser Ile Tyr Gly Asp  
 265 270 275  
 ttg gaa ttt atg aat gaa caa aag ctg agc aga tac cca gct cct tct 919  
 Leu Glu Phe Met Asn Glu Gln Lys Leu Ser Arg Tyr Pro Ala Pro Ser  
 280 285 290 295  
 ctt gtg att gtt agg tct cag act gaa gaa cat gag gag gca ggg ccc 967  
 Leu Val Ile Val Arg Ser Gln Thr Glu Glu His Glu Glu Ala Gly Pro  
 300 305 310

ctg ccc acc aag gtg aac ctt gct cac tca gaa atc taagcttttt 1013

Leu Pro Thr Lys Val Asn Leu Ala His Ser Glu Ile

315

320

aaaagagtcg tggacacata aacttccatt cctcatagag ctttttaaga tggtttcatt 1073

ggacataggc cttaagaaat cactataaaa tgcaataaaa gttaccaaac tctgtgaaga 1133

ctttatttgc tgtgacttta cctgtatttt tctagtcatt taagatggac attgggttgt 1193

atttttatatt tactaatatc tgtagctact tagttagttg cattgggtttt ggtttttttc 1253

ctctcttcgc caaattctat gagctgatca ttgtggcccc gccctgccca tgccccccgt 1313

cagtcacctc acttaataac cgaaacctta ggggtgtgatg cttctgcccc gaaatggcct 1373

ccaaactgtc ctctggatta tagcagaaat gttatttaat gacactacat tttcagttgt 1433

attgaattga aatcattaaa atctatttga ataattatgt tctg 1477

<210> 176

<211> 323

<212> PRT

<213> Mus musculus

<400> 176

Met Ala Ala Pro Lys Gly Lys Leu Trp Val Gln Ala Gln Leu Gly Leu

1

5

10

15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr

20

25

30

Ala Ala Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys

35

40

45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu

50

55

60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys

65

70

75

80

Gln Phe Val Asp Asp Gly Leu Asp Leu Asn Arg Thr Lys Leu Glu Cys  
85 90 95  
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Pro Asp Glu Gln Tyr Ala  
100 105 110  
Cys His Leu Gly Cys Gln Asp Gln Leu Pro Phe Ala Glu Leu Arg Gln  
115 120 125  
Glu Gln Leu Met Ser Leu Met Pro Arg Met His Leu Leu Phe Pro Leu  
130 135 140  
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser  
145 150 155 160  
Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys  
165 170 175  
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro Gln Leu  
180 185 190  
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser  
195 200 205  
Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Tyr Leu Glu Glu  
210 215 220  
Glu Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
225 230 235 240  
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile  
245 250 255  
Cys Cys Ala Ala Val Ala Thr Ala Val Glu Gln Tyr Val Pro Pro Glu  
260 265 270  
Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys Leu  
275 280 285  
Ser Arg Tyr Pro Ala Pro Ser Leu Val Ile Val Arg Ser Gln Thr Glu

290 295 300  
Glu His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala His  
305 310 315 320  
Ser Glu Ile

<210> 177

<211> 1696

## <212> DNA

<213> Homo sapiens

**<220>**

<221> CDS

$\langle 222 \rangle$  (251).. (1219)

<400> 177

aggccccgct tcgcgctaac gcttgcgatg gttgaattcc cctcctcacg ccagcctagg 60  
agaagaagtt cgtagtccca gaggtgaggc aggaggcggc agtttctggc gggtgagggc 120  
ggagctgaag tgacagcgga ggcggaagca acggtcggtg gggcggagaa gggggctggc 180  
cccaggagga ggaggaaacc cttccgagaa aacagcaaca agctgagctg ctgtgacaga 240  
ggggaacaag atg gcg gcg ccg aag ggg agc ctc tgg gtg agg acc caa 289

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln

1	5	10	
ctg ggg ctc ccg ccg ctg ctg ctg ctg acc atg gcc ttg gcc gga ggt			337
Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly			

15	20	25	
tcg ggg acc gct	tcg gct gaa gca ttt gac	tcg gtc ttg ggt gat acg	385
Ser Gly Thr Ala	Ser Ala Glu Ala Phe Asp	Ser Val Leu Gly Asp Thr	
30	35	40	45
gcg tct tgc cac	cgg gcc tgt cag ttg acc	tac ccc ttg cac acc tac	433

Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr	
50 55 60	
cct aag gaa gag gag ttg tac gca tgt cag aga ggt tgc agg ctg ttt	481
Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe	
65 70 75	
tca att tgt cag ttt gtg gat gat gga att gac tta aat cga act aaa	529
Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys	
80 85 90	
ttg gaa tgt gaa tct gca tgt aca gaa gca tat tcc caa tct gat gag	577
Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu	
95 100 105	
caa tat gct tgc cat ctt ggt tgc cag aat cag ctg cca ttc gct gaa	625
Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu	
110 115 120 125	
ctg aga caa gaa caa ctt atg tcc ctg atg cca aaa atg cac cta ctc	673
Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu	
130 135 140	
ttt cct cta act ctg gtg agg tca ttc tgg agt gac atg atg gac tcc	721
Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser	
145 150 155	
gca cag agc ttc ata acc tct tca tgg act ttt tat ctt caa gcc gat	769
Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp	
160 165 170	
gac gga aaa ata gtt ata ttc cag tct aag cca gaa atc cag tac gca	817
Asp Gly Lys Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala	
175 180 185	
cca cat ttg gag cag gag cct aca aat ttg aga gaa tca tct cta agc	865

Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser  
 190 195 200 205  
 aaa atg tcc tat ctg caa atg aga aat tca caa gcg cac agg aat ttt 913  
 Lys Met Ser Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe  
 210 215 220  
 ctt gaa gat gga gaa agt gat ggc ttt tta aga tgc ctc tct ctt aac 961  
 Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn  
 225 230 235  
 tct ggg tgg att tta act aca act ctt gtc ctc tcg gtg atg gta ttg 1009  
 Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu  
 240 245 250  
 ctt tgg att tgt tgt gca act gtt gct aca gct gtg gag cag tat gtt 1057  
 Leu Trp Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val  
 255 260 265  
 ccc tct gag aag ctg agt atc tat ggt gac ttg gag ttt atg aat gaa 1105  
 Pro Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu  
 270 275 280 285  
 caa aag cta aac aga tat cca gct tct tct ctt gtg gtt gtt aga tct 1153  
 Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser  
 290 295 300  
 aaa act gaa gat cat gaa gaa gca ggg cct cta cct aca aaa gtg aat 1201  
 Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn  
 305 310 315  
 ctt gct cat tct gaa att taagcatttt tcttttaaaa gacaagtgtg 1249  
 Leu Ala His Ser Glu Ile  
 320  
 atagacatct aaaattccac tctcataga gctttttaaaa tggtttcatt ggatataggc 1309

cttagaat cactataaaa tgcaaataaa gttactcaaa tctgtgaaga ctgtatttgc 1369  
 tataacttta ttggtattgt tttttagta atttaagagg tggatgtttg ggattgtatt 1429  
 attatatttac taatatctgt agctattttg ttttttgctt tggttattgt ttttttcct 1489  
 tttcttagct atgagctgat cattgctcct tctcacctcc tgccatgata ctgtcagtta 1549  
 ccttagttaa caagctgaat atttagtaga aatgatgctt ctgctcagga atggcccaca 1609  
 aatctgtaat ttgaaattta gcaggaaatg acctttaatg acactacatt ttcaggaact 1669  
 gaaatcatta aaattttatt tgaataa 1696

<210> 178

<211> 323

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu

1 5 10 15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr

20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys

35 40 45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu

50 55 60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys

65 70 75 80

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys

85 90 95

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala

100 105 110



Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln  
 115 120 125  
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu  
 130 135 140  
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser  
 145 150 155 160  
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys  
 165 170 175  
 Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu  
 180 185 190  
 Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser  
 195 200 205  
 Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp  
 210 215 220  
 Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
 225 230 235 240  
 Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile  
 245 250 255  
 Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser Glu  
 260 265 270  
 Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys Leu  
 275 280 285  
 Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr Glu  
 290 295 300  
 Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala His  
 305 310 315 320  
 Ser Glu Ile

&lt;210&gt; 179

&lt;211&gt; 1466

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (18).. (989)

&lt;400&gt; 179

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ggggagaggg gaacaag atg gcg gcg ccg aag ggg agc ctc tgg gtg agg      50
      Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg
              1              5              10

acc caa ctg ggg ctc ccg ccg ctg ctg ctg ctg acc atg gcc ttg gcc      98
Thr Gln Leu Gly Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala
              15              20              25

gga ggt tcg ggg acc gct tcg gct gaa gca ttt gac tcg gtc ttg ggt      146
Gly Gly Ser Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly
              30              35              40

gat acg gcg tct tgc cac ccg gcc tgt cag ttg acc tac ccc ttg cac      194
Asp Thr Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His
              45              50              55

acc tac cct aag gaa gag gag ttg tac gca tgt cag aga ggt tgc agg      242
Thr Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
              60              65              70              75

ctg ttt tca att tgt cag ttt gtg gat gat gga att gac tta aat cga      290
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg

```

80	85	90	
act aaa ttg gaa tgt gaa tct gca tgt aca gaa gca tat tcc caa tct			338
Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser			
95	100	105	
gat gag caa tat gct tgc cat ctt ggt tgc cag aat cag ctg cca ttc			386
Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe			
110	115	120	
gct gaa ctg aga caa gaa caa ctt atg tcc ctg atg cca aaa atg cac			434
Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His			
125	130	135	
cta ctc ttt cct cta act ctg gtg agg tca ttc tgg agt gac atg atg			482
Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met			
140	145	150	155
gac tcc gca cag agc ttc ata acc tct tca tgg act ttt tat ctt caa			530
Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln			
160	165	170	
gcc gat gac gga aaa ata gtt ata ttc cag tct aag cca gaa atc cag			578
Ala Asp Asp Gly Lys Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln			
175	180	185	
tac gca cca cat ttg gag cag gag cct aca aat ttg aga gaa tca tct			626
Tyr Ala Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser			
190	195	200	
cta agc aaa atg tcc tca gat ctg caa atg aga aat tca caa gcg cac			674
Leu Ser Lys Met Ser Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His			
205	210	215	
agg aat ttt ctt gaa gat gga gaa agt gat ggc ttt tta aga tgc ctc			722
Arg Asn Phe Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu			

220                      225                      230                      235  
 tct ctt aac tct ggg tgg att tta act aca act ctt gtc ctc tcg gtg 770  
 Ser Leu Asn Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val  
                     240                      245                      250  
 atg gta ttg ctt tgg att tgt tgt gca act gtt gct aca gct gtg gag 818  
 Met Val Leu Leu Trp Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu  
                     255                      260                      265  
 cag tat gtt ccc tct gag aag ctg agt atc tat ggt gac ttg gag ttt 866  
 Gln Tyr Val Pro Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe  
                     270                      275                      280  
 atg aat gaa caa aag cta aac aga tat cca gct tct tct ctt gtg gtt 914  
 Met Asn Glu Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val  
                     285                      290                      295  
 gtt aga tct aaa act gaa gat cat gaa gaa gca ggg cct cta cct aca 962  
 Val Arg Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr  
 300                      305                      310                      315  
 aaa gtg aat ctt gct cat tct gaa att taagcatttt tcttttaaaa 1009  
 Lys Val Asn Leu Ala His Ser Glu Ile  
                     320  
 gacaagtgta atagacatct aaaattccac tctcataga gcttttaaaa tggtttcatt 1069  
 ggatataggc cttaagaaat cactataaaa tgcaaataaa gttactcaaa tctgtgaaga 1129  
 ctgtatttgc tataacttta ttggtattgt tttttagta atttaagagg tggatgtttg 1189  
 ggattgtatt attattttac taatatctgt agctattttg ttttttgctt tggttattgt 1249  
 ttttttcct tttcttagct atgagctgat cattgctcct tctcacctcc tgccatgata 1309  
 ctgtcagtta ccttagtta caagctgaat atttagtaga aatgatgctt ctgctcagga 1369  
 atggcccaca aatctgtaat ttgaaattta gcaggaaatg acctttaatg aactacatt 1429  
 ttcaggaaact gaaatcatta aaattttatt tgaataa 1466

&lt;210&gt; 180

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu  
 1 5 10 15  
 Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr  
 20 25 30  
 Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys  
 35 40 45  
 His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu  
 50 55 60  
 Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys  
 65 70 75 80  
 Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys  
 85 90 95  
 Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala  
 100 105 110  
 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln  
 115 120 125  
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu  
 130 135 140  
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser  
 145 150 155 160  
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys

	165	170	175
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu			
	180	185	190
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser			
	195	200	205
Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu			
	210	215	220
Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly			
225	230	235	240
Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp			
	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser			
	260	265	270
Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys			
	275	280	285
Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr			
	290	295	300
Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala			
305	310	315	320
His Ser Glu Ile			

&lt;210&gt; 181

&lt;211&gt; 1831

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (226).. (1359)

&lt;400&gt; 181

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 ctgctaggtg tccactggag tgtgttacat ctcgggacct ttagaggaat tcggagtgcg 120  
 gggctgtggc tgctgtctcc ccattcagaa gccacttgct agtagctact gaaaggctct 180  
 tcattgtctc ttctgtcca ggaacaccgg tctaggaagc agaag atg cca tac tcc 237

Met Pro Tyr Ser

1

aac ctg cat cca gcc atc cca cgg ccc aga ggt cac cgc tcc aaa tat 285  
 Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His Arg Ser Lys Tyr  
 5 10 15 20  
 gta gcc ctc atc ttt ctg gtg gcc agc ctg atg atc ctt tgg gtg gca 333  
 Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile Leu Trp Val Ala  
 25 30 35  
 aag gat cca cca aat cac act ctg aag tac cta gca ctt cac cta gcc 381  
 Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala Leu His Leu Ala  
 40 45 50  
 tcg cac gaa ctt gga cta ctg ttg aaa aac ctc tgc tgt ctg gct gaa 429  
 Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys Cys Leu Ala Glu  
 55 60 65  
 gag ctg tgc cat gtc cag tcc agg tac cag ggc agc tac tgg aag gct 477  
 Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser Tyr Trp Lys Ala  
 70 75 80  
 gtg cgc gcc tgc ctg gga tgc ccc atc cac tgt atg gct atg att cta 525  
 Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met Ala Met Ile Leu  
 85 90 95 100  
 cta tcg tct tat ttc tat ttc ctc caa aac act gct gac ata tac ctc 573

Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala Asp Ile Tyr Leu	
105	110
115	
agt tgg atg ttt ggc ctt ctg gtc ctc tat aag tcc cta agc atg ctc	621
Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser Leu Ser Met Leu	
120	125
130	
ctg ggc ctt cag agc ttg act cca gcg gaa gtc tct gca gtc tgt gaa	669
Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser Ala Val Cys Glu	
135	140
145	
gaa aag aag tta aat gtt gcc cac ggg ctg gcc tgg tca tac tac att	717
Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile	
150	155
160	
ggg tac ttg cgg ttg atc tta cca ggg ctc cag gcc cgg atc cga atg	765
Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala Arg Ile Arg Met	
165	170
175	180
ttc aat cag cta cat aac aac atg ctc agt ggt gca ggg agc cga aga	813
Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala Gly Ser Arg Arg	
185	190
195	
ctg tac atc ctc ttt cca ttg gac tgt ggg gtg cct gac aac ctg agt	861
Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser	
200	205
210	
gta gtt gac ccc aac att cga ttc cga gat atg ctg ccc cag caa aac	909
Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu Pro Gln Gln Asn	
215	220
225	
atc gac cgt gct ggc atc aag aat cgg gtt tat tcc aac agc gtc tac	957
Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser Asn Ser Val Tyr	
230	235
240	
gag att ctg gag aac gga cag cca gca ggc gtc tgt atc ctg gag tac	1005



Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys Ile Leu Glu Tyr  
 245 250 255 260  
 gcc acc ccc ttg cag acc ctg ttt gcc atg tca cag gat gcc aaa gct 1053  
 Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Asp Ala Lys Ala  
 265 270 275  
 ggc ttc agt cgg gag gat cgg ctt gag cag gct aaa ctc ttc tgc cgg 1101  
 Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg  
 280 285 290  
 aca ctt gag gaa atc ctg gaa gat gtc ccc gag tct cga aat aac tgc 1149  
 Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser Arg Asn Asn Cys  
 295 300 305  
 cgc ctc att gtc tac caa gaa ccc aca gac gga aac agt ttc tca ctg 1197  
 Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn Ser Phe Ser Leu  
 310 315 320  
 tct cag gag gtg ctc cgg cac att cgt cag gaa gaa aag gag gag gtt 1245  
 Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu Lys Glu Glu Val  
 325 330 335 340  
 acc atg aat gcc ccc atg acc tca gtg gca cct cct ccc tcc gta ctg 1293  
 Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro Pro Ser Val Leu  
 345 350 355  
 tcc caa gag cca aga ctc ctc atc agt ggt atg gat cag cct ctc cca 1341  
 Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp Gln Pro Leu Pro  
 360 365 370  
 ctc cgc act gac ctc atc tgaggcatgg gacagccttg tctgggctct 1389  
 Leu Arg Thr Asp Leu Ile  
 375  
 agtgatcctt tagcctcctg actgagcctt ccttcaatgg ttgggggcct cagagacttc 1449

acatctccag atgagtccca cattcctggg caagccattt atttcacctc tctgagcctc 1509  
 aaccaaccct actatgaaag gaggtcataa tgcgttcctt gccagccaa aggattttat 1569  
 atatgtagaa gttggtgtca atgcctggta aacttgagag aaaggccaag tacttcccgt 1629  
 ggatgctgca gacattccct gctctctgtt gacctgtgtg gatggtacca gcagacttcc 1689  
 aacctccag cttctggtca cgtgtgttca atgggagctt aagtagatgg cgagaggag 1749  
 aaggaacatt tgttctgtta gctgtataca atcacagtgg gctggcctgt caactgcctt 1809  
 ctttaataaac acatctattc tc 1831

<210> 182

<211> 378

<212> PRT

<213> Mus musculus

<400> 182

Met Pro Tyr Ser Asn Leu His Pro Ala Ile Pro Arg Pro Arg Gly His

1 5 10 15

Arg Ser Lys Tyr Val Ala Leu Ile Phe Leu Val Ala Ser Leu Met Ile

20 25 30

Leu Trp Val Ala Lys Asp Pro Pro Asn His Thr Leu Lys Tyr Leu Ala

35 40 45

Leu His Leu Ala Ser His Glu Leu Gly Leu Leu Leu Lys Asn Leu Cys

50 55 60

Cys Leu Ala Glu Glu Leu Cys His Val Gln Ser Arg Tyr Gln Gly Ser

65 70 75 80

Tyr Trp Lys Ala Val Arg Ala Cys Leu Gly Cys Pro Ile His Cys Met

85 90 95

Ala Met Ile Leu Leu Ser Ser Tyr Phe Tyr Phe Leu Gln Asn Thr Ala

100 105 110

Asp Ile Tyr Leu Ser Trp Met Phe Gly Leu Leu Val Leu Tyr Lys Ser  
 115 120 125  
 Leu Ser Met Leu Leu Gly Leu Gln Ser Leu Thr Pro Ala Glu Val Ser  
 130 135 140  
 Ala Val Cys Glu Glu Lys Lys Leu Asn Val Ala His Gly Leu Ala Trp  
 145 150 155 160  
 Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Gly Leu Gln Ala  
 165 170 175  
 Arg Ile Arg Met Phe Asn Gln Leu His Asn Asn Met Leu Ser Gly Ala  
 180 185 190  
 Gly Ser Arg Arg Leu Tyr Ile Leu Phe Pro Leu Asp Cys Gly Val Pro  
 195 200 205  
 Asp Asn Leu Ser Val Val Asp Pro Asn Ile Arg Phe Arg Asp Met Leu  
 210 215 220  
 Pro Gln Gln Asn Ile Asp Arg Ala Gly Ile Lys Asn Arg Val Tyr Ser  
 225 230 235 240  
 Asn Ser Val Tyr Glu Ile Leu Glu Asn Gly Gln Pro Ala Gly Val Cys  
 245 250 255  
 Ile Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln  
 260 265 270  
 Asp Ala Lys Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala Lys  
 275 280 285  
 Leu Phe Cys Arg Thr Leu Glu Glu Ile Leu Glu Asp Val Pro Glu Ser  
 290 295 300  
 Arg Asn Asn Cys Arg Leu Ile Val Tyr Gln Glu Pro Thr Asp Gly Asn  
 305 310 315 320  
 Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Ile Arg Gln Glu Glu

325 330 335  
 Lys Glu Glu Val Thr Met Asn Ala Pro Met Thr Ser Val Ala Pro Pro  
 340 345 350  
 Pro Ser Val Leu Ser Gln Glu Pro Arg Leu Leu Ile Ser Gly Met Asp  
 355 360 365  
 Gln Pro Leu Pro Leu Arg Thr Asp Leu Ile  
 370 375

<210> 183

<211> 2109

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (243).. (1379)

<400> 183

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 gagtgtgtgg agtcctgctc aggtgttagg tacagtgtgt ttgatcgtgg tggcttgagg 120  
 ggaacccgct gttcagagct gtgactgcgg ctgcactcag agaagctgcc cttggctgct 180  
 cgtagcgccg ggccttctct cctcgtcatc atccagagca gccagtgtcc gggaggcaga 240  
 ag atg ccc cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt 287

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly

1 5 10 15  
 cac ggg gcc cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg 335  
 His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val  
 20 25 30  
 acc ctt tgg ggg cta gga gag cca cca gag cac act ctc cgg tac ctg 383

Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu  
                     35                                    40                                    45  
 gtc ctc cac cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc 431  
 Val Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val  
                     50                                    55                                    60  
 tgc agc ctg gct gag gag ctg cgc cac atc cac tcc agg tac cgg ggc 479  
 Cys Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly  
                     65                                    70                                    75  
 agc tac tgg agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt 527  
 Ser Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg  
                     80                                    85                                    90                                    95  
 ggg gcc ctg ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat 575  
 Gly Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn  
                                     100                                    105                                    110  
 gcg gtc ggc ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg 623  
 Ala Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser  
                                     115                                    120                                    125  
 cag gca ctg aac atc ctc ctg ggc ctc aag ggc ctg gcc cca gct gag 671  
 Gln Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu  
                                     130                                    135                                    140  
 atc tct gca gtg tgt gaa aaa ggg aat ttc aac gtg gcc cat ggg ctg 719  
 Ile Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu  
                                     145                                    150                                    155  
 gca tgg tca tat tac atc gga tat ctg cgg ctg atc ctg cca gag ctc 767  
 Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu  
                                     160                                    165                                    170                                    175  
 cag gcc cgg att cga act tac aat cag cat tac aac aac ctg cta cgg 815

Gln Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg  
 180 185 190  
 ggt gca gtg agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg 863  
 Gly Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly  
 195 200 205  
 gtg cct gat aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat 911  
 Val Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp  
 210 215 220  
 aaa ctg ccc cag cag acc ggt gac cgt gct ggc atc aag gat cgg gtt 959  
 Lys Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val  
 225 230 235  
 tac agc aac agc atc tat gag ctt ctg gag aac ggg cag cgg gcg ggc 1007  
 Tyr Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly  
 240 245 250 255  
 acc tgt gtc ctg gag tac gcc acc ccc ttg cag act ttg ttt gcc atg 1055  
 Thr Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met  
 260 265 270  
 tca caa tac agt caa gct ggc ttt agc cgg gag gat agg ctt gag cag 1103  
 Ser Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln  
 275 280 285  
 gcc aaa ctc ttc tgc cgg aca ctt gag gac atc ctg gca gat gcc cct 1151  
 Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro  
 290 295 300  
 gag tct cag aac aac tgc cgc ctc att gcc tac cag gaa cct gca gat 1199  
 Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp  
 305 310 315  
 gac agc agc ttc tcg ctg tcc cag gag gtt ctc cgg cac ctg cgg cag 1247

Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln  
 320 325 330 335  
 gag gaa aag gaa gag gtt act gtg ggc agc ttg aag acc tca gcg gtg 1295  
 Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val  
 340 345 350  
 ccc agt acc tcc acg atg tcc caa gag cct gag ctc ctc atc agt gga 1343  
 Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly  
 355 360 365  
 atg gaa aag ccc ctc cct ctc cgc acg gat ttc tct tgagaccag 1389  
 Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser  
 370 375  
 ggtcaccagg ccagagcctc cagtgggtctc caagcctctg gactgggggc tctcttcagt 1449  
 ggctgaatgt ccagcagagc tatttccttc cacagggggc cttgcaggga aggggtccagg 1509  
 acttgacatc ttaagatgcg tcttgctccc ttgggccagt catttcccct ctctgagcct 1569  
 cgggtgtcttc aacctgtgaa atgggatcat aatcaactgcc ttacctccct cacggttggtt 1629  
 gtgaggactg agtgtgtgga agtttttcat aaactttgga tgctagtgtgta cttaggggggt 1689  
 gtgccagggtg tctttcatgg ggccttcag acccaactccc cacccttctc cccttccttt 1749  
 gcccggggac gccgaactct ctcaatggta tcaacaggct ccttcgccct ctggctcctg 1809  
 gtcatgttcc attattgggg agccccagca gaagaatgga gaggaggagg aggctgagtt 1869  
 tgggggtattg aatcccccg cttccaccct gcagcatcaa ggttgctatg gactctcctg 1929  
 ccgggcaact cttgcgtaat catgactatc tctaggattc tggcaccact tccttcctg 1989  
 gcccttaag cctagctgtg tatcggcacc cccacccac tagagtactc cctctcactt 2049  
 gcggtttcct tatactccac ccctttctca acggtccttt tttaaagcac atctcagatt 2109

&lt;210&gt; 184

&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His  
 1 5 10 15  
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr  
 20 25 30  
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val  
 35 40 45  
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys  
 50 55 60  
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser  
 65 70 75 80  
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly  
 85 90 95  
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala  
 100 105 110  
 Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln  
 115 120 125  
 Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile  
 130 135 140  
 Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala  
 145 150 155 160  
 Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln  
 165 170 175  
 Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly  
 180 185 190  
 Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val



195	200	205
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys		
210	215	220
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr		
225	230	235
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr		
245	250	255
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser		
260	265	270
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala		
275	280	285
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu		
290	295	300
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp		
305	310	315
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu		
325	330	335
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro		
340	345	350
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly Met		
355	360	365
Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser		
370	375	

&lt;210&gt; 185

&lt;211&gt; 2262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (58)..(1482)

&lt;400&gt; 185

aagcccagtg gtcctggccg tgcgccggag gcagcggcgg cgtggcgcag cggcgac	57
atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc	105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr	
1                      5                      10                      15	
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt	153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu	
20                      25                      30	
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac	201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp	
35                      40                      45	
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt	249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser	
50                      55                      60	
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc	297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe	
65                      70                      75                      80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc	345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly	
85                      90                      95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc	393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr	
100                      105                      110	

gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg 441  
 Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg  
 115 120 125  
 gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc 489  
 Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala  
 130 135 140  
 atc ttc atg gtg ata act gca ctg gtg aag gtg gac act tcc tcc tgg 537  
 Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp  
 145 150 155 160  
 acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc 585  
 Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser  
 165 170 175  
 ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc 633  
 Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser  
 180 185 190  
 ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc 681  
 Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly  
 195 200 205  
 ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt 729  
 Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser  
 210 215 220  
 gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc acc atc ttc 777  
 Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
 225 230 235 240  
 ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat 825  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr  
 245 250 255

gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt	873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly	
260 265 270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275 280 285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290 295 300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser	
305 310 315 320	
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt	1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly	
325 330 335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc	1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe	
340 345 350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg	1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp	
355 360 365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc	1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu	
370 375 380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc	1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro	
385 390 395 400	

cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca 1305  
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala  
 405 410 415  
 ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353  
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
 420 425 430  
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401  
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
 435 440 445  
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449  
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly  
 450 455 460  
 tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga 1502  
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile  
 465 470 475  
 cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggctg ggggccatgg 1562  
 aggaaaggcc taaagtttca ctggtggaca gagagcagag cacactcggg cctcatccct 1622  
 cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcat 1682  
 attaacagaa cactcctgag acagttgaag aagaaatagc acaaatacagg ggtactccct 1742  
 tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtgtt 1802  
 cgccctagag ttattacaaa gccagtgcca aaaccagcc atgggctctt tgcaacctcc 1862  
 cagctgcgct cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1922  
 gaaggggtct ccttgaatg gaagtcccct ggcattgtca gtctcaggc ccaagactca 1982  
 agtgtgcaca gaccctgtg ttctgtgggt gaacaactgc ccactaacca gactggaaaa 2042  
 ccagaaaga tgggccttcc atgaatgctt cattccagag ggaccagagg gcctccctgt 2102  
 gcaagggatc aagcatgtct ggcctgggtt ttcaaaaaaa gagggatcct catgacctgg 2162  
 tgggtctatgg cctgggtcaa gatgagggtc ttttagtggt cctgtttaca acatgtcaaa 2222

gccattgggtt caaggcgta ataaatactt gcgtattcaa

2262

&lt;210&gt; 186

&lt;211&gt; 475

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

1 5 10 15

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

20 25 30

Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp

35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser

50 55 60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe

65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly

85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr

100 105 110

Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg

115 120 125

Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala

130 135 140

Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp

145 150 155 160

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser  
165 170 175  
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser  
180 185 190  
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly  
195 200 205  
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser  
210 215 220  
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
225 230 235 240  
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr  
245 250 255  
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly  
260 265 270  
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser  
275 280 285  
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys  
290 295 300  
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser  
305 310 315 320  
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly  
325 330 335  
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe  
340 345 350  
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp  
355 360 365  
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu

370                      375                      380  
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro  
 385                      390                      395                      400  
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala  
                          405                      410                      415  
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
                          420                      425                      430  
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
                          435                      440                      445  
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly  
                          450                      455                      460  
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile  
 465                      470                      475

<210> 187

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)..(1482)

<400> 187

aagcccagtg gtcctggccg tgcgccggag gcagcggcgg cgtggcgcag cggcgac 57  
 atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc 105  
 Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr  
 1                      5                      10                      15  
 tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt 153



Tyr	Arg	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	Leu	Leu				
20								25								30			
gag	aag	ctg	ctg	gac	cgc	ccg	ccc	cct	ggc	ctg	cag	agg	ccc	gag	gac	201			
Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	Pro	Glu	Asp				
35								40								45			
cgc	ttc	tgt	ggc	aca	tac	atc	atc	ttc	ttc	agc	ctg	ggc	att	ggc	agt	249			
Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	Gly	Ile	Gly	Ser				
50								55								60			
cta	ctg	cca	tgg	aac	ttc	ttt	atc	act	gcc	aag	gag	tac	tgg	atg	ttc	297			
Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	Glu	Tyr	Trp	Met	Phe				
65								70								75			
aaa	ctc	cgc	aac	tcc	tcc	agc	cca	gcc	acc	ggg	gag	gac	cct	gag	ggc	345			
Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	Gly	Glu	Asp	Pro	Glu	Gly				
				85								90							
tca	gac	atc	ctg	aac	tac	ttt	gag	agc	tac	ctt	gcc	gtt	gcc	tcc	acc	393			
Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	Tyr	Leu	Ala	Val	Ala	Ser	Thr				
100								105								110			
gtg	ccc	tcc	atg	ctg	tgc	ctg	gtg	gcc	aac	ttc	ctg	ctt	gtc	aac	agg	441			
Val	Pro	Ser	Met	Leu	Cys	Leu	Val	Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg				
115								120								125			
gtt	gca	gtc	cac	atc	cgt	gtc	ctg	gcc	tca	ctg	acg	gtc	atc	ctg	gcc	489			
Val	Ala	Val	His	Ile	Arg	Val	Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala				
130								135								140			
atc	ttc	atg	gtg	ata	act	gca	ctg	gtg	aag	gtg	gac	act	ttc	tcc	tgg	537			
Ile	Phe	Met	Val	Ile	Thr	Ala	Leu	Val	Lys	Val	Asp	Thr	Phe	Ser	Trp				
145								150								155			
acc	cgt	ggc	ttt	ttt	gcg	gtc	acc	att	gtc	tgc	atg	gtg	atc	ctc	agc	585			

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser	
165 170 175	
ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc	633
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser	
180 185 190	
ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc	681
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly	
195 200 205	
ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt	729
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser	
210 215 220	
gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc acc atc ttc	777
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	
225 230 235 240	
ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat	825
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr	
245 250 255	
gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt	873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly	
260 265 270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275 280 285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290 295 300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017

Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser  
 305 310 315 320  
 ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt 1065  
 Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly  
 325 330 335  
 tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc 1113  
 Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe  
 340 345 350  
 ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg 1161  
 Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp  
 355 360 365  
 atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc 1209  
 Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu  
 370 375 380  
 ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc 1257  
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro  
 385 390 395 400  
 cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca 1305  
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala  
 405 410 415  
 ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353  
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
 420 425 430  
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401  
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
 435 440 445  
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449

Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly

450

455

460

tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggagg gacacaagga 1502

Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile

465

470

475

cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggtg ggggccatgg 1562

aggaaaggcc taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1622

cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcatt 1682

attaacagaa cactcctgag acagttgaag aagaaatagc acaaatacagg ggtactccct 1742

tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtggt 1802

cgccttagag ttattacaaa gccagtgcca aaaccagcc atgggctctt tgcaacctcc 1862

cagctgcgt cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttacct 1922

gaaggggtct ccctggaatg gaagtccct ggcatggtca gtctcaggc ccaagactca 1982

agtgtgcaca gaccctgtg ttctgtgggt gaacaactgc ccactaacca gactggaaaa 2042

cccagaaaga tgggccttcc atgaatgctt cattccagag ggaccagagg gcctccctgt 2102

gcaagggatc aagcatgtct ggctgggtt ttcaaaaaaa gagggatcct catgacctgg 2162

tggtctatgg cctgggtcaa gatgagggtc ttttagtggt cctgtttaca acatgtcaaa 2222

gccattggtt caaggcgta ataaatactt gcgtattcaa 2262

<210> 188

<211> 475

<212> PRT

<213> Homo sapiens

<400> 188

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

1

5

10

15

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

20	25	30
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp		
35	40	45
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser		
50	55	60
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe		
65	70	75
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly		
85	90	95
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr		
100	105	110
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg		
115	120	125
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala		
130	135	140
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp		
145	150	155
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser		
165	170	175
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser		
180	185	190
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly		
195	200	205
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser		
210	215	220
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe		
225	230	235
		240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr  
245 250 255  
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly  
260 265 270  
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser  
275 280 285  
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys  
290 295 300  
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser  
305 310 315 320  
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly  
325 330 335  
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe  
340 345 350  
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp  
355 360 365  
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu  
370 375 380  
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro  
385 390 395 400  
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala  
405 410 415  
Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
420 425 430  
Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
435 440 445  
Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly

450	455	460	
Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile			
465	470	475	
<210>	189		
<211>	2262		
<212>	DNA		
<213>	Homo sapiens		
<220>			
<221>	CDS		
<222>	(58)..(1482)		
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atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc			105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr			
1                      5                      10                      15			
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt			153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu			
20                      25                      30			
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac			201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp			
35                      40                      45			
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt			249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser			
50                      55                      60			
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc			297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe			

65	70	75	80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc				345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly				
	85	90	95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc				393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr				
	100	105	110	
gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg				441
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg				
	115	120	125	
gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc				489
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala				
	130	135	140	
atc ttc atg gtg ata act gca ctg gtg aag gtg gac act tcc tcc tgg				537
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp				
	145	150	155	160
acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc				585
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser				
	165	170	175	
ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc				633
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser				
	180	185	190	
ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc				681
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly				
	195	200	205	
ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt				729
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser				



210	215	220	
gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc act gtc ttc			777
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe			
225	230	235	240
ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat			825
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr			
245	250	255	
gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt			873
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly			
260	265	270	
gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc			921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser			
275	280	285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag			969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys			
290	295	300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc			1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser			
305	310	315	320
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt			1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly			
325	330	335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc			1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe			
340	345	350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg			1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp			

355	360	365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc			1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu			
370	375	380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc			1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro			
385	390	395	400
cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca			1305
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala			
405	410	415	
ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg			1353
Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu			
420	425	430	
gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc			1401
Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala			
435	440	445	
acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc			1449
Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly			
450	455	460	
tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga			1502
Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile			
465	470	475	
cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggtg ggggccatgg			1562
aggaaaggcc taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct			1622
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcct			1682
attaacagaa cactcctgag acagttgaag aagaaatagc acaaatacagg ggtactccct			1742
tcacagctga tggttaacat tccaccttct ttctagccct tcaaagatgc tgccagtgtt			1802

cgccctagag	ttattacaaa	gccagtgcc	aaaccagcc	atgggctctt	tgcaacctcc	1862
cagctgcgct	cattccagct	gacagcgaga	tgcaagcaaa	tgctcagctc	tccttaccct	1922
gaaggggtct	ccctggaatg	gaagtcccct	ggcatggtca	gtcctcaggc	ccaagactca	1982
agtgtgcaca	gacccctgtg	ttctgtgggt	gaacaactgc	ccactaacca	gactggaaaa	2042
cccagaaaga	tgggccttcc	atgaatgctt	cattccagag	ggaccagagg	gcctccctgt	2102
gcaagggatc	aagcatgtct	ggcctggggt	ttcaaaaaaa	gagggatcct	catgacctgg	2162
tggtctatgg	cctgggtcaa	gatgagggtc	ttttagtgtt	cctgtttaca	acatgtcaaa	2222
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$\langle 210 \rangle$  190

**<211> 475**

&lt;212&gt; PRT

<213> Homo sapiens

<400> 190

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr

**1                  5                  10                  15**

Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu

20                      25                      30

Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp

35                      40                      45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser

50                      55                      60

Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe

65                      70                      75                      80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly

85                      90                      95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr

100 105 110  
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg  
115 120 125  
Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala  
130 135 140  
Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Ser Ser Trp  
145 150 155 160  
Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser  
165 170 175  
Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser  
180 185 190  
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly  
195 200 205  
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser  
210 215 220  
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe  
225 230 235 240  
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr  
245 250 255  
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly  
260 265 270  
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser  
275 280 285  
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys  
290 295 300  
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser  
305 310 315 320

Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly  
                             325                            330                            335  
 Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe  
                             340                            345                            350  
 Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp  
                             355                            360                            365  
 Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu  
                             370                            375                            380  
 Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro  
 385                            390                            395                            400  
 Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala  
                             405                            410                            415  
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
                             420                            425                            430  
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
                             435                            440                            445  
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly  
                             450                            455                            460  
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile  
 465                            470                            475

<210> 191

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

&lt;222&gt; (58)..(1482)

&lt;400&gt; 191

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atg gcc gtt gtc tca gag gac gac ttt cag cac agt tca aac tcc acc	105
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser Thr	
1                      5                      10                      15	
tac aga acc aca agc agc agt ctc cga gct gac cag gag gca ctg ctt	153
Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu	
20                      25                      30	
gag aag ctg ctg gac cgc ccg ccc cct ggc ctg cag agg ccc gag gac	201
Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp	
35                      40                      45	
cgc ttc tgt ggc aca tac atc atc ttc ttc agc ctg ggc att ggc agt	249
Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser	
50                      55                      60	
cta ctg cca tgg aac ttc ttt atc act gcc aag gag tac tgg atg ttc	297
Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe	
65                      70                      75                      80	
aaa ctc cgc aac tcc tcc agc cca gcc acc ggg gag gac cct gag ggc	345
Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly	
85                      90                      95	
tca gac atc ctg aac tac ttt gag agc tac ctt gcc gtt gcc tcc acc	393
Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr	
100                      105                      110	
gtg ccc tcc atg ctg tgc ctg gtg gcc aac ttc ctg ctt gtc aac agg	441
Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg	
115                      120                      125	

gtt gca gtc cac atc cgt gtc ctg gcc tca ctg acg gtc atc ctg gcc 489  
 Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala  
 130 135 140  
 atc ttc atg gtg ata act gca ctg gtg aag gtg gac act ttc tcc tgg 537  
 Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp  
 145 150 155 160  
 acc cgt ggc ttt ttt gcg gtc acc att gtc tgc atg gtg atc ctc agc 585  
 Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser  
 165 170 175  
 ggt gcc tcc act gtc ttc agc agc agc atc tac ggc atg acc ggc tcc 633  
 Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser  
 180 185 190  
 ttt cct atg agg aac tcc cag gca ctg ata tca gga gga gcc atg ggc 681  
 Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly  
 195 200 205  
 ggg acg gtc agc gcc gtg gcc tca ttg gtg gac ttg gct gca tcc agt 729  
 Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser  
 210 215 220  
 gat gtg agg aac agc gcc ctg gcc ttc ttc ctg acg gcc act gtc ttc 777  
 Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe  
 225 230 235 240  
 ctc gtg ctc tgc atg gga ctc tac ctg ctg ctg tcc agg ctg gag tat 825  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr  
 245 250 255  
 gcc agg tac tac atg agg cct gtt ctt gcg gcc cat gtg ttt tct ggt 873  
 Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly  
 260 265 270

gaa gag gag ctt ccc cag gac tcc ctc agt gcc cct tcg gtg gcc tcc	921
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser	
275 280 285	
aga ttc att gat tcc cac aca ccc cct ctc cgc ccc atc ctg aag aag	969
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys	
290 295 300	
acg gcc agc ctg ggc ttc tgt gtc acc tac gtc ttc ttc atc acc agc	1017
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser	
305 310 315 320	
ctc atc tac ccc gcc gtc tgc acc aac atc gag tcc ctc aac aag ggt	1065
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly	
325 330 335	
tcg ggc tca ctg tgg acc acc aag ttt ttc atc ccc ctc act acc ttc	1113
Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe	
340 345 350	
ctc ctg tac aac ttt gct gac cta tgt ggc cgg cag ctc acc gcc tgg	1161
Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp	
355 360 365	
atc cag gtg cca ggg ccc aat agc aag gcg ctc cca ggg ttc gtg ctc	1209
Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu	
370 375 380	
ctc cgg acc tgc ctc atc ccc ctc ttc gtg ctc tgt aac tac cag ccc	1257
Leu Arg Thr Cys Leu Ile Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro	
385 390 395 400	
cgc gtc cac ctg aag act gtg gtc ttc cag tcc gat gtg tac ccc gca	1305
Arg Val His Leu Lys Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala	
405 410 415	



ctc ctc agc tcc ctg ctg ggg ctc agc aac ggc tac ctc agc acc ctg 1353  
 Leu Leu Ser Ser Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu  
 420 425 430  
 gcc ctc ctc tac ggg cct aag att gtg ccc agg gag ctg gct gag gcc 1401  
 Ala Leu Leu Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala  
 435 440 445  
 acg gga gtg gtg atg tcc ttt tat gtg tgc ttg ggc tta aca ctg ggc 1449  
 Thr Gly Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly  
 450 455 460  
 tca gcc tgc tct acc ctc ctg gtg cac ctc atc tagaaggag gacacaagga 1502  
 Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile  
 465 470 475  
 cattggtgct tcagagcctt tgaagatgag aagagagtgc aggagggctg ggggccatgg 1562  
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 cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata ttccagtcat 1682  
 attaacagaa cactcctgag acagttgaag aagaaatagc acaaatcagg ggtactccct 1742  
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 cagctgcgct cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttacct 1922  
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&lt;211&gt; 475

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

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Tyr Arg Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala Leu Leu  
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Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg Pro Glu Asp  
 35 40 45

Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu Gly Ile Gly Ser  
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Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys Glu Tyr Trp Met Phe  
 65 70 75 80

Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr Gly Glu Asp Pro Glu Gly  
 85 90 95

Ser Asp Ile Leu Asn Tyr Phe Glu Ser Tyr Leu Ala Val Ala Ser Thr  
 100 105 110

Val Pro Ser Met Leu Cys Leu Val Ala Asn Phe Leu Leu Val Asn Arg  
 115 120 125

Val Ala Val His Ile Arg Val Leu Ala Ser Leu Thr Val Ile Leu Ala  
 130 135 140

Ile Phe Met Val Ile Thr Ala Leu Val Lys Val Asp Thr Phe Ser Trp  
 145 150 155 160

Thr Arg Gly Phe Phe Ala Val Thr Ile Val Cys Met Val Ile Leu Ser  
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Gly Ala Ser Thr Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser

180	185	190
Phe Pro Met Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly		
195	200	205
Gly Thr Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser		
210	215	220
Asp Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Val Phe		
225	230	235
240		
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu Tyr		
245	250	255
Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe Ser Gly		
260	265	270
Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser Val Ala Ser		
275	280	285
Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro Ile Leu Lys Lys		
290	295	300
Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val Phe Phe Ile Thr Ser		
305	310	315
320		
Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile Glu Ser Leu Asn Lys Gly		
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Ser Gly Ser Leu Trp Thr Thr Lys Phe Phe Ile Pro Leu Thr Thr Phe		
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Leu Leu Tyr Asn Phe Ala Asp Leu Cys Gly Arg Gln Leu Thr Ala Trp		
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Ile Gln Val Pro Gly Pro Asn Ser Lys Ala Leu Pro Gly Phe Val Leu		
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Ser Ala Cys Ser Thr Leu Leu Val His Leu Ile  
465 470 475

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 Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile  
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 Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln  
                             55                            60                            65  
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 Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro Asp Ile Leu Ala Pro  
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 Arg Pro Trp Ser Arg Asn Ala Ala Pro Ser Ser Thr Lys Arg Arg Asp  
                             85                            90                            95                            100  
 agc aag ctg tgg agt gag acc ttc gat gtg tgc gtc aat cag atg ctt 452  
 Ser Lys Leu Trp Ser Glu Thr Phe Asp Val Cys Val Asn Gln Met Leu  
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 aca tcc aag gaa atc aaa cgt cag gag gcg atc ttt gag ctt tcc caa 500  
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**589/861**

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aaa gac tcc ctg atc gac agc tct cga gtc ttg tgt tgt cat ggt gaa	1124
Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys Cys His Gly Glu	
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ctg aag aac aat cgg ggc gtg aaa ctg cat gtt ttc ctg ttc caa gaa	1172
Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe Leu Phe Gln Glu	
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gtg ctt gtg atc act cga gcc gtc acc cac aat gag cag ctt tgc tac	1220
Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu Gln Leu Cys Tyr	
360	365
cag ctg tac cgt cag cca atc ccc gtg aaa gac ctc ctg ctg gaa gac	1268
Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu Leu Leu Glu Asp	
375	380
ctc cag gat gga gaa gtg agg ctg ggt ggc tcc ctg cga ggg gca ttc	1316
Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu Arg Gly Ala Phe	
390	395
agc aac aat gag aga att aaa aac ttc ttc aga gtc agt ttc aaa aat	1364
Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val Ser Phe Lys Asn	
405	410
gga tcc caa agt cag acc cac tcg cta caa gcc aat gac act ttc aac	1412
Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn Asp Thr Phe Asn	
425	430
aaa cag cag tgg ctt aac tgt att cgt caa gcc aaa gaa aca gtt ttg	1460
Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys Glu Thr Val Leu	
440	445
tgt gct gcc ggg caa gct ggg gtg ctt gac tcc gag gga tcg ttc cta	1508

Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu Gly Ser Phe Leu  
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 Gly Asn Ser Arg His Gly Glu Ser Asn Val  
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<211> 526

<212> PRT

<213> Homo sapiens

<400> 194

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	35		40		45										
Ala	Asn	Leu	Ile	Pro	Pro	Val	Lys	Ala	Thr	Pro	Leu	Lys	Arg	Phe	Ser
	50		55		60										
Gln	Thr	Leu	Gln	Arg	Ser	Ile	Ser	Phe	Arg	Ser	Glu	Ser	Arg	Pro	Asp
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Ile	Leu	Ala	Pro	Arg	Pro	Trp	Ser	Arg	Asn	Ala	Ala	Pro	Ser	Ser	Thr
			85		90									95	
Lys	Arg	Arg	Asp	Ser	Lys	Leu	Trp	Ser	Glu	Thr	Phe	Asp	Val	Cys	Val
	100		105		110										
Asn	Gln	Met	Leu	Thr	Ser	Lys	Glu	Ile	Lys	Arg	Gln	Glu	Ala	Ile	Phe
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Glu	Leu	Ser	Gln	Gly	Glu	Glu	Asp	Leu	Ile	Glu	Asp	Leu	Lys	Leu	Ala
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Lys	Lys	Ala	Tyr	His	Asp	Pro	Met	Leu	Lys	Leu	Ser	Ile	Met	Thr	Glu
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Gln	Glu	Leu	Asn	Gln	Ile	Phe	Gly	Thr	Leu	Asp	Ser	Leu	Ile	Pro	Leu
			165		170									175	
His	Glu	Glu	Leu	Leu	Ser	Gln	Leu	Arg	Asp	Val	Arg	Lys	Pro	Asp	Gly
	180		185		190										
Ser	Thr	Glu	His	Val	Gly	Pro	Ile	Leu	Val	Gly	Trp	Leu	Pro	Cys	Leu
	195		200		205										
Ser	Ser	Tyr	Asp	Ser	Tyr	Cys	Ser	Asn	Gln	Val	Ala	Ala	Lys	Ala	Leu
	210		215		220										
Leu	Asp	His	Lys	Lys	Gln	Asp	His	Arg	Val	Gln	Asp	Phe	Leu	Gln	Arg
225			230		235									240	

Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp Leu Trp Asn Phe Leu  
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Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro Leu Leu Leu Arg Glu  
260 265 270  
Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp Gln Gln His Leu Glu  
275 280 285  
Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala Glu Ile Asn Thr Lys  
290 295 300  
Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu Arg Leu Leu Tyr Leu  
305 310 315 320  
Glu Glu Gly Gln Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys  
325 330 335  
Cys His Gly Glu Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe  
340 345 350  
Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu  
355 360 365  
Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu  
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Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu  
385 390 395 400  
Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val  
405 410 415  
Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn  
420 425 430  
Asp Thr Phe Asn Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys  
435 440 445  
Glu Thr Val Leu Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu

450                      455                      460  
 Gly Ser Phe Leu Asn Pro Thr Thr Gly Ser Arg Glu Leu Gln Gly Glu  
 465                      470                      475                      480  
 Thr Lys Leu Glu Gln Met Asp Gln Ser Asp Ser Glu Ser Asp Cys Ser  
                          485                      490                      495  
 Met Asp Thr Ser Glu Val Ser Leu Asp Cys Glu Arg Met Glu Gln Thr  
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<213> Homo sapiens

<220>

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 cggcggcggc cgggaacg atg cat cag aag ctg ctg aag agc gcg cat tac 231

Met His Gln Lys Leu Leu Lys Ser Ala His Tyr

1

5

10

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 Ile Glu Leu Gly Ser Tyr Gln Tyr Trp Pro Val Leu Val Pro Arg Gly

15

20

25

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Ile Arg Leu Tyr Thr Tyr Glu Gln Ile Pro Gly Ser Leu Lys Asp Asn	
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ccg tac atc acc gac ggc tac cgg gcc tac ctg ccg tcc agg ctg tgt	375
Pro Tyr Ile Thr Asp Gly Tyr Arg Ala Tyr Leu Pro Ser Arg Leu Cys	
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Ile Lys Ser Leu Phe Ile Leu Ser Asn Glu Thr Val Asn Ile Trp Ser	
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His Leu Leu Gly Phe Phe Leu Phe Phe Thr Leu Gly Ile Tyr Asp Met	
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Thr Ser Val Leu Pro Ser Ala Ser Ala Ser Arg Glu Asp Phe Val Ile	
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Cys Ser Ile Cys Leu Phe Cys Phe Gln Val Cys Met Leu Cys Ser Val	
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Gly Tyr His Leu Phe Ser Cys His Arg Ser Glu Lys Thr Cys Arg Arg	
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Trp Met Ala Leu Asp Tyr Ala Gly Ile Ser Ile Gly Ile Leu Gly Cys	
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Tyr Val Ser Gly Val Phe Tyr Ala Phe Tyr Cys Asn Asn Tyr Trp Arg	
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Gln Val Tyr Leu Ile Thr Val Leu Ala Met Ile Leu Ala Val Phe Phe	
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Ala Gln Ile His Pro Asn Tyr Leu Thr Gln Gln Trp Gln Arg Leu Arg	
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tct atc atc ttt tgt tct gtt tcg gga tat gga gtg att cct act ctt	855
Ser Ile Ile Phe Cys Ser Val Ser Gly Tyr Gly Val Ile Pro Thr Leu	
205 210 215	
cac tgg gtt tgg ctc aat gga gga att ggt gct cct att gta cag gac	903
His Trp Val Trp Leu Asn Gly Gly Ile Gly Ala Pro Ile Val Gln Asp	
220 225 230 235	
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Phe Ala Pro Arg Val Ile Val Met Tyr Met Ile Ala Leu Leu Ala Phe	
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Leu Phe Tyr Ile Ser Lys Val Pro Glu Arg Tyr Phe Pro Gly Gln Leu	
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Asn Tyr Leu Gly Ser Ser His Gln Ile Trp His Ile Leu Ala Val Val	
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Met Leu Tyr Trp Trp His Gln Ser Thr Val Tyr Val Met Gln Tyr Arg	
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<211> 311

<212> PRT

<213> Homo sapiens

<400> 196

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35 40 45

Gly Tyr Arg Ala Tyr Leu Pro Ser Arg Leu Cys Ile Lys Ser Leu Phe

50 55 60

Ile Leu Ser Asn Glu Thr Val Asn Ile Trp Ser His Leu Leu Gly Phe

65 70 75 80



Phe Leu Phe Phe Thr Leu Gly Ile Tyr Asp Met Thr Ser Val Leu Pro  
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                     115                    120                    125  
 Ser Cys His Arg Ser Glu Lys Thr Cys Arg Arg Trp Met Ala Leu Asp  
                     130                    135                    140  
 Tyr Ala Gly Ile Ser Ile Gly Ile Leu Gly Cys Tyr Val Ser Gly Val  
 145                    150                    155                    160  
 Phe Tyr Ala Phe Tyr Cys Asn Asn Tyr Trp Arg Gln Val Tyr Leu Ile  
                     165                    170                    175  
 Thr Val Leu Ala Met Ile Leu Ala Val Phe Phe Ala Gln Ile His Pro  
                     180                    185                    190  
 Asn Tyr Leu Thr Gln Gln Trp Gln Arg Leu Arg Ser Ile Ile Phe Cys  
                     195                    200                    205  
 Ser Val Ser Gly Tyr Gly Val Ile Pro Thr Leu His Trp Val Trp Leu  
                     210                    215                    220  
 Asn Gly Gly Ile Gly Ala Pro Ile Val Gln Asp Phe Ala Pro Arg Val  
 225                    230                    235                    240  
 Ile Val Met Tyr Met Ile Ala Leu Leu Ala Phe Leu Phe Tyr Ile Ser  
                     245                    250                    255  
 Lys Val Pro Glu Arg Tyr Phe Pro Gly Gln Leu Asn Tyr Leu Gly Ser  
                     260                    265                    270  
 Ser His Gln Ile Trp His Ile Leu Ala Val Val Met Leu Tyr Trp Trp  
                     275                    280                    285  
 His Gln Ser Thr Val Tyr Val Met Gln Tyr Arg His Ser Lys Pro Cys

290  
Pro Asp Tyr Val Ser His Leu

295

300

305

310

&lt;210&gt; 197

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (644).. (937)

&lt;400&gt; 197

gtgtagttga gcacactaaa gtcttgttcc cttagtcatt cctccttctg ctgccccgtg 60  
 ggggagggtc ttgctgcctg tacccacctc tgacatttgc actccttagac aacatagccg 120  
 ctaatttggtt ggaaaggcgt taaaagaaaa aaaaaaaagt gctattttacc gcctccctct 180  
 ttgacagaag actgtctgtc aaagtaacct cgccccaagt gacttttttaa ggggtggctc 240  
 accaggaggg agtcagagca gaacttggac tgagtcctgc aggacacagg tattagcttt 300  
 tctcttttat ttgctttatg tttcatttac ttctttggat cgaatagctc caattgtatt 360  
 gctgttattt ggtttttcat tttgttgttg ggttttttga tgtggtgttt ttttgttttg 420  
 ttttgtttct ttttgtcttt ttagaaagag ggtttcctc tattgccctg gctggagtac 480  
 agtggtggaa tcaactgttca ctacagcctc caacttattc ctgggctcaa gcaatccttc 540  
 tgtctccatc tcctgagcag ctgggactct aggcatattgc caccgtgcc aatttttttt 600  
 taattccttt ttaaaaatat tttaatcctt tccggaaaaa aat atg ttt tcc atg 655

Met Phe Ser Met

1

gac ttg ctt att tcc ttt ata cag tcc att gtc gtt gaa ttc tta ttt 703  
 Asp Leu Leu Ile Ser Phe Ile Gln Ser Ile Val Val Glu Phe Leu Phe

5	10	15	20	
gaa ttt gtg ata cac cct ctc ata ggg aac ata aca aat ttc ctc cca				751
Glu Phe Val Ile His Pro Leu Ile Gly Asn Ile Thr Asn Phe Leu Pro				
25	30	35		
cag caa tta atg acg agt gcg atg aga agc ata atg aca atg att aac				799
Gln Gln Leu Met Thr Ser Ala Met Arg Ser Ile Met Thr Met Ile Asn				
40	45	50		
ttg ata att aaa aat cta atc aac caa ctg ttg atg att gta cta aac				847
Leu Ile Ile Lys Asn Leu Ile Asn Gln Leu Leu Met Ile Val Leu Asn				
55	60	65		
aaa ata att tca ttt tta cac aac cag ttg tat gtg aac tat gtt gaa				895
Lys Ile Ile Ser Phe Leu His Asn Gln Leu Tyr Val Asn Tyr Val Glu				
70	75	80		
aac agg atg cat gac tgg cgg cca gaa caa aga agt ttg gtt				937
Asn Arg Met His Asp Trp Arg Pro Glu Gln Arg Ser Leu Val				
85	90	95		
taatttctat ctatacaccc agtaaaatat ctgtaatacc actggaaaac cttaaaatac				997
attatctatt tcttgtaaaa gaatgatgaa atgtgaattt gaacagcata aatatgtaca				1057
agtatctctt ctcaacggaa aaaattatgt ttgtggatga aatatgaacc gagtttgtgg				1117
atgaaatatg agcagcatga ataagcacag atatctctcc tcaatggaaa aaatcacgta				1177
caaaatataa gaaccagtt tgtggatgcg tga				1210

&lt;210&gt; 198

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 198

Met Phe Ser Met Asp Leu Leu Ile Ser Phe Ile Gln Ser Ile Val Val  
 1 5 10 15  
 Glu Phe Leu Phe Glu Phe Val Ile His Pro Leu Ile Gly Asn Ile Thr  
 20 25 30  
 Asn Phe Leu Pro Gln Gln Leu Met Thr Ser Ala Met Arg Ser Ile Met  
 35 40 45  
 Thr Met Ile Asn Leu Ile Ile Lys Asn Leu Ile Asn Gln Leu Leu Met  
 50 55 60  
 Ile Val Leu Asn Lys Ile Ile Ser Phe Leu His Asn Gln Leu Tyr Val  
 65 70 75 80  
 Asn Tyr Val Glu Asn Arg Met His Asp Trp Arg Pro Glu Gln Arg Ser  
 85 90 95  
 Leu Val

&lt;210&gt; 199

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (99).. (665)

&lt;400&gt; 199

gacgcgccgc ggtccccgcc tgccgctgct ccgccgcagt cgccgctcca gtctatccgg 60  
 cactaggaac agccccgagc ggcgagacgg tccccgcc atg tct gcg gcc atg agg 116  
 Met Ser Ala Ala Met Arg  
 1 5  
 gag agg ttc gac cgg ttc ctg cac gag aag aac tgc atg act gac ctt 164

Glu Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu	
10 15 20	
ctg gcc aag ctc gag gcc aaa acc ggc gtg aac agg agc ttc atc gct	212
Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala	
25 30 35	
ctt ggt gtc atc gga ctg gtg gcc ttg tac ctg gtg ttc ggt tat gga	260
Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly	
40 45 50	
gcc tct ctc ctc tgc aac ctg ata gga ttt ggc tac cca gcc tac atc	308
Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile	
55 60 65 70	
tca att aaa gct ata gag agt ccc aac aaa gaa gat gat acc cag tgg	356
Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp	
75 80 85	
ctg acc tac tgg gta gtg tat ggt gtg ttc agc att gct gaa ttc ttc	404
Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe	
90 95 100	
tct gat atc ttc ctg tca tgg ttc ccc ttc tac tac atg ctg aag tgt	452
Ser Asp Ile Phe Leu Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys	
105 110 115	
ggc ttc ctg ttg tgg tgc atg gcc ccg agc cct tct aat ggg gct gaa	500
Gly Phe Leu Leu Trp Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu	
120 125 130	
ctg ctc tac aag cgc atc atc cgt cct ttc ttc ctg aag cac gag tcc	548
Leu Leu Tyr Lys Arg Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser	
135 140 145 150	
cag atg gac agt gtg gtc aag gac ctt aaa gac aag gcc aaa gag act	596

Gln Met Asp Ser Val Val Lys Asp Leu Lys Asp Lys Ala Lys Glu Thr  
                             155                            160                            165  
 gca gat gcc atc act aaa gaa gcg aag aaa gct acc gtg aat tta ctg 644  
 Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu  
                             170                            175                            180  
 ggt gaa gaa aag aag agc acc taaaccagac tggatggaaa cttcctgccc 695  
 Gly Glu Glu Lys Lys Ser Thr  
                             185  
 tctctgtacc ttctactgg agcttgatgt tatattaggg actgtggtat aattatttta 755  
 ataatgttgc cttggaaaca tttttgagat attaaagatt ggaatgtgtt gtaagtttct 815  
 ttgcttactt ttactgtcta tatatatagg gagcacttta aacttaatgc agtgggcagt 875  
 gtccacgttt ttggaaaatg tattttgcct ctgggtagga aaagatgtat gttgctatcc 935  
 tgcaggaaat ataaacttaa aataaaatta tataccccac aggctgtgta cttta 990

<210> 200

<211> 189

<212> PRT

<213> Homo sapiens

<400> 200

Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg Phe Leu His Glu Lys  
 1                            5                            10                            15  
 Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val  
                             20                            25                            30  
 Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr  
                             35                            40                            45  
 Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe  
                             50                            55                            60

606/861

aagtatttgt ggtaataacc cttaccggga gtttactga agctactctc cagagagacc 180  
ggatcttcaa acattttacc aggaagcgcc aaagggct atg cga agg cga gtc cac 236  
Met Arg Arg Arg Val His  
1 5  
cag atc aat gga cac aag ttc atg gcc acg tat ctg agg cag ccc acc 284  
Gln Ile Asn Gly His Lys Phe Met Ala Thr Tyr Leu Arg Gln Pro Thr  
10 15 20  
tac tgc tct cac tgc agg gag ttt atc tgg gga gtg ttt ggg aaa cag 332  
Tyr Cys Ser His Cys Arg Glu Phe Ile Trp Gly Val Phe Gly Lys Gln  
25 30 35  
ggg tat cag tgc caa gtg tgc acc tgt gtc gtc cat aaa cgc tgc cat 380  
Gly Tyr Gln Cys Gln Val Cys Thr Cys Val Val His Lys Arg Cys His  
40 45 50  
cat cta att gtt aca gcc tgt act tgc caa aac aat att aac aaa gtg 428  
His Leu Ile Val Thr Ala Cys Thr Cys Gln Asn Asn Ile Asn Lys Val  
55 60 65 70  
gat tca aag att gca gaa cag agg ttc ggg atc aac atc cca cac aag 476  
Asp Ser Lys Ile Ala Glu Gln Arg Phe Gly Ile Asn Ile Pro His Lys  
75 80 85  
ttc agc atc cac aac tac aaa gtg cca aca ttc tgc gat cac tgt ggc 524  
Phe Ser Ile His Asn Tyr Lys Val Pro Thr Phe Cys Asp His Cys Gly  
90 95 100  
tca ctg ctc tgg gga ata atg cga caa gga ctt cag tgt aaa ata tgt 572  
Ser Leu Leu Trp Gly Ile Met Arg Gln Gly Leu Gln Cys Lys Ile Cys  
105 110 115  
aaa atg aat gtg cat att cga tgt caa gcg aac gtg gcc cct aac tgt 620  
Lys Met Asn Val His Ile Arg Cys Gln Ala Asn Val Ala Pro Asn Cys



120	125	130	
ggg gta aat gcg gtg gaa ctt gcc aag acc ctg gca ggg atg ggt ctc			668
Gly Val Asn Ala Val Glu Leu Ala Lys Thr Leu Ala Gly Met Gly Leu			
135	140	145	150
caa ccc gga aat att tct cca acc tcg aaa ctc gtt tcc aga tcg acc			716
Gln Pro Gly Asn Ile Ser Pro Thr Ser Lys Leu Val Ser Arg Ser Thr			
	155	160	165
cta aga cga cag gga aag gag agc agc aaa gaa gga aat ggg att ggg			764
Leu Arg Arg Gln Gly Lys Glu Ser Ser Lys Glu Gly Asn Gly Ile Gly			
	170	175	180
gtt aat tct tcc aac cga ctt ggt atc gac aac ttt gag ttc atc cga			812
Val Asn Ser Ser Asn Arg Leu Gly Ile Asp Asn Phe Glu Phe Ile Arg			
	185	190	195
gtg ttg ggg aag ggg agt ttt ggg aag gtg atg ctt gca aga gta aaa			860
Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Arg Val Lys			
200	205	210	
gaa aca gga gac ctc tat gct gtg aag gtg ctg aag aag gac gtg att			908
Glu Thr Gly Asp Leu Tyr Ala Val Lys Val Leu Lys Lys Asp Val Ile			
215	220	225	230
ctg cag gat gat gat gtg gaa tgc acc atg acc gag aaa agg atc ctg			956
Leu Gln Asp Asp Asp Val Glu Cys Thr Met Thr Glu Lys Arg Ile Leu			
	235	240	245
tct ctg gcc cgc aat cac ccc ttc ctc act cag ttg ttc tgc tgc ttt			1004
Ser Leu Ala Arg Asn His Pro Phe Leu Thr Gln Leu Phe Cys Cys Phe			
	250	255	260
cag acc ccc gat cgt ctg ttt ttt gtg atg gag ttt gtg aat ggg ggt			1052
Gln Thr Pro Asp Arg Leu Phe Phe Val Met Glu Phe Val Asn Gly Gly			

265	270	275	
gac ttg atg ttc cac att cag aag tct cgt cgt ttt gat gaa gca cga			1100
Asp Leu Met Phe His Ile Gln Lys Ser Arg Arg Phe Asp Glu Ala Arg			
280	285	290	
gct cgc ttc tat gct gca gaa atc att tcg gct ctc atg ttc ctc cat			1148
Ala Arg Phe Tyr Ala Ala Glu Ile Ile Ser Ala Leu Met Phe Leu His			
295	300	305	310
gat aaa gga atc atc tat aga gat ctg aaa ctg gac aat gtc ctg ttg			1196
Asp Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu			
315	320	325	
gac cac gag ggt cac tgt aaa ctg gca gac ttc gga atg tgc aag gag			1244
Asp His Glu Gly His Cys Lys Leu Ala Asp Phe Gly Met Cys Lys Glu			
330	335	340	
ggg att tgc aat ggt gtc acc acg gcc aca ttc tgt ggc acg cca gac			1292
Gly Ile Cys Asn Gly Val Thr Thr Ala Thr Phe Cys Gly Thr Pro Asp			
345	350	355	
tat atc gct cca gag atc ctc cag gaa atg ctg tac ggg cct gca gta			1340
Tyr Ile Ala Pro Glu Ile Leu Gln Glu Met Leu Tyr Gly Pro Ala Val			
360	365	370	
gac tgg tgg gca atg ggc gtg ttg ctc tat gag atg ctc tgt ggt cac			1388
Asp Trp Trp Ala Met Gly Val Leu Leu Tyr Glu Met Leu Cys Gly His			
375	380	385	390
gcg cct ttt gag gca gag aat gaa gat gac ctc ttt gag gcc ata ctg			1436
Ala Pro Phe Glu Ala Glu Asn Glu Asp Asp Leu Phe Glu Ala Ile Leu			
395	400	405	
aat gat gag gtg gtc tac cct acc tgg ctc cat gaa gat gcc aca ggg			1484
Asn Asp Glu Val Val Tyr Pro Thr Trp Leu His Glu Asp Ala Thr Gly			

410	415	420	
atc cta aaa tct ttc atg acc aag aac ccc acc atg cgc ttg ggc agc			1532
Ile Leu Lys Ser Phe Met Thr Lys Asn Pro Thr Met Arg Leu Gly Ser			
425	430	435	
ctg act cag gga ggc gag cac gcc atc ttg aga cat cct ttt ttt aag			1580
Leu Thr Gln Gly Gly Glu His Ala Ile Leu Arg His Pro Phe Phe Lys			
440	445	450	
gaa atc gac tgg gcc cag ctg aac cat cgc caa ata gaa ccg cct ttc			1628
Glu Ile Asp Trp Ala Gln Leu Asn His Arg Gln Ile Glu Pro Pro Phe			
455	460	465	470
aga ccc aga atc aaa tcc cga gaa gat gtc agt aat ttt gac cct gac			1676
Arg Pro Arg Ile Lys Ser Arg Glu Asp Val Ser Asn Phe Asp Pro Asp			
475	480	485	
ttc ata aag gaa gag cca gtt tta act cca att gat gag gga cat ctt			1724
Phe Ile Lys Glu Glu Pro Val Leu Thr Pro Ile Asp Glu Gly His Leu			
490	495	500	
cca atg att aac cag gat gag ttt aga aac ttt tcc tat gtg tct cca			1772
Pro Met Ile Asn Gln Asp Glu Phe Arg Asn Phe Ser Tyr Val Ser Pro			
505	510	515	
gaa ttg caa cca tagccttatg gggagtgaga gagagggcac gagaacccaa			1824
Glu Leu Gln Pro			
520			
agggaataga gattctccag gaatttcctc tatgggacct tcccagcatc agccttagaa			1884
caagaacctt accttcaagg agcaagtga gaactctgtg aaggatggaa ctttcagata			1944
tcaactatth agagtccaga gggagccatg gcactagaaa tagttgataa tgaaatgaga			2004
ttttatgaag tataccgctc cacctatgag cgtctgtctc tgtgggcttg ggatgttaac			2064
aggagccaaa aggagggaaa gtgtgaagaa taaagtagat ctgagaaatt ctgagccaat			2124

caggcttctt aattcaagag acaaaccaag acgttctgtc aactgtgctg tgctcttctt 2184  
 taagccaatg aacccaatt cctggcagtc tacaagaagt ctcttaatgc taatgaagaa 2244  
 tttaaaggtc tttttaagga aatgaagggc tttccaaata gaatgattta ctctgaagaa 2304  
 acaaacaatg gtatctctga aactcacaac ctaaagccca atcttgaaaa tatgttgtgc 2364  
 accaagacga ctgcttcagc ttcttctctt atccttactt tctttaatag atatttatta 2424  
 aactgtccag tgaaaagggt ccacaatgcc cagtattgta aacaacaggt ttgcattcat 2484  
 gaagctttca ttcattctgg agtctactaa tttacctgaa tgggtgttgc attctgtgaa 2544  
 atgcctctcc acgttgcata tgtcacactt ttgtctgcac ataactcttt tttcacaaga 2604  
 agggtcactg ccacaacagc acagtcagcg ggtgaattac aggtgcctgc tgcctgccta 2664  
 cctgggtaat ctgatcttgt ctgtatcgcc gtgtgctcat cactgaggaa ttgcaggcca 2724  
 ctcatgtcag tgaccagatt tgtggcttat aaacattagc agtttatatta tgttttaaga 2784  
 tgcaaagatg tgtgtttgat attcacttta ataattagaa atggatcttg taaacagggc 2844  
 atatatcaaa gatgacctta taatatgtac ccgaatatac agttcaagaa ttttgtctga 2904  
 ctggaaataa atgcattttg tagcaaaa 2932

<210> 202

<211> 522

<212> PRT

<213> Homo sapiens

<400> 202

Met Arg Arg Arg Val His Gln Ile Asn Gly His Lys Phe Met Ala Thr

1

5

10

15

Tyr Leu Arg Gln Pro Thr Tyr Cys Ser His Cys Arg Glu Phe Ile Trp

20

25

30

Gly Val Phe Gly Lys Gln Gly Tyr Gln Cys Gln Val Cys Thr Cys Val

35

40

45

Val His Lys Arg Cys His His Leu Ile Val Thr Ala Cys Thr Cys Gln

50	55	60
Asn Asn Ile Asn Lys Val Asp Ser Lys Ile Ala Glu Gln Arg Phe Gly		
65	70	75
Ile Asn Ile Pro His Lys Phe Ser Ile His Asn Tyr Lys Val Pro Thr		80
	85	90
Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Ile Met Arg Gln Gly		95
	100	105
Leu Gln Cys Lys Ile Cys Lys Met Asn Val His Ile Arg Cys Gln Ala		110
	115	120
Asn Val Ala Pro Asn Cys Gly Val Asn Ala Val Glu Leu Ala Lys Thr		125
	130	135
Leu Ala Gly Met Gly Leu Gln Pro Gly Asn Ile Ser Pro Thr Ser Lys		140
	145	150
Leu Val Ser Arg Ser Thr Leu Arg Arg Gln Gly Lys Glu Ser Ser Lys		155
	160	165
Glu Gly Asn Gly Ile Gly Val Asn Ser Ser Asn Arg Leu Gly Ile Asp		170
	175	180
Asn Phe Glu Phe Ile Arg Val Leu Gly Lys Gly Ser Phe Gly Lys Val		185
	190	195
Met Leu Ala Arg Val Lys Glu Thr Gly Asp Leu Tyr Ala Val Lys Val		200
	205	210
Leu Lys Lys Asp Val Ile Leu Gln Asp Asp Asp Val Glu Cys Thr Met		215
	220	225
Thr Glu Lys Arg Ile Leu Ser Leu Ala Arg Asn His Pro Phe Leu Thr		230
	235	240
Gln Leu Phe Cys Cys Phe Gln Thr Pro Asp Arg Leu Phe Phe Val Met		245
	250	255
	260	265
		270

Glu Phe Val Asn Gly Gly Asp Leu Met Phe His Ile Gln Lys Ser Arg  
275 280 285  
Arg Phe Asp Glu Ala Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ile Ser  
290 295 300  
Ala Leu Met Phe Leu His Asp Lys Gly Ile Ile Tyr Arg Asp Leu Lys  
305 310 315 320  
Leu Asp Asn Val Leu Leu Asp His Glu Gly His Cys Lys Leu Ala Asp  
325 330 335  
Phe Gly Met Cys Lys Glu Gly Ile Cys Asn Gly Val Thr Thr Ala Thr  
340 345 350  
Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Leu Gln Glu Met  
355 360 365  
Leu Tyr Gly Pro Ala Val Asp Trp Trp Ala Met Gly Val Leu Leu Tyr  
370 375 380  
Glu Met Leu Cys Gly His Ala Pro Phe Glu Ala Glu Asn Glu Asp Asp  
385 390 395 400  
Leu Phe Glu Ala Ile Leu Asn Asp Glu Val Val Tyr Pro Thr Trp Leu  
405 410 415  
His Glu Asp Ala Thr Gly Ile Leu Lys Ser Phe Met Thr Lys Asn Pro  
420 425 430  
Thr Met Arg Leu Gly Ser Leu Thr Gln Gly Gly Glu His Ala Ile Leu  
435 440 445  
Arg His Pro Phe Phe Lys Glu Ile Asp Trp Ala Gln Leu Asn His Arg  
450 455 460  
Gln Ile Glu Pro Pro Phe Arg Pro Arg Ile Lys Ser Arg Glu Asp Val  
465 470 475 480  
Ser Asn Phe Asp Pro Asp Phe Ile Lys Glu Glu Pro Val Leu Thr Pro

485 490 495  
 Ile Asp Glu Gly His Leu Pro Met Ile Asn Gln Asp Glu Phe Arg Asn  
 500 505 510  
 Phe Ser Tyr Val Ser Pro Glu Leu Gln Pro  
 515 520

&lt;210&gt; 203

&lt;211&gt; 3585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (389).. (2437)

&lt;400&gt; 203

agcgggaaga gacgcttggg gctggggctc accggacggg taggtccggc tctccaggga 60  
 gaggagctgc ccggccctgg agaaggggcg agtcctgcgc gagtccccgg gaggcgccgc 120  
 gcgcttgga gggacggctg ggcttccccg gcccgctgag ggctaggcgg cgggctcccc 180  
 tcctttccac ctcggcaggg aggggaaggag gggagggaaa agtcccacgg aggaggcaga 240  
 atggccagtc gaggggcgct taggcgctgc ctttccccag ggctgcctcg actcctgcac 300  
 ctgtcccagag ggctggcctg agacgggact cccggttctc ccgctgcgaa gcagcgcggc 360  
 cccccggggc cggggcagcg gcgccggc atg tgc tct ggc acc atg aag ttc 412  
 Met Ser Ser Gly Thr Met Lys Phe

1

5

aat ggc tat ttg agg gtc cgc atc ggt gag gca gtg ggg ctg cag ccc 460  
 Asn Gly Tyr Leu Arg Val Arg Ile Gly Glu Ala Val Gly Leu Gln Pro  
 10 15 20  
 acc cgc tgg tcc ctg cgc cac tgc ctc ttc aag aag ggc cac cag ctg 508

615/861



Ile Asn Gly His Lys Phe Met Ala Thr Tyr Leu Arg Gln Pro Thr Tyr	
170	175
180	
tgc tct cac tgc agg gag ttt atc tgg gga gtg ttt ggg aaa cag ggt	988
Cys Ser His Cys Arg Glu Phe Ile Trp Gly Val Phe Gly Lys Gln Gly	
185	190
195	200
tat cag tgc caa gtg tgc acc tgt gtc gtc cat aaa cgc tgc cat cat	1036
Tyr Gln Cys Gln Val Cys Thr Cys Val Val His Lys Arg Cys His His	
205	210
215	
cta att gtt aca gcc tgt act tgc caa aac aat att aac aaa gtg gat	1084
Leu Ile Val Thr Ala Cys Thr Cys Gln Asn Asn Ile Asn Lys Val Asp	
220	225
230	
tca aag att gca gaa cag agg ttc ggg atc aac atc cca cac aag ttc	1132
Ser Lys Ile Ala Glu Gln Arg Phe Gly Ile Asn Ile Pro His Lys Phe	
235	240
245	
agc atc cac aac tac aaa gtg cca aca ttc tgc gat cac tgt ggc tca	1180
Ser Ile His Asn Tyr Lys Val Pro Thr Phe Cys Asp His Cys Gly Ser	
250	255
260	
ctg ctc tgg gga ata atg cga caa gga ctt cag tgt aaa ata tgt aaa	1228
Leu Leu Trp Gly Ile Met Arg Gln Gly Leu Gln Cys Lys Ile Cys Lys	
265	270
275	280
atg aat gtg cat att cga tgt caa gcg aac gtg gcc cct aac tgt ggg	1276
Met Asn Val His Ile Arg Cys Gln Ala Asn Val Ala Pro Asn Cys Gly	
285	290
295	
gta aat gcg gtg gaa ctt gcc aag acc ctg gca ggg atg ggt ctc caa	1324
Val Asn Ala Val Glu Leu Ala Lys Thr Leu Ala Gly Met Gly Leu Gln	
300	305
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ccc gga aat att tct cca acc tcg aaa ctc gtt tcc aga tcg acc cta	1372

Pro Gly Asn Ile Ser Pro Thr Ser Lys Leu Val Ser Arg Ser Thr Leu	
315 320 325	
aga cga cag gga aag gag agc agc aaa gaa gga aat ggg att ggg gtt	1420
Arg Arg Gln Gly Lys Glu Ser Ser Lys Glu Gly Asn Gly Ile Gly Val	
330 335 340	
aat tct tcc aac cga ctt ggt atc gac aac ttt gag ttc atc cga gtg	1468
Asn Ser Ser Asn Arg Leu Gly Ile Asp Asn Phe Glu Phe Ile Arg Val	
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Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Arg Val Lys Glu	
365 370 375	
aca gga gac ctc tat gct gtg aag gtg ctg aag aag gac gtg att ctg	1564
Thr Gly Asp Leu Tyr Ala Val Lys Val Leu Lys Lys Asp Val Ile Leu	
380 385 390	
cag gat gat gat gtg gaa tgc acc atg acc gag aaa agg atc ctg tct	1612
Gln Asp Asp Asp Val Glu Cys Thr Met Thr Glu Lys Arg Ile Leu Ser	
395 400 405	
ctg gcc cgc aat cac ccc ttc ctc act cag ttg ttc tgc tgc ttt cag	1660
Leu Ala Arg Asn His Pro Phe Leu Thr Gln Leu Phe Cys Cys Phe Gln	
410 415 420	
acc ccc gat cgt ctg ttt ttt gtg atg gag ttt gtg aat ggg ggt gac	1708
Thr Pro Asp Arg Leu Phe Phe Val Met Glu Phe Val Asn Gly Gly Asp	
425 430 435 440	
ttg atg ttc cac att cag aag tct cgt cgt ttt gat gaa gca cga gct	1756
Leu Met Phe His Ile Gln Lys Ser Arg Arg Phe Asp Glu Ala Arg Ala	
445 450 455	
cgc ttc tat gct gca gaa atc att tcg gct ctc atg ttc ctc cat gat	1804

Arg Phe Tyr Ala Ala Glu Ile Ile Ser Ala Leu Met Phe Leu His Asp	
460 465 470	
aaa gga atc atc tat aga gat ctg aaa ctg gac aat gtc ctg ttg gac	1852
Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp	
475 480 485	
cac gag ggt cac tgt aaa ctg gca gac ttc gga atg tgc aag gag ggg	1900
His Glu Gly His Cys Lys Leu Ala Asp Phe Gly Met Cys Lys Glu Gly	
490 495 500	
att tgc aat ggt gtc acc acg gcc aca ttc tgt ggc acg cca gac tat	1948
Ile Cys Asn Gly Val Thr Thr Ala Thr Phe Cys Gly Thr Pro Asp Tyr	
505 510 515 520	
atc gct cca gag atc ctc cag gaa atg ctg tac ggg cct gca gta gac	1996
Ile Ala Pro Glu Ile Leu Gln Glu Met Leu Tyr Gly Pro Ala Val Asp	
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tgg tgg gca atg ggc gtg ttg ctc tat gag atg ctc tgt ggt cac gcg	2044
Trp Trp Ala Met Gly Val Leu Leu Tyr Glu Met Leu Cys Gly His Ala	
540 545 550	
cct ttt gag gca gag aac gaa gat gac ctc ttt gag gcc ata ctg aat	2092
Pro Phe Glu Ala Glu Asn Glu Asp Asp Leu Phe Glu Ala Ile Leu Asn	
555 560 565	
gat gag gtg gtc tac cct acc tgg ctc cat gaa gat gcc aca ggg atc	2140
Asp Glu Val Val Tyr Pro Thr Trp Leu His Glu Asp Ala Thr Gly Ile	
570 575 580	
cta aaa tct ttc atg acc aag aac ccc acc atg cgc ttg ggc agc ctg	2188
Leu Lys Ser Phe Met Thr Lys Asn Pro Thr Met Arg Leu Gly Ser Leu	
585 590 595 600	
act cag gga ggc gag cac gcc atc ttg aga cat cct ttt ttt aag gaa	2236

Thr Gln Gly Gly Glu His Ala Ile Leu Arg His Pro Phe Phe Lys Glu  
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 atc gac tgg gcc cag ctg aac cat cgc caa ata gaa ccg cct ttc aga 2284  
 Ile Asp Trp Ala Gln Leu Asn His Arg Gln Ile Glu Pro Pro Phe Arg  
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 ccc aga atc aaa tcc cga gaa gat gtc agt aat ttt gac cct gac ttc 2332  
 Pro Arg Ile Lys Ser Arg Glu Asp Val Ser Asn Phe Asp Pro Asp Phe  
 635 640 645  
 ata aag gaa gag cca gtt tta act cca att gat gag gga cat ctt cca 2380  
 Ile Lys Glu Glu Pro Val Leu Thr Pro Ile Asp Glu Gly His Leu Pro  
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 Leu Gln Pro  
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<210> 204

<211> 683

<212> PRT

<213> Homo sapiens

<400> 204

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Leu Phe Lys Lys Gly His Gln Leu Leu Asp Pro Tyr Leu Thr Val Ser
           35           40           45
Val Asp Gln Val Arg Val Gly Gln Thr Ser Thr Lys Gln Lys Thr Asn
           50           55           60
Lys Pro Thr Tyr Asn Glu Glu Phe Cys Ala Asn Val Thr Asp Gly Gly
65           70           75           80
His Leu Glu Leu Ala Val Phe His Glu Thr Pro Leu Gly Tyr Asp His
           85           90           95
Phe Val Ala Asn Cys Thr Leu Gln Phe Gln Glu Leu Leu Arg Thr Thr

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100 105 110  
Gly Ala Ser Asp Thr Phe Glu Gly Trp Val Asp Leu Glu Pro Glu Gly  
115 120 125  
Lys Val Phe Val Val Ile Thr Leu Thr Gly Ser Phe Thr Glu Ala Thr  
130 135 140  
Leu Gln Arg Asp Arg Ile Phe Lys His Phe Thr Arg Lys Arg Gln Arg  
145 150 155 160  
Ala Met Arg Arg Arg Val His Gln Ile Asn Gly His Lys Phe Met Ala  
165 170 175  
Thr Tyr Leu Arg Gln Pro Thr Tyr Cys Ser His Cys Arg Glu Phe Ile  
180 185 190  
Trp Gly Val Phe Gly Lys Gln Gly Tyr Gln Cys Gln Val Cys Thr Cys  
195 200 205  
Val Val His Lys Arg Cys His His Leu Ile Val Thr Ala Cys Thr Cys  
210 215 220  
Gln Asn Asn Ile Asn Lys Val Asp Ser Lys Ile Ala Glu Gln Arg Phe  
225 230 235 240  
Gly Ile Asn Ile Pro His Lys Phe Ser Ile His Asn Tyr Lys Val Pro  
245 250 255  
Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Ile Met Arg Gln  
260 265 270  
Gly Leu Gln Cys Lys Ile Cys Lys Met Asn Val His Ile Arg Cys Gln  
275 280 285  
Ala Asn Val Ala Pro Asn Cys Gly Val Asn Ala Val Glu Leu Ala Lys  
290 295 300  
Thr Leu Ala Gly Met Gly Leu Gln Pro Gly Asn Ile Ser Pro Thr Ser  
305 310 315 320

Lys Leu Val Ser Arg Ser Thr Leu Arg Arg Gln Gly Lys Glu Ser Ser  
325 330 335

Lys Glu Gly Asn Gly Ile Gly Val Asn Ser Ser Asn Arg Leu Gly Ile  
340 345 350

Asp Asn Phe Glu Phe Ile Arg Val Leu Gly Lys Gly Ser Phe Gly Lys  
355 360 365

Val Met Leu Ala Arg Val Lys Glu Thr Gly Asp Leu Tyr Ala Val Lys  
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Val Leu Lys Lys Asp Val Ile Leu Gln Asp Asp Asp Val Glu Cys Thr  
385 390 395 400

Met Thr Glu Lys Arg Ile Leu Ser Leu Ala Arg Asn His Pro Phe Leu  
405 410 415

Thr Gln Leu Phe Cys Cys Phe Gln Thr Pro Asp Arg Leu Phe Phe Val  
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Met Glu Phe Val Asn Gly Gly Asp Leu Met Phe His Ile Gln Lys Ser  
435 440 445

Arg Arg Phe Asp Glu Ala Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ile  
450 455 460

Ser Ala Leu Met Phe Leu His Asp Lys Gly Ile Ile Tyr Arg Asp Leu  
465 470 475 480

Lys Leu Asp Asn Val Leu Leu Asp His Glu Gly His Cys Lys Leu Ala  
485 490 495

Asp Phe Gly Met Cys Lys Glu Gly Ile Cys Asn Gly Val Thr Thr Ala  
500 505 510

Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Leu Gln Glu  
515 520 525

Met Leu Tyr Gly Pro Ala Val Asp Trp Trp Ala Met Gly Val Leu Leu

530 535 540  
Tyr Glu Met Leu Cys Gly His Ala Pro Phe Glu Ala Glu Asn Glu Asp  
545 550 555 560  
Asp Leu Phe Glu Ala Ile Leu Asn Asp Glu Val Val Tyr Pro Thr Trp  
565 570 575  
Leu His Glu Asp Ala Thr Gly Ile Leu Lys Ser Phe Met Thr Lys Asn  
580 585 590  
Pro Thr Met Arg Leu Gly Ser Leu Thr Gln Gly Gly Glu His Ala Ile  
595 600 605  
Leu Arg His Pro Phe Phe Lys Glu Ile Asp Trp Ala Gln Leu Asn His  
610 615 620  
Arg Gln Ile Glu Pro Pro Phe Arg Pro Arg Ile Lys Ser Arg Glu Asp  
625 630 635 640  
Val Ser Asn Phe Asp Pro Asp Phe Ile Lys Glu Glu Pro Val Leu Thr  
645 650 655  
Pro Ile Asp Glu Gly His Leu Pro Met Ile Asn Gln Asp Glu Phe Arg  
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Asn Phe Ser Tyr Val Ser Pro Glu Leu Gln Pro  
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&lt;210&gt; 205

&lt;211&gt; 2874

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (160).. (1272)



&lt;400&gt; 205

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cttatcttag agccacactg agattggaac ccgcaaaat atg cca gga aac gcc 174

Met Pro Gly Asn Ala

1

5

acc cca gtg acc acc act gcc ccg tgg gcc tcc ctg ggc ctc tcc gcc 222

Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser Leu Gly Leu Ser Ala

10

15

20

aag acc tgc aac aac gtg tcc ttc gaa gag agc agg ata gtc ctg gtc 270

Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser Arg Ile Val Leu Val

25

30

35

gtg gtg tac agc gcg gtg tgc acg ctg ggg gtg ccg gcc aac tgc ctg 318

Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu

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45

50

act gcg tgg ctg gcg ctg ctg cag gta ctg cag ggc aac gtg ctg gcc 366

Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala

55

60

65

gtc tac ctg ctc tgc ctg gca ctc tgc gag ctg ctg tac aca ggc acg 414

Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr

70

75

80

85

ctg cca ctc tgg gtc atc tat atc cgc aac cag cac cgc tgg acc cta 462

Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu

90

95

100

ggc ctg ctg gcc tgc aag gtg acc gcc tac atc ttc ttc tgc aac atc 510

Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile

105

110

115

tac gtc agc atc ctc ttc ctg tgc tgc atc tcc tgc gac cgc ttc gtg	558
Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val	
120 125 130	
gcc gtg gtg tac gcg ctg gag agt cgg ggc cgc cgc cgc cgg agg acc	606
Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr	
135 140 145	
gcc atc ctc atc tcc gcc tgc atc ttc atc ctc gtc ggg atc gtt cac	654
Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His	
150 155 160 165	
tac ccg gtg ttc cag acg gaa gac aag gag acc tgc ttt gac atg ctg	702
Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu	
170 175 180	
cag atg gac agc agg att gcc ggg tac tac tac gcc agg ttc acc gtt	750
Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val	
185 190 195	
ggc ttt gcc atc cct ctc tcc atc atc gcc ttc acc aac cac cgg att	798
Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile	
200 205 210	
ttc agg agc atc aag cag agc atg ggc tta agc gct gcc cag aag gcc	846
Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala	
215 220 225	
aag gtg aag cac tcg gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc	894
Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys	
230 235 240 245	
ttc gcc ccg tac cac ctg gtt ctc ctc gtc aaa gcc gct gcc ttt tcc	942
Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser	
250 255 260	

tac tac aga gga gac agg aac gcc atg tgc ggc ttg gag gaa agg ctg	990
Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu	
265 270 275	
tac aca gcc tct gtg gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg	1038
Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val	
280 285 290	
gct gac ccc att atc tac gtg ctg gcc acg gac cat tcc cgc caa gaa	1086
Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu	
295 300 305	
gtg tcc aga atc cat aag ggg tgg aaa gag tgg tcc atg aag aca gac	1134
Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp	
310 315 320 325	
gtc acc agg ctc acc cac agc agg gac acc gag gag ctg cag tcg ccc	1182
Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro	
330 335 340	
gtg gcc ctt gca gac cac tac acc ttc tcc agg ccc gtg cac cca cca	1230
Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro	
345 350 355	
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Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys	
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<210> 206

<211> 371

<212> PRT

<213> Homo sapiens

<400> 206

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                     20                      25                      30  
 Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
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 Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln  
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 Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
 65                      70                      75                      80  
 Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
                     85                      90                      95  
 His Arg Trp Thr Leu Gly Leu Leu Ala Cys Lys Val Thr Ala Tyr Ile  
                     100                      105                      110  
 Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
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 Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
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 Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
 145                      150                      155                      160  
 Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
                     165                      170                      175  
 Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
                     180                      185                      190  
 Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
                     195                      200                      205  
 Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser

210 215 220  
Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
225 230 235 240  
Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
245 250 255  
Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
260 265 270  
Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
275 280 285  
Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
290 295 300  
His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
305 310 315 320  
Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335  
Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
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<210> 207

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<212> DNA

<213> Homo sapiens

<220>

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&lt;222&gt; (901).. (2040)

&lt;400&gt; 207

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cggaaagcag ggacgtgaac agccctctc atgttcttga caccgtcatt ctccagcagct      420
cagctaaggc acagaggcag ccgagcgtct gtcagcagag tcgtggctga gcagaacacg      480
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atg tgc cca atg cta ctg aaa aac ggt tac aat gga aac gcc acc cca      948
Met Cys Pro Met Leu Leu Lys Asn Gly Tyr Asn Gly Asn Ala Thr Pro
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gtg acc acc act gcc ccg tgg gcc tcc ctg ggc ctc tcc gcc aag acc      996
Val Thr Thr Thr Ala Pro Trp Ala Ser Leu Gly Leu Ser Ala Lys Thr
           20           25           30
tgc aac aac gtg tcc ttc gaa gag agc agg ata gtc ctg gtc gtg gtg      1044
Cys Asn Asn Val Ser Phe Glu Glu Ser Arg Ile Val Leu Val Val Val
           35           40           45

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tac agc gcg gtg tgc acg ctg ggg gtg ccg gcc aac tgc ctg act gcg	1092
Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu Thr Ala	
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tgg ctg gcg ctg ctg cag gta ctg cag ggc aac gtg ctg gcc gtc tac	1140
Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala Val Tyr	
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ctg ctc tgc ctg gca ctc tgc gag ctg ctg tac aca ggc acg ctg cca	1188
Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr Leu Pro	
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ctc tgg gtc atc tat atc cgc aac cag cac cgc tgg acc cta ggc ctg	1236
Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu Gly Leu	
100 105 110	
ctg gcc tgc aag gtg acc gcc tac atc ttc ttc tgc aac atc tac gtc	1284
Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile Tyr Val	
115 120 125	
agc atc ctc ttc ctg tgc tgc atc tcc tgc gac cgc ttc gtg gcc gtg	1332
Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val Ala Val	
130 135 140	
gtg tac gcg ctg gag agt cgg ggc cgc cgc cgc cgg agg acc gcc atc	1380
Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr Ala Ile	
145 150 155 160	
ctc atc tcc gcc tgc atc ttc atc ctc gtc ggg atc gtt cac tac ccg	1428
Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His Tyr Pro	
165 170 175	
gtg ttc cag acg gaa gac aag gag acc tgc ttt gac atg ctg cag atg	1476
Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu Gln Met	
180 185 190	



gac agc agg att gcc ggg tac tac tac gcc agg ttc acc gtt ggc ttt	1524
Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe	
195 200 205	
gcc atc cct ctc tcc atc atc gcc ttc acc aac cac cgg att ttc agg	1572
Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg	
210 215 220	
agc atc aag cag agc atg ggc tta agc gct gcc cag aag gcc aag gtg	1620
Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val	
225 230 235 240	
aag cac tcg gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc ttc gcc	1668
Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala	
245 250 255	
ccg tac cac ctg gtt ctc ctc gtc aaa gcc gct gcc ttt tcc tac tac	1716
Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr	
260 265 270	
aga gga gac agg aac gcc atg tgc ggc ttg gag gaa agg ctg tac aca	1764
Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr	
275 280 285	
gcc tct gtg gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg gct gac	1812
Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp	
290 295 300	
ccc att atc tac gtg ctg gcc acg gac cat tcc cgc caa gaa gtg tcc	1860
Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser	
305 310 315 320	
aga atc cat aag ggg tgg aaa gag tgg tcc atg aag aca gac gtc acc	1908
Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr	
325 330 335	

agg ctc acc cac agc agg gac acc gag gag ctg cag tcg ccc gtg gcc 1956  
 Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala  
 340 345 350

ctt gca gac cac tac acc ttc tcc agg ccc gtg cac cca cca ggg tca 2004  
 Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser  
 355 360 365

cca tgc cct gca aag agg ctg att gag gag tcc tgc tgagcccact 2050  
 Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys  
 370 375 380

gtgtggcagg gggatggcag gttgggggtc ctggggccag caatgtgggtt cctgtgcact 2110  
 gagcccacca gccacagtgc ccatgtcccc tctggaagac aaactaccaa tttctcgttc 2170  
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 tgcctcaaaa tgtcagtgag caccatgctg gaagtcacca tcaactgtggc agcggccagg 2530  
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<210> 208

<211> 380

<212> PRT

<213> Homo sapiens

<400> 208

Met Cys Pro Met Leu Leu Lys Asn Gly Tyr Asn Gly Asn Ala Thr Pro  
 1 5 10 15  
 Val Thr Thr Thr Ala Pro Trp Ala Ser Leu Gly Leu Ser Ala Lys Thr

20	25	30
Cys Asn Asn Val Ser Phe Glu Glu Ser Arg Ile Val Leu Val Val Val		
35	40	45
Tyr Ser Ala Val Cys Thr Leu Gly Val Pro Ala Asn Cys Leu Thr Ala		
50	55	60
Trp Leu Ala Leu Leu Gln Val Leu Gln Gly Asn Val Leu Ala Val Tyr		
65	70	75
80		
Leu Leu Cys Leu Ala Leu Cys Glu Leu Leu Tyr Thr Gly Thr Leu Pro		
85	90	95
Leu Trp Val Ile Tyr Ile Arg Asn Gln His Arg Trp Thr Leu Gly Leu		
100	105	110
Leu Ala Cys Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile Tyr Val		
115	120	125
Ser Ile Leu Phe Leu Cys Cys Ile Ser Cys Asp Arg Phe Val Ala Val		
130	135	140
Val Tyr Ala Leu Glu Ser Arg Gly Arg Arg Arg Arg Arg Thr Ala Ile		
145	150	155
160		
Leu Ile Ser Ala Cys Ile Phe Ile Leu Val Gly Ile Val His Tyr Pro		
165	170	175
Val Phe Gln Thr Glu Asp Lys Glu Thr Cys Phe Asp Met Leu Gln Met		
180	185	190
Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe		
195	200	205
Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg		
210	215	220
Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val		
225	230	235
240		

Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala  
245 250 255  
Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr  
260 265 270  
Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr  
275 280 285  
Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp  
290 295 300  
Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser  
305 310 315 320  
Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr  
325 330 335  
Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala  
340 345 350  
Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser  
355 360 365  
Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys  
370 375 380

<210> 209

<211> 3347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1175)..(1750)

<400> 209

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 cacactgaat acaatggaat accatcccgc ctttgaaagg aagggaatc ctggcacacg 120  
 ctgcaacagg agggagcttg aggacactgt ggtgagtga gcacgtgaga cacggaagga 180  
 cacacgctga agacacgcag agatgcccac ccacgtgggg aggtgacagg ggagcccagc 240  
 gcacagagac aaagtggaat ggaggcctgg gggctgggag caaatgcgga gcgagtgcctt 300  
 cctggggcag agtctccgtt tgggaagatg agaaggttct gccgacggat gctggcgatg 360  
 gttgcagaag aatgtgaatg tgcccaatgc tactgaaaaa cggttacaat ggtgctgagg 420  
 ccaggtctgt ctgcggttc ctgctgacct ggaggtggga ctccatgac tgtaaccaca 480  
 gaaggcccag aagcatgaac tcagccagag tgggcagcca ggacactgga gctggtggcg 540  
 ctggcagagc ttggggaagt cacaccactg cacaccctgc gtgacctcta gcaacccctt 600  
 ggctggaaag gatgagtttc tgacctcgga gagctgtgtt tgaggaaacg ccaccccagt 660  
 gaccaccact gcccgtggg cctccctggg cctctccgcc aagacctgca acaacgtgtc 720  
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 ctgcgaccgc ttcgtggccg tgggtgtacgc gctggagagt cggggccgcc gccgccggag 1080  
 gaccgccatc ctcatctccg cctgcatctt catcctcgtc gggatcggtc actaccgggt 1140  
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Met Leu Gln Met Asp Ser Arg

1

5

att gcc ggg tac tac tac gcc agg ttc acc gtt ggc ttt gcc atc cct 1243  
 Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe Thr Val Gly Phe Ala Ile Pro  
 10 15 20  
 ctc tcc atc atc gcc ttc acc aac cac cgg att ttc agg agc atc aag 1291  
 Leu Ser Ile Ile Ala Phe Thr Asn His Arg Ile Phe Arg Ser Ile Lys

25	30	35	
cag agc atg ggc tta agc gct gcc cag aag gcc aag gtg aag cac tcg			1339
Gln Ser Met Gly Leu Ser Ala Ala Gln Lys Ala Lys Val Lys His Ser			
40	45	50	55
gcc atc gcg gtg gtt gtc atc ttc cta gtc tgc ttc gcc ccg tac cac			1387
Ala Ile Ala Val Val Val Ile Phe Leu Val Cys Phe Ala Pro Tyr His			
60	65	70	
ctg gtt ctc ctc gtc aaa gcc gct gcc ttt tcc tac tac aga gga gac			1435
Leu Val Leu Leu Val Lys Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp			
75	80	85	
agg aac gcc atg tgc ggc ttg gag gaa agg ctg tac aca gcc tct gtg			1483
Arg Asn Ala Met Cys Gly Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val			
90	95	100	
gtg ttt ctg tgc ctg tcc acg gtg aac ggc gtg gct gac ccc att atc			1531
Val Phe Leu Cys Leu Ser Thr Val Asn Gly Val Ala Asp Pro Ile Ile			
105	110	115	
tac gtg ctg gcc acg gac cat tcc cgc caa gaa gtg tcc aga atc cat			1579
Tyr Val Leu Ala Thr Asp His Ser Arg Gln Glu Val Ser Arg Ile His			
120	125	130	135
aag ggg tgg aaa gag tgg tcc atg aag aca gac gtc acc agg ctc acc			1627
Lys Gly Trp Lys Glu Trp Ser Met Lys Thr Asp Val Thr Arg Leu Thr			
140	145	150	
cac agc agg gac acc gag gag ctg cag tcg ccc gtg gcc ctt gca gac			1675
His Ser Arg Asp Thr Glu Glu Leu Gln Ser Pro Val Ala Leu Ala Asp			
155	160	165	
cac tac acc ttc tcc agg ccc gtg cac cca cca ggg tca cca tgc cct			1723
His Tyr Thr Phe Ser Arg Pro Val His Pro Pro Gly Ser Pro Cys Pro			

170	175	180	
gca aag agg ctg att gag gag tcc tgc tgagcccact gtgtggcagg			1770
Ala Lys Arg Leu Ile Glu Glu Ser Cys			
185	190		
,gggatggcag gttgggggtc ctggggccag caatgtggtt cctgtgcaact gagcccacca			1830
gccacagtgc ccatgtcccc tctggaagac aaactaccaa tttctcgttc ctgaagccac			1890
tccctccgtg accactggcc ccaggctttc ccacatggaa ggtggctgca tgccaagggg			1950
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cccaggcgtc ctcaacgggg agccccaat gtccacgcc agaacaacag ttggcaggac			2430
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ggggagtgca gcagttggcc tgcttgtctg gcggagaaag ccagctccct gcaccctcg			2610
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ctggtttccc tatctgtaaa atggggccaa tgacacctac ctactgggt caccatcgag			2730
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cgggcagacg cagcacctgc atggggagcc cagtgcccg cacagcacag gggcttcag			2850
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acagggcctt gctctgttgc ctgggctgga gaacagtggc accatcatag ctactgcag			3030
cctcaaactc ctgggctcaa gcgacctcc ccgctcagcc tctgagtag ctgggactac			3090
aggtgtgcac caccacaccc agccaaaaca gccatcctcc cttgagagt catcagaaaa			3150

atacattagg aaaatgtgtt tagaaataaa agcacaaggc agggcagtgc tcacgcctgt 3210  
 catcccagca ctttgggagg ccgagacggg aggatcagtt gaggtcagga gtttgagacc 3270  
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<210> 210

<211> 192

<212> PRT

<213> Homo sapiens

<400> 210

Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr Ala Arg Phe  
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 Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe Thr Asn His  
 20 25 30  
 Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser Ala Ala Gln  
 35 40 45  
 Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val Ile Phe Leu  
 50 55 60  
 Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys Ala Ala Ala  
 65 70 75 80  
 Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly Leu Glu Glu  
 85 90 95  
 Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser Thr Val Asn  
 100 105 110  
 Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp His Ser Arg  
 115 120 125  
 Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp Ser Met Lys



130	135	140	
Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu Glu Leu Gln			
145	150	155	160
Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg Pro Val His			
	165	170	175
Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu Glu Ser Cys			
180	185	190	

&lt;210&gt; 211

&lt;211&gt; 2304

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (362).. (1729)

&lt;400&gt; 211

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ggactcagtt tgtttctgct gattacaccc gtgcccagga gcttgacgcc ttagataaca	180
gccatcctat tgaagtcagt gtgggccatc catctgaggt tgatgagata tttgatgcta	240
tatcatatag caaaggtgca tctgtcatcc gaatgctgca tgactacatt ggggataagg	300
actttaagaa aggaatgaac atgtatttaa ccaagttcca acaaaagaat gctgccgcag	360
g atg gac gtg gta gag gtc gcg ggc agt tgg tgg gca caa gag cga gag	409
Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu	
1 5 10 15	
gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag	457
Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu	

20	25	30	
gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat			505
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His			
35	40	45	
ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag			553
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu			
50	55	60	
gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat			601
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp			
65	70	75	80
atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat			649
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp			
85	90	95	
cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca			697
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser			
100	105	110	
gtc ctc ctg aac act gag gaa atg aag ttg aaa aac ccc gga aga tac			745
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr			
115	120	125	
cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc			793
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg			
130	135	140	
atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg			841
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg			
145	150	155	160
gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca			889
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala			

165	170	175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac			937
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His			
180	185	190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg			985
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp			
195	200	205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt			1033
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe			
210	215	220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag			1081
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu			
225	230	235	240
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag			1129
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys			
245	250	255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata			1177
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile			
260	265	270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg			1225
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val			
275	280	285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc			1273
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala			
290	295	300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg			1321
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro			

305	310	315	320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag				1369
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu				
325	330	335		
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga				1417
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg				
340	345	350		
aag cag ggg gac ctg caa ccc cca gcc aaa ccc gag caa ggg tcg tcg				1465
Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser				
355	360	365		
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag				1513
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys				
370	375	380		
ggg gac agg cag gcc cct cca ggc cca ttt ggt cag ctt ccc cgc cac				1561
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His				
385	390	395	400	
ggg cac ctc gtt ctt cca cac cct gtc ctg gtg ggg ctg tcc ggg aag				1609
Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys				
405	410	415		
aca cct acc ctg tgg gca ctc agg gtg tgc cca gcc cgg ccc tgg ctc				1657
Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu				
420	425	430		
agg gag gac ctc agg gtt cct gga gat tcc tgc agt gga act cca tgc				1705
Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys				
435	440	445		
ccc gcc tcc caa cgg acc tgg acg tagagggccc ttggttccgc cattatgatt				1759
Pro Ala Ser Gln Arg Thr Trp Thr				

450  
 455  
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 aggctgaaca ccctgcgag cgggtgagat cggttttcgc tgcaccacagc actgattccg 1879  
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 gcctctgcgg cctccacttg gaaagttctc agttccctcc aggcttctag aagcatctgg 1999  
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 aatga 2304

<210> 212

<211> 456

<212> PRT

<213> Homo sapiens

<400> 212

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

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Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu

20 25 30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His

35 40 45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50 55 60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp

65 70 75 80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp  
                             85                            90                            95  
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser  
                             100                            105                            110  
 Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr  
                             115                            120                            125  
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg  
                             130                            135                            140  
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg  
 145                            150                            155                            160  
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala  
                             165                            170                            175  
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His  
                             180                            185                            190  
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp  
                             195                            200                            205  
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe  
                             210                            215                            220  
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu  
 225                            230                            235                            240  
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys  
                             245                            250                            255  
 Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile  
                             260                            265                            270  
 Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val  
                             275                            280                            285  
 Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala

290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
305	310	315 320
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
325	330	335
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
340	345	350
Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
355	360	365
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His		
385	390	395 400
Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys		
405	410	415
Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu		
420	425	430
Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys		
435	440	445
Pro Ala Ser Gln Arg Thr Trp Thr		
450	455	

<210> 213

<211> 2304

<212> DNA

<213> Homo sapiens

**<220>**

&lt;221&gt; CDS

&lt;222&gt; (362).. (1729)

&lt;400&gt; 213

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ggactcagtt tgtttctgct gattacaccc gtgccagga gcttgacgcc ttagataaca      180
gccatcctat tgaagtcagt gtgggccatc catctgaggt tgatgagata tttgatgcta      240
tatcatatag caaaggtgca tctgtcatcc gaatgctgca tgactacatt ggggataagg      300
actttaagaa aggaatgaac atgtatttaa ccaagttcca acaaaagaat gctgccgcag      360
g atg gac gtg gta gag gtc gcg ggc agt tgg tgg gca caa gag cga gag      409
Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu
1           5           10           15
gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag      457
Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
20           25           30
gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat      505
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
35           40           45
ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag      553
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50           55           60
gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat      601
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65           70           75           80
atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat      649
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85           90           95

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cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca	697
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser	
100 105 110	
gtc ctc ctg aac act gag gaa atg aag ttg aaa aac ccc gga aga tac	745
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr	
115 120 125	
cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc	793
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg	
130 135 140	
atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg	841
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg	
145 150 155 160	
gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca	889
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala	
165 170 175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac	937
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His	
180 185 190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg	985
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	1033
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	1081
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	

cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	1129
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	1177
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	1225
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	1273
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	1321
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro	
305 310 315 320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag	1369
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu	
325 330 335	
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga	1417
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg	
340 345 350	
aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa ggg tcg tcg	1465
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser	
355 360 365	
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag	1513
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys	
370 375 380	

ggg gac agg cag gcc cct cca ggc cca ttt ggt cag ctt ccc cgc cac 1561  
 Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His  
 385 390 395 400  
 ggg cac ctc gtt ctt cca cac cct gtc ctg gtg ggg ctg tcc ggg aag 1609  
 Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys  
 405 410 415  
 aca cct acc ctg tgg gca ctc agg gtg tgc cca gcc cgg ccc tgg ctc 1657  
 Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu  
 420 425 430  
 agg gag gac ctc agg gtt cct gga gat tcc tgc agt gga act cca tgc 1705  
 Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys  
 435 440 445  
 ccc gcc tcc caa cgg acc tgg acg tagagggcc ttggttcgc cattatgatt 1759  
 Pro Ala Ser Gln Arg Thr Trp Thr  
 450 455  
 tcagacagag ctgctgggtc cgtgccatat cccaggagga ccagctggcc ccctgctggc 1819  
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 gcctctgcgg cctccacttg gaaagtctc agttccctcc aggcttctag aagcatctgg 1999  
 gccagggctc atggctggat aatttccta ggcttaacaa cccaagcaag cttcgcatcc 2059  
 tcgttttatt tttggttaaa cttatgaaaa tgtattaaga aagagtgcag ctgagagag 2119  
 attcagagat ggaacacacc agacccaga tcacaaagcc aaccatgccc agcccctccc 2179  
 agcaccacca gcccacgac catcgttctg aattctgacg acaccgtgag cctgcctttg 2239  
 tacttcaaac tcatggaagg ataaccacct tcatgttttg aaataaatgt ttctgttga 2299  
 aatga 2304

&lt;210&gt; 214

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 214

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

1

5

10

15

Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu

20

25

30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His

35

40

45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50

55

60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp

65

70

75

80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp

85

90

95

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser

100

105

110

Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr

115

120

125

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg

130

135

140

Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg

145

150

155

160

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala

165

170

175

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His

180	185	190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp		
195	200	205
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe		
210	215	220
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu		
225	230	235
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys		
245	250	255
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile		
260	265	270
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val		
275	280	285
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala		
290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
305	310	315
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
325	330	335
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
340	345	350
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
355	360	365
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Phe Gly Gln Leu Pro Arg His		
385	390	395
		400

Gly His Leu Val Leu Pro His Pro Val Leu Val Gly Leu Ser Gly Lys  
                     405                    410                    415  
 Thr Pro Thr Leu Trp Ala Leu Arg Val Cys Pro Ala Arg Pro Trp Leu  
                     420                    425                    430  
 Arg Glu Asp Leu Arg Val Pro Gly Asp Ser Cys Ser Gly Thr Pro Cys  
                     435                    440                    445  
 Pro Ala Ser Gln Arg Thr Trp Thr  
                     450                    455

<210> 215

<211> 1964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1647)

<400> 215

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 1                    5                    10                    15  
 gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag 96  
 Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu  
                     20                    25                    30  
 gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat 144  
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His  
                     35                    40                    45  
 ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag 192

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu	
50	55
60	
gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat	240
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp	
65	70
75	80
atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat	288
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp	
85	90
95	
cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca	336
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser	
100	105
110	
gtc ctc ctg aac att gag gaa atg aag ttg aaa aac ccc gga aga tac	384
Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr	
115	120
125	
cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc	432
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg	
130	135
140	
atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg	480
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg	
145	150
155	160
gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca	528
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala	
165	170
175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac	576
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His	
180	185
190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg	624

Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	672
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	720
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	768
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	816
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	864
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	912
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	960
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro	
305 310 315 320	
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag	1008
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu	
325 330 335	
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga	1056



Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg	
340	345
350	
aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa ggg tcg tcg	1104
Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser	
355	360
365	
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag	1152
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys	
370	375
380	
ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc ccg cgg ccc	1200
Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro	
385	390
395	400
att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc aca ccc tgt	1248
Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys	
405	410
415	
cct ggt ggg gct gtc ccg gaa gac acc tac cct gtg ggc act cag ggt	1296
Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly	
420	425
430	
gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt tcc tgg aga	1344
Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg	
435	440
445	
ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac ctg gac gta	1392
Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val	
450	455
460	
gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc tgc tgg gtc	1440
Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val	
465	470
475	480
cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg cag gct gaa	1488

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu  
 485 490 495  
 cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc agc act gat 1536  
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp  
 500 505 510  
 tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag ccg tgt gct 1584  
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala  
 515 520 525  
 ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa agt tct cag 1632  
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln  
 530 535 540  
 ttc cct cca ggc ttc tagaagcatc tgggccaggg ctcatggctg gataatttcc 1687  
 Phe Pro Pro Gly Phe  
 545  
 ctaggcttaa caacccaagc aagcttcgcg tcctcgtttt atttttgggtt aaacttatga 1747  
 aaatgtatta agaaagagtg cagctcgaga gagattcaga gatggaacac accagacccc 1807  
 agatcacaaa gccaaccatg cccagcccct cccagcaccc ccagccccac gaccatcggt 1867  
 ctgaattctg acgacaccgt gagcctgcct ttgtacttta aactcatgga aggataacta 1927  
 ccttcacgtt ttgaaataaa tgtttcctgt tgaaatg 1964

&lt;210&gt; 216

&lt;211&gt; 549

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 216

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

1

5

10

15

Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu  
 20 25 30  
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His  
 35 40 45  
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu  
 50 55 60  
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp  
 65 70 75 80  
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp  
 85 90 95  
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser  
 100 105 110  
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr  
 115 120 125  
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg  
 130 135 140  
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg  
 145 150 155 160  
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala  
 165 170 175  
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His  
 180 185 190  
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp  
 195 200 205  
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe  
 210 215 220  
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu

225                                      230                                      235                                      240  
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys  
    245                                      250                                      255  
 Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile  
    260                                      265                                      270  
 Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val  
    275                                      280                                      285  
 Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala  
    290                                      295                                      300  
 Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro  
 305                                      310                                      315                                      320  
 Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu  
    325                                      330                                      335  
 Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg  
    340                                      345                                      350  
 Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser  
    355                                      360                                      365  
 Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys  
    370                                      375                                      380  
 Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro  
 385                                      390                                      395                                      400  
 Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys  
    405                                      410                                      415  
 Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly  
    420                                      425                                      430  
 Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg  
    435                                      440                                      445

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val  
 450 455 460  
 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val  
 465 470 475 480  
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu  
 485 490 495  
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp  
 500 505 510  
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala  
 515 520 525  
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln  
 530 535 540  
 Phe Pro Pro Gly Phe  
 545

<210> 217

<211> 1964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1647)

<400> 217

atg gac gtg gta gag gtc gcg ggc agt tgg tgg gca caa gag cga gag 48  
 Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu  
 1 5 10 15  
 gac atc att atg aaa tac gaa aag gga cac cga gct ggg ctg cca gag 96

Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu  
 20 25 30  
 gac aag ggg cct aag cct ttt cga agc tac aac aac aac gtc gat cat 144  
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His  
 35 40 45  
 ttg ggg att gta cat gag acg gag ctg cct cct ctg act gcg cgg gag 192  
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu  
 50 55 60  
 gcg aag caa att cgg cgg gag atc agc cga aag agc aag tgg gtg gat 240  
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp  
 65 70 75 80  
 atg ctg gga gac tgg gag aaa tac aaa agc agc aga aag ctc ata gat 288  
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp  
 85 90 95  
 cga gcg tac aag gga atg ccc atg aac atc cgg ggc ccg atg tgg tca 336  
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser  
 100 105 110  
 gtc ctc ctg aac att gag gaa atg aag ttg aaa aac ccc gga aga tac 384  
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr  
 115 120 125  
 cag atc atg aag gag aag ggc aag agg tca tct gag cac atc cag cgc 432  
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg  
 130 135 140  
 atc gac cgg gac gta agc ggg aca tta agg aag cat ata ttc ttc agg 480  
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg  
 145 150 155 160  
 gat cga tac gga acc aag cag cgg gaa cta ctc cac atc ctc ctg gca 528

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala	
165 170 175	
tat gag gag tat aac ccg gag gtg ggc tac tgc agg gac ctg agc cac	576
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His	
180 185 190	
atc gcc gcc ttg ttc ctc ctc tat ctt cct gag gag gat gca ttc tgg	624
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp	
195 200 205	
gca ctg gtg cag ctg ctg gcc agt gag agg cac tcc ctg cag gga ttt	672
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe	
210 215 220	
cac agc cca aat ggc ggg acc gtc cag ggg ctc caa gac caa cag gag	720
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu	
225 230 235 240	
cat gtg gta gcc acg tca caa ccc aag acc atg ggg cat cag gac aag	768
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys	
245 250 255	
aaa gat cta tgt ggg cag tgt tcc ccg tta ggc tgc ctc atc cgg ata	816
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile	
260 265 270	
ttg att gac ggg atc tct ctc ggg ctc acc ctg cgc ctg tgg gac gtg	864
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val	
275 280 285	
tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca aga atc gcc	912
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala	
290 295 300	
ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg tgt ggc ccg	960

Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro	
305	310
315	320
tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc agg gat gag	1008
Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu	
325	330
335	
gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa cta aca aga	1056
Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg	
340	345
350	
aag cag ggg gac ctg caa ccc cca gcc aaa ccc gag caa ggg tcg tcg	1104
Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser	
355	360
365	
gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc ctc tgc aag	1152
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys	
370	375
380	
ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc ccg cgg ccc	1200
Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro	
385	390
395	400
att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc aca ccc tgt	1248
Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys	
405	410
415	
cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc act cag ggt	1296
Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly	
420	425
430	
gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt tcc tgg aga	1344
Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg	
435	440
445	
ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac ctg gac gta	1392



Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val  
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 gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc tgc tgg gtc 1440  
 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val  
 465 470 475 480  
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 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu  
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 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp  
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 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala  
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 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln  
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 Phe Pro Pro Gly Phe  
 545  
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&lt;210&gt; 218

&lt;211&gt; 549

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 218

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

1 5 10 15

Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu

20 25 30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His

35 40 45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50 55 60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp

65 70 75 80

Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp

85 90 95

Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser

100 105 110

Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr

115 120 125

Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg

130 135 140

Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg

145 150 155 160

Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala

165 170 175

Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His

180	185	190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp		
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Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe		
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His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu		
225	230	235
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys		
245	250	255
Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile		
260	265	270
Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val		
275	280	285
Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala		
290	295	300
Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro		
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Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu		
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Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg		
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Lys Gln Gly Asp Leu Gln Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser		
355	360	365
Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys		
370	375	380
Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro		
385	390	395
		400

Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys  
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 Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg  
                             435                            440                            445  
 Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val  
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 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val  
 465                            470                            475                            480  
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu  
                             485                            490                            495  
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp  
                             500                            505                            510  
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala  
                             515                            520                            525  
 Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln  
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<210> 219

<211> 2647

<212> DNA

<213> Homo sapiens

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<221> CDS

&lt;222&gt; (755).. (2335)

&lt;400&gt; 219

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 aatgggtggac tccacagtcc ctccgcgaga gacgttggtt ccatgcgtac aatagatctt 180  
 cctcatcccc caaacccaac accctcctgc tcaacaggcg ttattcctaa agtggcttca 240  
 ctgttcagac tgaagagcca cggtagccaa agtgatgagc ggagtagaac cgagcagtcg 300  
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 gccgattgca cagagacctc tggtcgctga cccagtcctg cctccacatc cctggaatag 420  
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 gccagccagc atctgggagc ccggcgagag cggttcaggt gttctccgaa gccgccgcgt 720  
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Met Asp Val Val Glu Val Ala

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ggc agt tgg tgg gca caa gag cga gag gac atc att atg aaa tac gaa 823  
 Gly Ser Trp Trp Ala Gln Glu Arg Glu Asp Ile Ile Met Lys Tyr Glu

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aag gga cac cga gct ggg ctg cca gag gac aag ggg cct aag cct ttt 871  
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25

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cga agc tac aac aac aac gtc gat cat ttg ggg att gta cat gag acg 919  
 Arg Ser Tyr Asn Asn Asn Val Asp His Leu Gly Ile Val His Glu Thr

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gag ctg cct cct ctg act gcg cgg gag gcg aag caa att cgg cgg gag 967

Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln Ile Arg Arg Glu	
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atc agc cga aag agc aag tgg gtg gat atg ctg gga gac tgg gag aaa	1015
Ile Ser Arg Lys Ser Lys Trp Val Asp Met Leu Gly Asp Trp Glu Lys	
75 80 85	
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Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr Lys Gly Met Pro	
90 95 100	
atg aac atc cgg ggc ccg atg tgg tca gtc ctc ctg aac act gag gaa	1111
Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu Asn Thr Glu Glu	
105 110 115	
atg aag ttg aaa aac ccc gga aga tac cag atc atg aag gag aag ggc	1159
Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met Lys Glu Lys Gly	
120 125 130 135	
aag agg tca tct gag cac atc cag cgc atc gac cgg gac gta agc ggg	1207
Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg Asp Val Ser Gly	
140 145 150	
aca tta agg aag cat ata ttc ttc agg gat cga tac gga acc aag cag	1255
Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr Gly Thr Lys Gln	
155 160 165	
cgg gaa cta ctc cac atc ctc ctg gca tat gag gag tat aac ccg gag	1303
Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu Tyr Asn Pro Glu	
170 175 180	
gtg ggc tac tgc agg gac ctg agc cac atc gcc gcc ttg ttc ctc ctc	1351
Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala Leu Phe Leu Leu	
185 190 195	
tat ctt cct gag gag gat gca ttc tgg gca ctg gtg cag ctg ctg gcc	1399

Tyr	Leu	Pro	Glu	Glu	Asp	Ala	Phe	Trp	Ala	Leu	Val	Gln	Leu	Leu	Ala		
200						205					210				215		
agt	gag	agg	cac	tcc	ctg	cag	gga	ttt	cac	agc	cca	aat	ggc	ggg	acc	1447	
Ser	Glu	Arg	His	Ser	Leu	Gln	Gly	Phe	His	Ser	Pro	Asn	Gly	Gly	Thr		
				220					225					230			
gtc	cag	ggg	ctc	caa	gac	caa	cag	gag	cat	gtg	gta	gcc	acg	tca	caa	1495	
Val	Gln	Gly	Leu	Gln	Asp	Gln	Gln	Glu	His	Val	Val	Ala	Thr	Ser	Gln		
			235					240					245				
ccc	aag	acc	atg	ggg	cat	cag	atc	tct	ctc	ggg	ctc	acc	ctg	cgc	ctg	1543	
Pro	Lys	Thr	Met	Gly	His	Gln	Ile	Ser	Leu	Gly	Leu	Thr	Leu	Arg	Leu		
	250					255					260						
tgg	gac	gtg	tat	ctg	gta	gaa	ggc	gaa	cag	gcg	ttg	atg	ccg	ata	aca	1591	
Trp	Asp	Val	Tyr	Leu	Val	Glu	Gly	Glu	Gln	Ala	Leu	Met	Pro	Ile	Thr		
	265					270				275							
aga	atc	gcc	ttt	aag	gtt	cag	cag	aag	cgc	ctc	acg	aag	acg	tcc	agg	1639	
Arg	Ile	Ala	Phe	Lys	Val	Gln	Gln	Lys	Arg	Leu	Thr	Lys	Thr	Ser	Arg		
280				285					290				295				
tgt	ggc	ccg	tgg	gca	cgt	ttt	tgc	aac	cgg	ttc	gtt	gat	acc	tgg	gcc	1687	
Cys	Gly	Pro	Trp	Ala	Arg	Phe	Cys	Asn	Arg	Phe	Val	Asp	Thr	Trp	Ala		
			300					305					310				
agg	gat	gag	gac	act	gtg	ctc	aag	cat	ctt	agg	gcc	tct	atg	aag	aaa	1735	
Arg	Asp	Glu	Asp	Thr	Val	Leu	Lys	His	Leu	Arg	Ala	Ser	Met	Lys	Lys		
			315					320				325					
cta	aca	aga	aag	cag	ggg	gac	ctg	caa	ccc	cca	gcc	aaa	ccc	gag	caa	1783	
Leu	Thr	Arg	Lys	Gln	Gly	Asp	Leu	Gln	Pro	Pro	Ala	Lys	Pro	Glu	Gln		
		330				335					340						
ggg	tcg	tcg	gca	tcc	agg	cct	gtg	ccg	gct	tca	cgt	ggc	ggg	aag	acc	1831	

Gly Ser Ser Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr	
345 350 355	
ctc tgc aag ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc	1879
Leu Cys Lys Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe	
360 365 370 375	
ccg cgg ccc att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc	1927
Pro Arg Pro Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser	
380 385 390	
aca ccc tgt cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc	1975
Thr Pro Cys Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly	
395 400 405	
act cag ggt gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt	2023
Thr Gln Gly Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly	
410 415 420	
tcc tgg aga ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac	2071
Ser Trp Arg Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp	
425 430 435	
ctg gac gta gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc	2119
Leu Asp Val Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser	
440 445 450 455	
tgc tgg gtc cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg	2167
Cys Trp Val Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp	
460 465 470	
cag gct gaa cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc	2215
Gln Ala Glu His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro	
475 480 485	
agc act gat tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag	2263



Ser Thr Asp Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln

490

495

500

ccg tgt gct ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa 2311

Pro Cys Ala Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu

505

510

515

agt tct cag ttc cct cca ggc ttc tagaagcatc tgggccaggg ctcattggctg 2365

Ser Ser Gln Phe Pro Pro Gly Phe

520

525

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aaacttatga aaatgtatta agaaagagtg cagctcgaga gagattcaga gatggaacac 2485

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<211> 527

<212> PRT

<213> Homo sapiens

<400> 220

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu

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Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu

20

25

30

Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His

35

40

45

Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu

50

55

60

Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp  
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 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp  
    85                                      90                                      95  
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser  
    100                                      105                                      110  
 Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr  
    115                                      120                                      125  
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg  
    130                                      135                                      140  
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg  
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 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala  
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 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His  
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 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe  
    210                                      215                                      220  
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu  
 225                                      230                                      235                                      240  
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Ile Ser  
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 Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr Leu Val Glu Gly Glu  
    260                                      265                                      270  
 Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys Val Gln Gln Lys

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Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr Val Leu Lys His		
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Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly Asp Leu Gln		
325	330	335
Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg Pro Val Pro		
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Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg Gln Ala Pro		
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Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp Ser Ala Ser Pro		
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Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly Gly Ala Val Arg		
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Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser Pro Ala Leu		
405	410	415
Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Gln Trp Asn Ser		
420	425	430
Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly Pro Trp Phe Arg		
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His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala Ile Ser Gln Glu		
450	455	460
Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro Ala Glu Arg Val		
465	470	475
Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln Gly Thr Pro		
485	490	495

Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr Ser Gly Pro Cys

500

505

510

Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro Pro Gly Phe

515

520

525

&lt;210&gt; 221

&lt;211&gt; 2647

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (755).. (2335)

&lt;400&gt; 221

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Met Asp Val Val Glu Val Ala

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aag gga cac cga gct ggg ctg cca gag gac aag ggg cct aag cct ttt			871
Lys Gly His Arg Ala Gly Leu Pro Glu Asp Lys Gly Pro Lys Pro Phe			
25	30	35	
cga agc tac aac aac aac gtc gat cat ttg ggg att gta cat gag acg			919
Arg Ser Tyr Asn Asn Asn Val Asp His Leu Gly Ile Val His Glu Thr			
40	45	50	55
gag ctg cct cct ctg act gcg cgg gag gcg aag caa att cgg cgg gag			967
Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln Ile Arg Arg Glu			
60	65	70	
atc agc cga aag agc aag tgg gtg gat atg ctg gga gac tgg gag aaa			1015
Ile Ser Arg Lys Ser Lys Trp Val Asp Met Leu Gly Asp Trp Glu Lys			
75	80	85	
tac aaa agc agc aga aag ctc ata gat cga gcg tac aag gga atg ccc			1063
Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr Lys Gly Met Pro			
90	95	100	
atg aac atc cgg ggc ccg atg tgg tca gtc ctc ctg aac act gag gaa			1111
Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu Asn Thr Glu Glu			
105	110	115	
atg aag ttg aaa aac ccc gga aga tac cag atc atg aag gag aag ggc			1159
Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met Lys Glu Lys Gly			
120	125	130	135
aag agg tca tct gag cac atc cag cgc atc gac cgg gac gta agc ggg			1207
Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg Asp Val Ser Gly			

140	145	150	
aca tta agg aag cat ata ttc ttc agg gat cga tac gga acc aag cag			1255
Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr Gly Thr Lys Gln			
155	160	165	
cgg gaa cta ctc cac atc ctc ctg gca tat gag gag tat aac ccg gag			1303
Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu Tyr Asn Pro Glu			
170	175	180	
gtg ggc tac tgc agg gac ctg agc cac atc gcc gcc ttg ttc ctc ctc			1351
Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala Leu Phe Leu Leu			
185	190	195	
tat ctt cct gag gag gat gca ttc tgg gca ctg gtg cag ctg ctg gcc			1399
Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala Leu Val Gln Leu Leu Ala			
200	205	210	215
agt gag agg cac tcc ctg cag gga ttt cac agc cca aat ggc ggg acc			1447
Ser Glu Arg His Ser Leu Gln Gly Phe His Ser Pro Asn Gly Gly Thr			
220	225	230	
gtc cag ggg ctc caa gac caa cag gag cat gtg gta gcc acg tca caa			1495
Val Gln Gly Leu Gln Asp Gln Gln Glu His Val Val Ala Thr Ser Gln			
235	240	245	
ccc aag acc atg ggg cat cag atc tct ctc ggg ctc acc ctg cgc ctg			1543
Pro Lys Thr Met Gly His Gln Ile Ser Leu Gly Leu Thr Leu Arg Leu			
250	255	260	
tgg gac gtg tat ctg gta gaa ggc gaa cag gcg ttg atg ccg ata aca			1591
Trp Asp Val Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr			
265	270	275	
aga atc gcc ttt aag gtt cag cag aag cgc ctc acg aag acg tcc agg			1639
Arg Ile Ala Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg			

280	285	290	295	
tgt ggc ccg tgg gca cgt ttt tgc aac cgg ttc gtt gat acc tgg gcc	1687			
Cys Gly Pro Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala				
300	305	310		
agg gat gag gac act gtg ctc aag cat ctt agg gcc tct atg aag aaa	1735			
Arg Asp Glu Asp Thr Val Leu Lys His Leu Arg Ala Ser Met Lys Lys				
315	320	325		
cta aca aga aag cag ggg gac ctg cca ccc cca gcc aaa ccc gag caa	1783			
Leu Thr Arg Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln				
330	335	340		
ggg tcg tcg gca tcc agg cct gtg ccg gct tca cgt ggc ggg aag acc	1831			
Gly Ser Ser Ala Ser Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr				
345	350	355		
ctc tgc aag ggg gac agg cag gcc cct cca ggc cca cca gcc cgg ttc	1879			
Leu Cys Lys Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe				
360	365	370	375	
ccg cgg ccc att tgg tca gct tcc ccg cca cgg gca cct cgt tct tcc	1927			
Pro Arg Pro Ile Trp Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser				
380	385	390		
aca ccc tgt cct ggt ggg gct gtc cgg gaa gac acc tac cct gtg ggc	1975			
Thr Pro Cys Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly				
395	400	405		
act cag ggt gtg ccc agc ccg gcc ctg gct cag gga gga cct cag ggt	2023			
Thr Gln Gly Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly				
410	415	420		
tcc tgg aga ttc ctg cag tgg aac tcc atg ccc cgc ctc cca acg gac	2071			
Ser Trp Arg Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp				

425	430	435	
ctg gac gta gag ggc cct tgg ttc cgc cat tat gat ttc aga cag agc			2119
Leu Asp Val Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser			
440	445	450	455
tgc tgg gtc cgt gcc ata tcc cag gag gac cag ctg gcc ccc tgc tgg			2167
Cys Trp Val Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp			
460	465	470	
cag gct gaa cac cct gcg gag cgg gtg aga tcg gct ttc gct gca ccc			2215
Gln Ala Glu His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro			
475	480	485	
agc act gat tcc gac cag ggc acc ccc ttc aga gct agg gac gaa cag			2263
Ser Thr Asp Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln			
490	495	500	
ccg tgt gct ccc acc tca ggg cct tgc ctc tgc ggc ctc cac ttg gaa			2311
Pro Cys Ala Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu			
505	510	515	
agt tct cag ttc cct cca ggc ttc tagaagcatc tgggccaggg ctcatggctg			2365
Ser Ser Gln Phe Pro Pro Gly Phe			
520	525		
gataatttcc ctaggcttaa caaccgaagc aagcttcgca tcctcgtttt atttttggtt			2425
aaacttatga aaatgtatta agaaagagtg cagctcgaga gagattcaga gatggaacac			2485
accagacccc agatcacaaa gccaaaccatg cccagcccct cccagcaccc ccagccccac			2545
gaccatcggt ctgaattctg acgacaccgt gagcctgcct ttgtacttca aactcatgga			2605
aggataacca ctttcatggt ttgaaataaa tgtttcctgt tg			2647

&lt;210&gt; 222

&lt;211&gt; 527



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

Met Asp Val Val Glu Val Ala Gly Ser Trp Trp Ala Gln Glu Arg Glu  
1                    5                    10                    15  
Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu  
                  20                    25                    30  
Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His  
                  35                    40                    45  
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu  
                  50                    55                    60  
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp  
65                    70                    75                    80  
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp  
                  85                    90                    95  
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser  
                  100                    105                    110  
Val Leu Leu Asn Thr Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr  
                  115                    120                    125  
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg  
                  130                    135                    140  
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg  
145                    150                    155                    160  
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala  
                  165                    170                    175  
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His  
                  180                    185                    190

Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp  
195 200 205  
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe  
210 215 220  
His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu  
225 230 235 240  
His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Ile Ser  
245 250 255  
Leu Gly Leu Thr Leu Arg Leu Trp Asp Val Tyr Leu Val Glu Gly Glu  
260 265 270  
Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys Val Gln Gln Lys  
275 280 285  
Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro Trp Ala Arg Phe Cys Asn  
290 295 300  
Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr Val Leu Lys His  
305 310 315 320  
Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly Asp Leu Pro  
325 330 335  
Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg Pro Val Pro  
340 345 350  
Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg Gln Ala Pro  
355 360 365  
Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp Ser Ala Ser Pro  
370 375 380  
Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly Gly Ala Val Arg  
385 390 395 400  
Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser Pro Ala Leu

405	410	415
Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Gln Trp Asn Ser		
420	425	430
Met Pro Arg Leu Pro Thr Asp Leu Asp Val Glu Gly Pro Trp Phe Arg		
435	440	445
His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala Ile Ser Gln Glu		
450	455	460
Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu His Pro Ala Glu Arg Val		
465	470	475
Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln Gly Thr Pro		
485	490	495
Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr Ser Gly Pro Cys		
500	505	510
Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro Pro Gly Phe		
515	520	525

&lt;210&gt; 223

&lt;211&gt; 1817

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (119)..(415)

&lt;400&gt; 223

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cgcagctccc tttgccttc cttggccggg gttccctccc tccccagct gccagtc	118
atg ggg gct gct gtg ttt ttc gga tgc acc ttc gtc gcg ttc ggc cca	166

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro  
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 gcc ttc tcc ctt ttc ctg atc act gta gct gga gac cca ctt cgg gtt 214  
 Ala Phe Ser Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val  
 20 25 30  
 atc atc ctg gtg gcg gga gcc ttt ttc tgg ctg gtc tcc ctg ctc ttg 262  
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu  
 35 40 45  
 gct tct gtg gtc tgg ttc atc ttg gtc cac gtg aca gac cga tca gat 310  
 Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp  
 50 55 60  
 gca cgg ctc cag tat ggc ctc ctg att ttt ggt gct gct gtc tct gtc 358  
 Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val  
 65 70 75 80  
 ctt cta cag gaa gtg ttc cgt ttt gct tac tac aag ctc ctt aag cag 406  
 Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Gln  
 85 90 95  
 atg agg gct tagcatcact gaggtaggac ggaagatcac ccatctccat 455  
 Met Arg Ala  
 ccgacagatg gcctatgttt ctggtctgtc cticgggtatc atcagtgggtg tcttctctgt 515  
 tatcaatatt ttggctgatg cacttgggcc aggtgtgggtt gggatccatg gagactcacc 575  
 ctattacttc ctgacttcag cttttctgac agcagccatt atcctgctcc acaccttttg 635  
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 gggaggtttt ctatcactgt gttgtttttc tgctgagggt ggaatattct gtccttttaa 1775  
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<210> 224

<211> 99

<212> PRT

<213> Mus musculus

<400> 224

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 20 25 30  
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu  
 35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp

50

55

60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val

65

70

75

80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Gln

85

90

95

Met Arg Ala

<210> 225

<211> 1997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136)..(876)

<400> 225

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cccacctgac cagcc atg ggg gct gcg gtg ttt ttc ggc tgc act ttc gtc 171

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val

1

5

10

gcg ttc ggc ccg gcc ttc gcg ctt ttc ttg atc act gtg gct ggg gac 219

Ala Phe Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp

15

20

25

ccg ctt cgc gtt atc atc ctg gtc gca ggg gca ttt ttc tgg ctg gtc 267

Pro Leu Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val

30

35

40

tcc	ctg	ctc	ctg	gcc	tct	gtg	gtc	tgg	ttc	atc	ttg	gtc	cat	gtg	acc	315
Ser	Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	
45				50					55					60		
gac	cgg	tca	gat	gcc	cgg	ctc	cag	tac	ggc	ctc	ctg	att	ttt	ggg	gct	363
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	
				65					70					75		
gct	gtc	tct	gtc	ctt	cta	cag	gag	gtg	ttc	cgc	ttt	gcc	tac	tac	aag	411
Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	
				80					85					90		
ctg	ctt	aag	aag	gca	gat	gag	ggg	tta	gca	tcg	ctg	agt	gag	gac	gga	459
Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	
				95					100					105		
aga	tca	ccc	atc	tcc	atc	cgc	cag	atg	gcc	tat	gtt	tct	ggg	ctc	tcc	507
Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	
				110					115					120		
ttc	ggg	atc	atc	agt	ggg	gtc	ttc	tct	gtt	atc	aat	att	ttg	gct	gat	555
Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	
125					130					135				140		
gca	ctt	ggg	cca	ggg	gtg	gtt	ggg	atc	cat	gga	gac	tca	ccc	tat	tac	603
Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	
				145					150					155		
ttc	ctg	act	tca	gcc	ttt	ctg	aca	gca	gcc	att	atc	ctg	ctc	cat	acc	651
Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	
				160					165					170		
ttt	tgg	gga	gtt	gtg	ttc	ttt	gat	gcc	tgt	gag	agg	aga	cgg	tac	tgg	699
Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	
				175					180					185		

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 Ala Leu Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr  
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 Phe Leu Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val  
 205 210 215 220  
 act gtt tcc atg ggg ctc tgg gcc ttc atc aca gct gga ggg tcc ctc 843  
 Thr Val Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu  
 225 230 235  
 cga agt att cag cgc agc ctc ttg tgt aag gac tgactacctg gactgatcgc 896  
 Arg Ser Ile Gln Arg Ser Leu Leu Cys Lys Asp  
 240 245  
 ctgacagatc ccacctgcct gtccactgcc catgactgag cccagcccca gcccgggtcc 956  
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<210> 226

<211> 247

<212> PRT

<213> Homo sapiens

<400> 226

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1 5 10 15

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20 25 30

Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu

35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp

50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val

65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys

85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile

100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile

115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro

130                      135                      140  
 Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser  
 145                      150                      155                      160  
 Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val  
                     165                      170                      175  
 Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu  
                     180                      185                      190  
 Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro  
                     195                      200                      205  
 Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met  
                     210                      215                      220  
 Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln  
 225                      230                      235                      240  
 Arg Ser Leu Leu Cys Lys Asp  
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<210> 227

<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190).. (984)

<400> 227

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 ccagctggcg cgcccctccc atttgctgt cctgggtcagg cccccacccc ctttcccacc    180

tgaccagcc atg ggg gct gcg gtg ttt ttc ggc tgc act ttc gtc gcg ttc 231  
 Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe  
 1 5 10  
 ggc ccg gcc ttc gcg ctt ttc ttg atc act gtg gct ggg gac ccg ctt 279  
 Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu  
 15 20 25 30  
 cgc gtt atc atc ctg gtc gca ggg gca ttt ttc tgg ctg gtc tcc ctg 327  
 Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu  
 35 40 45  
 ctc ctg gcc tct gtg gtc tgg ttc atc ttg gtc cat gtg acc gac cgg 375  
 Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg  
 50 55 60  
 tca gat gcc cgg ctc cag tac ggc ctc ctg att ttt ggt gct gct gtc 423  
 Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val  
 65 70 75  
 tct gtc ctt cta cag gag gtg ttc cgc ttt gcc tac tac aag ctg ctt 471  
 Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu  
 80 85 90  
 aag aag gca gat gag ggg tta gca tcg ctg agt gag gac gga aga tca 519  
 Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser  
 95 100 105 110  
 ccc atc tcc atc cgc cag atg gcc tat gtt tct ggt ctc tcc ttc ggt 567  
 Pro Ile Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly  
 115 120 125  
 atc atc agt ggt gtc ttc tct gtt atc aat att ttg gct gat gca ctt 615  
 Ile Ile Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu  
 130 135 140

ggg cca ggt gtg gtt ggg atc cat gga gac tca ccc tat tac ttc ctg 663  
 Gly Pro Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu  
 145 150 155  
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 Thr Ser Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp  
 160 165 170  
 gga gtt gtg ttc ttt gat gcc tgt gag agg aga cgg tac tgg gct ttg 759  
 Gly Val Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu  
 175 180 185 190  
 ggc ctg gtg gtt ggg agt cac cta ctg aca tcg gga ctg aca ttc ctg 807  
 Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu  
 195 200 205  
 aac ccc tgg tat gag gcc agc ctg ctg ccc atc tat gca gtc act gtt 855  
 Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val  
 210 215 220  
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 Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser  
 225 230 235  
 att cag cgc agc ctc ttg tgc cga cgg cag gag gac agt cgg gtg atg 951  
 Ile Gln Arg Ser Leu Leu Cys Arg Arg Gln Glu Asp Ser Arg Val Met  
 240 245 250  
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 Val Tyr Ser Ala Leu Arg Ile Pro Pro Glu Asp  
 255 260 265  
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 atggaggctc aaggatagat gagctctgag tttctcagta ctccctcaag actggacatc 1184

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ccttttttttc ttttttgagg tggggggagg gaggaggat attggaactc ttctaacctc 1304
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taccatgaca tcgtagggaa ggaggggaga tttttttgta gtttttaatt ggggtgtggg 1604
aggggcgggg aggttttcta taaactgtat cattttctgc tgagggtgga gtgtcccatc 1664
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<210> 228

<211> 265

<212> PRT

<213> Homo sapiens

<400> 228

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          20           25           30
Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
          35           40           45
Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
          50           55           60
Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65           70           75           80
Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
          85           90           95

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Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile  
                     100                    105                    110  
 Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile  
                     115                    120                    125  
 Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro  
                     130                    135                    140  
 Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser  
 145                    150                    155                    160  
 Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val  
                     165                    170                    175  
 Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu  
                     180                    185                    190  
 Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro  
                     195                    200                    205  
 Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met  
                     210                    215                    220  
 Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln  
 225                    230                    235                    240  
 Arg Ser Leu Leu Cys Arg Arg Gln Glu Asp Ser Arg Val Met Val Tyr  
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 Ser Ala Leu Arg Ile Pro Pro Glu Asp  
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<210> 229

<211> 2212

<212> DNA

<213> Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (43).. (813)

&lt;400&gt; 229

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Met Ala Ala Asp

1

ggg gtg gac gaa cgt tcg cct ctg ctg tca gca tcc cat tcg gga aat 102

Gly Val Asp Glu Arg Ser Pro Leu Leu Ser Ala Ser His Ser Gly Asn

5 10 15 20

gtc act ccc aca gcc ccg ccg tac ttg cag gaa agc agc ccc aga gct 150

Val Thr Pro Thr Ala Pro Pro Tyr Leu Gln Glu Ser Ser Pro Arg Ala

25 30 35

gaa ctc cca cct ccg tat aca gcc atc gcc agt cca gga aca agt ggt 198

Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro Gly Thr Ser Gly

40 45 50

att ccc gtg atc aac tgt cgt gtg tgc caa tct cta atc aac ctg gat 246

Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu Ile Asn Leu Asp

55 60 65

ggt aaa ctt cac cag cat gtg gtt aag tgc aca gtt tgc aat gaa gct 294

Gly Lys Leu His Gln His Val Val Lys Cys Thr Val Cys Asn Glu Ala

70 75 80

acg cca atc aaa acc ccc cca aca ggg aag aaa tat gtt aga tgc cct 342

Thr Pro Ile Lys Thr Pro Pro Thr Gly Lys Lys Tyr Val Arg Cys Pro

85 90 95 100

tgt aat tgt cta ctc att tgt aag gat aca tct cgg cga ata gga tgt 390

Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg Arg Ile Gly Cys

105	110	115	
ccg aga ccc aac tgt cga cgc ata att aac ctt ggc ccc gta atg ctc			438
Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly Pro Val Met Leu			
120	125	130	
att tct gaa gag caa cca gcc caa cct gca ttg ccg atc cag cca gaa			486
Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro Ile Gln Pro Glu			
135	140	145	
ggc aca agg gta gtg tgc ggg cac tgc ggg aac aca ttc ctg tgg atg			534
Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr Phe Leu Trp Met			
150	155	160	
gaa ctg agg ttc aac act ctg gca aaa tgc cca cac tgc aaa aaa atc			582
Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His Cys Lys Lys Ile			
165	170	175	180
tcc tcg gta ggt agc gcc ctt ccc cgg aga cgc tgc tgt gcg tat gtc			630
Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys Cys Ala Tyr Val			
185	190	195	
acc atc gga atg ata tgt att ttc att gca gtt gga tta act gtt ggc			678
Thr Ile Gly Met Ile Cys Ile Phe Ile Ala Val Gly Leu Thr Val Gly			
200	205	210	
aca caa gat ttt tca agg cga ttt cat gca acc tat gtg tct tgg gca			726
Thr Gln Asp Phe Ser Arg Arg Phe His Ala Thr Tyr Val Ser Trp Ala			
215	220	225	
att gct tat ctg cta ggt ttg att tgc ctt atc cga gct tgt tac tgg			774
Ile Ala Tyr Leu Leu Gly Leu Ile Cys Leu Ile Arg Ala Cys Tyr Trp			
230	235	240	
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Gly Ala Ile Arg Val Ser Tyr Pro Glu His Gly Phe Ala			



245	250	255	
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attcaaaaa			2212

&lt;210&gt; 230

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 230

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His Ser Gly Asn Val Thr Pro Thr Ala Pro Pro Tyr Leu Gln Glu Ser

20 25 30

Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro

35 40 45

Gly Thr Ser Gly Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu

50 55 60

Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val Lys Cys Thr Val

65 70 75 80

Cys Asn Glu Ala Thr Pro Ile Lys Thr Pro Pro Thr Gly Lys Lys Tyr

85 90 95

Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg

100 105 110

Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly

115 120 125

Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro

130 135 140

Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr

145 150 155 160

Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His

165 170 175

Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys

180 185 190  
 Cys Ala Tyr Val Thr Ile Gly Met Ile Cys Ile Phe Ile Ala Val Gly  
 195 200 205  
 Leu Thr Val Gly Thr Gln Asp Phe Ser Arg Arg Phe His Ala Thr Tyr  
 210 215 220  
 Val Ser Trp Ala Ile Ala Tyr Leu Leu Gly Leu Ile Cys Leu Ile Arg  
 225 230 235 240  
 Ala Cys Tyr Trp Gly Ala Ile Arg Val Ser Tyr Pro Glu His Gly Phe  
 245 250 255  
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<210> 231

<211> 2255

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (77)..(847)

<400> 231

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 Met Ala Ala Asp Gly Val Asp Glu Arg Ser Pro Leu  
 1 5 10  
 ctg tca gca tcc cac tcc gga aat gtc act ccc acc gcc cca ccg tac 160  
 Leu Ser Ala Ser His Ser Gly Asn Val Thr Pro Thr Ala Pro Pro Tyr  
 15 20 25  
 ttg caa gaa agc agc ccc aga gcg gag ctc cca cct cca tat aca gcc 208

Leu Gln Glu Ser Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala  
 30 35 40  
 att gcc agt cca gac gcc agt ggt att cca gta ata aac tgc cgt gtg 256  
 Ile Ala Ser Pro Asp Ala Ser Gly Ile Pro Val Ile Asn Cys Arg Val  
 45 50 55 60  
 tgc caa tca cta atc aat ttg gat ggc aag ctt cac cag cat gtg gtt 304  
 Cys Gln Ser Leu Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val  
 65 70 75  
 aag tgc aca gtt tgc aat gaa gct acg cca atc aaa aac ccc cca aca 352  
 Lys Cys Thr Val Cys Asn Glu Ala Thr Pro Ile Lys Asn Pro Pro Thr  
 80 85 90  
 ggc aag aaa tat gtt aga tgc cct tgt aat tgt ctt ctc att tgt aag 400  
 Gly Lys Lys Tyr Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys  
 95 100 105  
 gac aca tct cgg cga ata gga tgc cca aga ccc aac tgt aga cgg ata 448  
 Asp Thr Ser Arg Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile  
 110 115 120  
 att aac ctt ggc cca gta atg ctt att tct gaa gaa caa cca gct cag 496  
 Ile Asn Leu Gly Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln  
 125 130 135 140  
 cct gca ttg cca atc caa cca gaa ggt aca agg gtc gtg tgt ggg cac 544  
 Pro Ala Leu Pro Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His  
 145 150 155  
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 Cys Gly Asn Thr Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala  
 160 165 170  
 aaa tgc cca cac tgc aaa aaa atc tcc tca gtg ggt agt gca ctt cca 640

Lys Cys Pro His Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro  
 175 180 185  
 cga aga cgc tgc tgt gca tat att acc att gga atg ata tgt att ttc 688  
 Arg Arg Arg Cys Cys Ala Tyr Ile Thr Ile Gly Met Ile Cys Ile Phe  
 190 195 200  
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 Ile Gly Val Gly Leu Thr Val Gly Thr Pro Asp Phe Ala Arg Arg Phe  
 205 210 215 220  
 cga gca acc tat gtt tct tgg gca att gct tat ctc cta gga ttg atc 784  
 Arg Ala Thr Tyr Val Ser Trp Ala Ile Ala Tyr Leu Leu Gly Leu Ile  
 225 230 235  
 tgc ctt atc cga gct tgt tat tgg gga gcc ata aga gtc agt tat cca 832  
 Cys Leu Ile Arg Ala Cys Tyr Trp Gly Ala Ile Arg Val Ser Tyr Pro  
 240 245 250  
 gaa cac agt ttt gca taagcttggt tatgattcag taatgcaggt gagagtgtct 887  
 Glu His Ser Phe Ala  
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 agtagaatta gacagtgaga tcatctgagt aaattgattg gtgattccag agataagact 2087  
 aatattttta attatttatg atactgatta gtataaaaac gtactcatca cagaatttga 2147  
 agcaaaatac atgtacactt caaagagtaa atgacaaatg tataaatgct gtagctcagg 2207  
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<210> 232

<211> 257

<212> PRT

<213> Homo sapiens

<400> 232

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                     20                      25                      30  
 Ser Pro Arg Ala Glu Leu Pro Pro Pro Tyr Thr Ala Ile Ala Ser Pro  
                     35                      40                      45  
 Asp Ala Ser Gly Ile Pro Val Ile Asn Cys Arg Val Cys Gln Ser Leu  
                     50                      55                      60

Ile Asn Leu Asp Gly Lys Leu His Gln His Val Val Lys Cys Thr Val  
 65                                70                                75                                80  
 Cys Asn Glu Ala Thr Pro Ile Lys Asn Pro Pro Thr Gly Lys Lys Tyr  
                                  85                                90                                95  
 Val Arg Cys Pro Cys Asn Cys Leu Leu Ile Cys Lys Asp Thr Ser Arg  
                                  100                                105                                110  
 Arg Ile Gly Cys Pro Arg Pro Asn Cys Arg Arg Ile Ile Asn Leu Gly  
                                  115                                120                                125  
 Pro Val Met Leu Ile Ser Glu Glu Gln Pro Ala Gln Pro Ala Leu Pro  
                                  130                                135                                140  
 Ile Gln Pro Glu Gly Thr Arg Val Val Cys Gly His Cys Gly Asn Thr  
 145                                150                                155                                160  
 Phe Leu Trp Met Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His  
                                  165                                170                                175  
 Cys Lys Lys Ile Ser Ser Val Gly Ser Ala Leu Pro Arg Arg Arg Cys  
                                  180                                185                                190  
 Cys Ala Tyr Ile Thr Ile Gly Met Ile Cys Ile Phe Ile Gly Val Gly  
                                  195                                200                                205  
 Leu Thr Val Gly Thr Pro Asp Phe Ala Arg Arg Phe Arg Ala Thr Tyr  
                                  210                                215                                220  
 Val Ser Trp Ala Ile Ala Tyr Leu Leu Gly Leu Ile Cys Leu Ile Arg  
 225                                230                                235                                240  
 Ala Cys Tyr Trp Gly Ala Ile Arg Val Ser Tyr Pro Glu His Ser Phe  
                                  245                                250                                255  
 Ala

<210> 233

&lt;211&gt; 1915

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (80)..(1297)

&lt;400&gt; 233

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agagttcctg atctatgaa atg gca gag aat gga aaa aat tgt gac cag aga 112
      Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg
              1              5              10
cgc ata gca atg agt aag gat cag cac aat gga agt ctc aca gac ccc 160
Arg Ile Ala Met Ser Lys Asp Gln His Asn Gly Ser Leu Thr Asp Pro
              15              20              25
tct tca gtt cat gag aag aag aga agg gat cgg gaa gaa aga cag aat 208
Ser Ser Val His Glu Lys Lys Arg Arg Asp Arg Glu Glu Arg Gln Asn
              30              35              40
att gtc ctg tgg aga cag cca ctc att acc ttg cag tat ttc tct ctg 256
Ile Val Leu Trp Arg Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu
              45              50              55
gaa act ctt gta gtt ttg aag gaa tgg acc tca aaa ttg tgg cat cgt 304
Glu Thr Leu Val Val Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg
              60              65              70              75
caa agc att gtg gtg tcc ttt tta ctg ctg ctt gct gcg ctt gta gct 352
Gln Ser Ile Val Val Ser Phe Leu Leu Leu Leu Ala Ala Leu Val Ala
              80              85              90
acg tat tat gtg gaa gga gcg cac caa cag tat gtg cag cgg ata gag 400

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Thr Tyr Tyr Val Glu Gly Ala His Gln Gln Tyr Val Gln Arg Ile Glu	
95 100 105	
aag cag ttt ctt ttg tat gca tac tgg ata ggc ctg ggg att ttg tcc	448
Lys Gln Phe Leu Leu Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser	
110 115 120	
tct gtt ggt ctt gga aca gga ctg cac acc ttt ctg ctt tat ctg ggc	496
Ser Val Gly Leu Gly Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly	
125 130 135	
cca cat ata gct tca gtt aca tta gct gct tat gaa tgc aat tcg gtg	544
Pro His Ile Ala Ser Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val	
140 145 150 155	
aat ttc cct gag cca ccc tat cct gac cag att atc tgc cca gag gaa	592
Asn Phe Pro Glu Pro Pro Tyr Pro Asp Gln Ile Ile Cys Pro Glu Glu	
160 165 170	
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Glu Gly Ala Glu Gly Ala Ile Ser Leu Trp Ser Ile Ile Ser Lys Val	
175 180 185	
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Arg Ile Glu Ala Cys Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu	
190 195 200	
cct cca tat ttc atg gcc agg gca gct cgc ctc tca ggt gct gaa cca	736
Pro Pro Tyr Phe Met Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro	
205 210 215	
gat gat gaa gag tat cag gaa ttt gaa gaa atg ctg gaa cat gca gag	784
Asp Asp Glu Glu Tyr Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu	
220 225 230 235	
gct gca caa gac ttt gca tca cgg gct aaa ctg gca gtt caa aaa cta	832

Ala Ala Gln Asp Phe Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu	
240	245
gta cag aaa gtt gga ttt ttt gga att ttg gcc tgt gct tct att cca	880
Val Gln Lys Val Gly Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro	
255	260
aac ccc ctg ttt gac ctg gct gga ata acg tgt ggg cac ttc ctt gta	928
Asn Pro Leu Phe Asp Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val	
270	275
cct ttc tgg acc ttc ttt ggt gca acc ctg att ggg aaa gca atc att	976
Pro Phe Trp Thr Phe Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile	
285	290
aaa atg cat atc cag aaa ata ttt gtt ata gta act ttc agc aag cac	1024
Lys Met His Ile Gln Lys Ile Phe Val Ile Val Thr Phe Ser Lys His	
300	305
atc gtg gag cag atg gtg act ttc att ggt gct gtc ccc ggc ata ggt	1072
Ile Val Glu Gln Met Val Thr Phe Ile Gly Ala Val Pro Gly Ile Gly	
320	325
ccg tct ctg cag aag cct ttt caa gag tac ctg gag gcg cag cgg cag	1120
Pro Ser Leu Gln Lys Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln	
335	340
aag ctt cat cac aga agt gaa gcg ggc aca ccg cag gga gaa aac tgg	1168
Lys Leu His His Arg Ser Glu Ala Gly Thr Pro Gln Gly Glu Asn Trp	
350	355
tta tcc tgg atg ttt gag aag ctg gtg gtt gca atg gtg tgt tac ttt	1216
Leu Ser Trp Met Phe Glu Lys Leu Val Val Ala Met Val Cys Tyr Phe	
365	370
gtc ctg tct att att aac tcc atg gca caa aac tat gcc aaa cga atc	1264

Val Leu Ser Ile Ile Asn Ser Met Ala Gln Asn Tyr Ala Lys Arg Ile

380

385

390

395

cag cag cgc ttg aac tca gag gag aaa act aaa taagcagaga gtttttatct 1317

Gln Gln Arg Leu Asn Ser Glu Glu Lys Thr Lys

400

405

gcagaagtta acatggtgga gtcctgcctt acactgggag ggctctaacc aggaaggaag 1377

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tatgttacac tgacatactt tatttgtaa ggtaagggtg ctacaccctc agttcaatcc 1497

acgtcgtatt ctttagggtg gatgtgatgt tctgctgcaa acttaacaaa aactggcctt 1557

ctgatacctt cacagggccca cacagaacct tctgaagtat gttaaataatg tcaggctttt 1617

taggcttgtc acaaatgatt gtttttttct aagtccecaa atgtatataa gttatatata 1677

ttggatagca atcttgcatt tctatcatgg aacaatttaa catgccttcc tttcccaccc 1737

tcaaaaaggc cattttatga cgcattgcac accctctggg gaaattgata tttaaatttt 1797

gaaacagtat aaggaaaatc tgggtggtgt ctcacaaatg agtacgccat tttttattct 1857

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<210> 234

<211> 406

<212> PRT

<213> Mus musculus

<400> 234

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10

15

Lys Asp Gln His Asn Gly Ser Leu Thr Asp Pro Ser Ser Val His Glu

20

25

30

Lys Lys Arg Arg Asp Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg

35

40

45

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Thr Leu Val Val  
50 55 60  
Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val  
65 70 75 80  
Ser Phe Leu Leu Leu Leu Ala Ala Leu Val Ala Thr Tyr Tyr Val Glu  
85 90 95  
Gly Ala His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu  
100 105 110  
Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly  
115 120 125  
Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser  
130 135 140  
Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro  
145 150 155 160  
Pro Tyr Pro Asp Gln Ile Ile Cys Pro Glu Glu Glu Gly Ala Glu Gly  
165 170 175  
Ala Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys  
180 185 190  
Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met  
195 200 205  
Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr  
210 215 220  
Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ala Ala Gln Asp Phe  
225 230 235 240  
Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly  
245 250 255  
Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp

260                                      265                                      270  
 Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe  
 275                                      280                                      285  
 Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln  
 290                                      295                                      300  
 Lys Ile Phe Val Ile Val Thr Phe Ser Lys His Ile Val Glu Gln Met  
 305                                      310                                      315                                      320  
 Val Thr Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys  
 325                                      330                                      335  
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Arg  
 340                                      345                                      350  
 Ser Glu Ala Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe  
 355                                      360                                      365  
 Glu Lys Leu Val Val Ala Met Val Cys Tyr Phe Val Leu Ser Ile Ile  
 370                                      375                                      380  
 Asn Ser Met Ala Gln Asn Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn  
 385                                      390                                      395                                      400  
 Ser Glu Glu Lys Thr Lys  
 405

<210> 235

<211> 2515

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114)..(1331)

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Met	
1	
gca gag aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag	164
Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys	
5 10 15	
gaa cat cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag	212
Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys	
20 25 30	
aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag	260
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln	
35 40 45	
ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg	308
Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu	
50 55 60 65	
aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct	356
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser	
70 75 80	
ttt tta ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga	404
Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly	
85 90 95	
gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat	452
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr	
100 105 110	
gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca	500

Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr	
115 120 125	
ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt	548
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val	
130 135 140 145	
aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc	596
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro	
150 155 160	
tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc	644
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr	
165 170 175	
att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg	692
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met	
180 185 190	
tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc	740
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala	
195 200 205	
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag	788
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln	
210 215 220 225	
gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc	836
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala	
230 235 240	
tcc cgg gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt	884
Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe	
245 250 255	
ttt gga att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg	932

Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu  
 260 265 270  
 gct gga ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt 980  
 Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe  
 275 280 285  
 ggt gca acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa 1028  
 Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys  
 290 295 300 305  
 att ttt gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg 1076  
 Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val  
 310 315 320  
 gct ttc att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca 1124  
 Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro  
 325 330 335  
 ttt cag gag tac ctg gag gct caa cgg cag aag ctt cac cac aaa agc 1172  
 Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser  
 340 345 350  
 gaa atg ggc aca cca cag gga gaa aac tgg ttg tcc tgg atg ttt gaa 1220  
 Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu  
 355 360 365  
 aag ttg gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac 1268  
 Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn  
 370 375 380 385  
 tcc atg gca caa agt tat gcc aaa cga atc cag cag cgg ttg aac tca 1316  
 Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser  
 390 395 400  
 gag gag aaa act aaa taagtagaga aagttttaaa ctgcagaaat tggagtggat 1371



Glu Glu Lys Thr Lys

405

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gggttctgcc ttaaattggg aggactccaa gccgggaagg aaaattccct tttccaacct 1431
gtatcaattt ttacaacttt tttcctgaaa gcagtttagt ccatactttg cactgacata 1491
ctttttcctt ctgtgctaag gtaaggatc caccctcgat gcaatccacc ttgtgttttc 1551
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tatgttaa atgtcaagct ttttaggctt gtcacaaatg attgctttgt tttcctaagt 1731
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agtcttgaaa aaaactttat aaagacatct ttaatcattc caaaattgtg tccgttttct 2031
tgagcgtttt gattttttac ttttagctta taccagctga atggcagcct tgcctaatec 2091
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gttttcttgc cgttctgtaa gtgttttatt cttagtgtga tttttttcca ttgggatgtt 2451
tttgattgaa cttgttcatt ttgttttgct tgggaggaaa ataaacaatt ttactttttt 2511
cctt 2515

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&lt;210&gt; 236

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn  
 1                      5                      10                      15  
 Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu  
                     20                      25                      30  
 Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg  
                     35                      40                      45  
 Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile  
                     50                      55                      60  
 Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val  
 65                      70                      75                      80  
 Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu  
                     85                      90                      95  
 Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu  
                     100                      105                      110  
 Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly  
                     115                      120                      125  
 Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser  
                     130                      135                      140  
 Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro  
 145                      150                      155                      160  
 Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly  
                     165                      170                      175  
 Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys  
                     180                      185                      190  
 Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met  
                     195                      200                      205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr  
210 215 220  
Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe  
225 230 235 240  
Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly  
245 250 255  
Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp  
260 265 270  
Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe  
275 280 285  
Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln  
290 295 300  
Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met  
305 310 315 320  
Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys  
325 330 335  
Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys  
340 345 350  
Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe  
355 360 365  
Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile  
370 375 380  
Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn  
385 390 395 400  
Ser Glu Glu Lys Thr Lys  
405

&lt;210&gt; 237

&lt;211&gt; 2302

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (659).. (1510)

&lt;400&gt; 237

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ggacccccctt gatgtccagc actgggctct gaccatcctg aagacatggt gccccaggg      180
acctttgaca ccctggggtc tgaggggtcc tgactacaag gaggaatgaa taggggggtg      240
ccatgggtctt cgtgtccctt gccaacctct gtcccctctc cttcctgcct ataggtggtt      300
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aatgctaata acatgaactt ggtttacaca attagaccag attgctaaga gacatctctg      420
tcatgccgct cttgggaacc cccatgatgt atatagcact gggctctgac caccatgggtg      480
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gatgctgggt gggagtgtag ccctttgtca cctaccagct tgccctgtgt ctttgcagcc      600
tctgcgacag cattgcttct agccctcttg ctattcttac cttgagactg tgagggcc      658
atg gct gag aga gtg ctg gtg ccc acc cag ata ggc cgg ggg gac cgc      706
Met Ala Glu Arg Val Leu Val Pro Thr Gln Ile Gly Arg Gly Asp Arg
1           5           10           15
tac tac aca tac acg gag ttg ttg gct atc tca cgg cgt ttc aag cag      754
Tyr Tyr Thr Tyr Thr Glu Leu Leu Ala Ile Ser Arg Arg Phe Lys Gln
20           25           30
aac ccc aat gag ctc atg gtc acc tgg atc ctg cgg gtg tat gac cag      802
Asn Pro Asn Glu Leu Met Val Thr Trp Ile Leu Arg Val Tyr Asp Gln

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35	40	45	
gga ggc cct gcc ctg tcc ctg aat tct ggg gag ctg ggg ctg ctg ggt			850
Gly Gly Pro Ala Leu Ser Leu Asn Ser Gly Glu Leu Gly Leu Leu Gly			
50	55	60	
gac ctc acc cat gat gcc atc ttt aac tac cgc tgc aag gcc ctg cgg			898
Asp Leu Thr His Asp Ala Ile Phe Asn Tyr Arg Cys Lys Ala Leu Arg			
65	70	75	80
ggg gct ggc tgc cag act ctc ctg agc tgg ctg ctg cag gcc tgg cgt			946
Gly Ala Gly Cys Gln Thr Leu Leu Ser Trp Leu Leu Gln Ala Trp Arg			
	85	90	95
cag cgt tgg gaa tcc tcc ctg cat ttt gag gcc acc gag tta ccc ttc			994
Gln Arg Trp Glu Ser Ser Leu His Phe Glu Ala Thr Glu Leu Pro Phe			
100	105	110	
agg ccc tgg acc acc atg gag gaa ggc atc cag ttg gtg cgt gag ctg			1042
Arg Pro Trp Thr Thr Met Glu Glu Gly Ile Gln Leu Val Arg Glu Leu			
115	120	125	
ggc atg att gag tgg atc tac ctt gac cca gaa ggg ccc gtg gac ctg			1090
Gly Met Ile Glu Trp Ile Tyr Leu Asp Pro Glu Gly Pro Val Asp Leu			
130	135	140	
gcc cca gag gat gtg gcc ttc act caa ggc ctg cag cgg cgc ctg ctc			1138
Ala Pro Glu Asp Val Ala Phe Thr Gln Gly Leu Gln Arg Arg Leu Leu			
145	150	155	160
aca gca gcc ccc tct gag ctg cgg ctt tca ctg gtc agc ctg ctg gta			1186
Thr Ala Ala Pro Ser Glu Leu Arg Leu Ser Leu Val Ser Leu Leu Val			
	165	170	175
cgt ggc atg aca gtg ttg gag gct gtg atg gag atc cag act att gct			1234
Arg Gly Met Thr Val Leu Glu Ala Val Met Glu Ile Gln Thr Ile Ala			

180	185	190	
gac gtg ggt ctg ctc tgg cgc cag agc cat cca ggc cgc acc aag ctc			1282
Asp Val Gly Leu Leu Trp Arg Gln Ser His Pro Gly Arg Thr Lys Leu			
195	200	205	
atg ttg ggg ccc aac cca act cgt aag gac ctc cta ggc tgg ctg ctc			1330
Met Leu Gly Pro Asn Pro Thr Arg Lys Asp Leu Leu Gly Trp Leu Leu			
210	215	220	
agc cac ggt gta ccc cgg gag caa gta gac aga cag ccc acc aag gta			1378
Ser His Gly Val Pro Arg Glu Gln Val Asp Arg Gln Pro Thr Lys Val			
225	230	235	240
ctc cta gaa ctc tac atc aaa gaa gcc aag cgc agt cgc ggc cac ccc			1426
Leu Leu Glu Leu Tyr Ile Lys Glu Ala Lys Arg Ser Arg Gly His Pro			
245	250	255	
aac tat ggg ctg aac gag gag cag ccc cca cca ccc cct tac tcc gac			1474
Asn Tyr Gly Leu Asn Glu Glu Gln Pro Pro Pro Pro Pro Tyr Ser Asp			
260	265	270	
cag gcc tgt ggg gaa gag caa ccg gtg cgt cat gac taagtcctgg			1520
Gln Ala Cys Gly Glu Glu Gln Pro Val Arg His Asp			
275	280		
actgacgtca agaggacact tacaccccag ggttgaaggt gggaaagtga attgcagaga			1580
ggctgtctgt aaccaggtg actaggaagc agcttgggga gcgccaagt ggacattccc			1640
atcctatagc acttaatgcc aagctcgggtg gcccacaaaga gaagtgtgca tgttcctagc			1700
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catcagggtc cccaccctc tgctccaca tggaccccaa agcactacat acaggccatc			1880
ttgaattttt tactttttca atgcaacact tacatagtat tttaggtata ggccgtactt			1940
ccatggcctt ttactggatg tttgacactt tagggccagt ctcctagtg taaaggctta			2000

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 tccccctggct gcacagatgg cccctggcca atgcagatct ggatttagtg gaggggtgag 2240  
 gtgggcagcc ctggaacttc tgccttcgtg agtttctatt aaatggctgg ttcatggccc 2300  
 tc 2302

<210> 238

<211> 284

<212> PRT

<213> Mus musculus

<400> 238

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1 5 10 15

Tyr Tyr Thr Tyr Thr Glu Leu Leu Ala Ile Ser Arg Arg Phe Lys Gln

20 25 30

Asn Pro Asn Glu Leu Met Val Thr Trp Ile Leu Arg Val Tyr Asp Gln

35 40 45

Gly Gly Pro Ala Leu Ser Leu Asn Ser Gly Glu Leu Gly Leu Leu Gly

50 55 60

Asp Leu Thr His Asp Ala Ile Phe Asn Tyr Arg Cys Lys Ala Leu Arg

65 70 75 80

Gly Ala Gly Cys Gln Thr Leu Leu Ser Trp Leu Leu Gln Ala Trp Arg

85 90 95

Gln Arg Trp Glu Ser Ser Leu His Phe Glu Ala Thr Glu Leu Pro Phe

100 105 110

Arg Pro Trp Thr Thr Met Glu Glu Gly Ile Gln Leu Val Arg Glu Leu

115                                      120                                      125  
 Gly Met Ile Glu Trp Ile Tyr Leu Asp Pro Glu Gly Pro Val Asp Leu  
 130                                      135                                      140  
 Ala Pro Glu Asp Val Ala Phe Thr Gln Gly Leu Gln Arg Arg Leu Leu  
 145                                      150                                      155                                      160  
 Thr Ala Ala Pro Ser Glu Leu Arg Leu Ser Leu Val Ser Leu Leu Val  
 165                                      170                                      175  
 Arg Gly Met Thr Val Leu Glu Ala Val Met Glu Ile Gln Thr Ile Ala  
 180                                      185                                      190  
 Asp Val Gly Leu Leu Trp Arg Gln Ser His Pro Gly Arg Thr Lys Leu  
 195                                      200                                      205  
 Met Leu Gly Pro Asn Pro Thr Arg Lys Asp Leu Leu Gly Trp Leu Leu  
 210                                      215                                      220  
 Ser His Gly Val Pro Arg Glu Gln Val Asp Arg Gln Pro Thr Lys Val  
 225                                      230                                      235                                      240  
 Leu Leu Glu Leu Tyr Ile Lys Glu Ala Lys Arg Ser Arg Gly His Pro  
 245                                      250                                      255  
 Asn Tyr Gly Leu Asn Glu Glu Gln Pro Pro Pro Pro Pro Tyr Ser Asp  
 260                                      265                                      270  
 Gln Ala Cys Gly Glu Glu Gln Pro Val Arg His Asp  
 275                                      280

&lt;210&gt; 239

&lt;211&gt; 1942

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;



<221> CDS

<222> (102).. (710)

<400> 239

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caagcagcca ttcttgccctg tggattcaga gccccaggcc tgaccacagt gccagaaact    60
gccacccccct gccctaaagg agccccaagg ctgctgtgag c atg gca gaa gct cct    116
                                     Met Ala Glu Ala Pro
                                     1             5

gtt gac ttg agc aca gga gac aat ctg gag caa aag atc ctg cag gtg    164
Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln Lys Ile Leu Gln Val
                10             15             20

ttg agc gat gac ggc ggc cct gtg aag att ggc cag ctg gtg aag aaa    212
Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly Gln Leu Val Lys Lys
                25             30             35

tgc caa gtg ccc aag aaa acc ctc aat caa gtc ctt tac cgc ctg aag    260
Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val Leu Tyr Arg Leu Lys
                40             45             50

aag gag gac aga gtg tcc tcc cca gag cct gca aca tgg agc ata ggc    308
Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala Thr Trp Ser Ile Gly
                55             60             65

ggg gct gct tct gga gat ggg gct cct gca atc cct gag aac tcc agt    356
Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile Pro Glu Asn Ser Ser
                70             75             80             85

gcc cag cct agc ctt gat gaa aga ata tta aga ttc ctg gaa gcc aat    404
Ala Gln Pro Ser Leu Asp Glu Arg Ile Leu Arg Phe Leu Glu Ala Asn
                90             95             100

ggg cct cac agg gcc ctg cac atc gcc aag gct ctg gga atg acg aca    452
Gly Pro His Arg Ala Leu His Ile Ala Lys Ala Leu Gly Met Thr Thr

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105	110	115	
gcc aaa gaa gtg aac cca ctc ctg tat tcc atg aga aat aag cac ctt			500
Ala Lys Glu Val Asn Pro Leu Leu Tyr Ser Met Arg Asn Lys His Leu			
120	125	130	
ctg agc tat gac gga cag acg tgg aag atc tac cac tca cgt cag gaa			548
Leu Ser Tyr Asp Gly Gln Thr Trp Lys Ile Tyr His Ser Arg Gln Glu			
135	140	145	
ggc caa gac ata gct cat tct gga gtc aca caa gag tcc cct gcg att			596
Gly Gln Asp Ile Ala His Ser Gly Val Thr Gln Glu Ser Pro Ala Ile			
150	155	160	165
att tgt cag cac aat ccg gtc aac atg atc tgc caa caa gga gcc aac			644
Ile Cys Gln His Asn Pro Val Asn Met Ile Cys Gln Gln Gly Ala Asn			
170	175	180	
agc cac atc tcc att gcc aat tca aac gcc atc cag att ggt cac ggg			692
Ser His Ile Ser Ile Ala Asn Ser Asn Ala Ile Gln Ile Gly His Gly			
185	190	195	
aat gtc ata gta aga gag taagcctgtg gtgagccagg tcccaggacc			740
Asn Val Ile Val Arg Glu			
200			
tctcaccctc tacccttggc atgggacgcc tctgctcagg acatgcccc tggtgcccac			800
ggagctcagt acatctacat ggacaagtcc ttgctccaac aagtgcagct tggccaccac			860
aacgagatga gcctcgtggg ggatgcaggg aagcaccctt cttatagctt ttctgacagc			920
ccccagaag tgtcaaccac cactgctgac ccaggagctt cattcaacat gcaaacatct			980
gagccaggcc ctcaccctga gggagacaca gtccagacag tccacatcaa atcctgcttt			1040
ctagaggacg ccaccattgg taacggcaac aagatgacca tccaccttag gtcaaagggt			1100
gaagtcattg agtctggaga cagtgaagag ccgaagaagg aagacacagg tacaagctct			1160
gaagccactc caccagaag ctgccagcac acgccagtg actccatgct gccacctct			1220

gagctgagag ctatggctct gggagacagt agccccaga ccacagaacc tgtgcttaga 1280  
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 tgtgggacca taggctgacc cctctgccac tataagtcaa atcaaccttt cctgcctcaa 1400  
 gatcaatcaa tcgatcaacc gcaggagcca gttctaccac tcctggatgc tcacccaaag 1460  
 gcaaaagtca acacagagag atctccgcat atccatgtag attgggacac tgttcacagc 1520  
 agctaagaag tggaaccgac ctigtacccc agcagtaaaa gatgggtgaa ttggagtatg 1580  
 cacacagcca tgggaaatac tgaggctgtc attggccaga agaggatgtg accagaggcc 1640  
 accatgttga atgaatgaaa gccatcttag aaagacaagg gccacatttt ctctgctgtg 1700  
 gctcctagac tttagataga tttataaaat catatacaca gatgtgacat gaaagtacat 1760  
 gtaacaccaa ccaggggatg aggatggtgc atggggagga gaggcggggg tcacagcctg 1820  
 ggggggggtc acggtctggg aggggtgtcac cacctaaaga gatcacagct ggggggatca 1880  
 gggccgggag gggggacact gctgaatgca ctgtactttt ataaaaaggt gtacctctga 1940  
 aa 1942

<210> 240

<211> 203

<212> PRT

<213> Mus musculus

<400> 240

Met Ala Glu Ala Pro Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln

1 5 10 15

Lys Ile Leu Gln Val Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly

20 25 30

Gln Leu Val Lys Lys Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val

35 40 45

Leu Tyr Arg Leu Lys Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala

50 55 60

<210>	241
<211>	1942
<212>	DNA
<213>	Mus musculus
<220>	
<221>	CDS
<222>	(102)..(1334)
<400>	241

caagcagcca ttcttgctg tggattcaga gcccaggcc tgaccacagt gccagaaact 60  
 gccaccccct gccctaaagg agccccaagg ctgctgtgag c atg gca gaa gct cct 116  
 Met Ala Glu Ala Pro  
 1 5  
 gtt gac ttg agc aca gga gac aat ctg gag caa aag atc ctg cag gtg 164  
 Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln Lys Ile Leu Gln Val  
 10 15 20  
 ttg agc gat gac ggc ggc cct gtg aag att ggc cag ctg gtg aag aaa 212  
 Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly Gln Leu Val Lys Lys  
 25 30 35  
 tgc caa gtg ccc aag aaa acc ctc aat caa gtc ctt tac cgc ctg aag 260  
 Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val Leu Tyr Arg Leu Lys  
 40 45 50  
 aag gag gac aga gtg tcc tcc cca gag cct gca aca tgg agc ata ggc 308  
 Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala Thr Trp Ser Ile Gly  
 55 60 65  
 ggg gct gct tct gga gat ggg gct cct gca atc cct gag aac tcc agt 356  
 Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile Pro Glu Asn Ser Ser  
 70 75 80 85  
 gcc cag cct agc ctt gat gaa aga ata tta aga ttc ctg gaa gcc aat 404  
 Ala Gln Pro Ser Leu Asp Glu Arg Ile Leu Arg Phe Leu Glu Ala Asn  
 90 95 100  
 ggg cct cac agg gcc ctg cac atc gcc aag gct ctg gga atg acg aca 452  
 Gly Pro His Arg Ala Leu His Ile Ala Lys Ala Leu Gly Met Thr Thr  
 105 110 115  
 gcc aaa gaa gtg aac cca ctc ctg tat tcc atg aga aat aag cac ctt 500  
 Ala Lys Glu Val Asn Pro Leu Leu Tyr Ser Met Arg Asn Lys His Leu

120	125	130	
ctg agc tat gac gga cag acg tgg aag atc tac cac tca cgt cag gaa			548
Leu Ser Tyr Asp Gly Gln Thr Trp Lys Ile Tyr His Ser Arg Gln Glu			
135	140	145	
ggc caa gac ata gct cat tct gga gtc aca caa gag tcc cct gcg att			596
Gly Gln Asp Ile Ala His Ser Gly Val Thr Gln Glu Ser Pro Ala Ile			
150	155	160	165
att tgt cag cac aat ccg gtc aac atg atc tgc caa caa gga gcc aac			644
Ile Cys Gln His Asn Pro Val Asn Met Ile Cys Gln Gln Gly Ala Asn			
170	175	180	
agc cac atc tcc att gcc aat tca aac gcc atc cag att ggt cac ggg			692
Ser His Ile Ser Ile Ala Asn Ser Asn Ala Ile Gln Ile Gly His Gly			
185	190	195	
aat gtc ata gta aga gag aaa gcc tgt ggt gag cca ggt ccc agg acc			740
Asn Val Ile Val Arg Glu Lys Ala Cys Gly Glu Pro Gly Pro Arg Thr			
200	205	210	
tct cac cct cta ccc ttg gca tgg gac gcc tct gct cag gac atg ccc			788
Ser His Pro Leu Pro Leu Ala Trp Asp Ala Ser Ala Gln Asp Met Pro			
215	220	225	
cct gtt gcc cac gga gct cag tac atc tac atg gac aag tcc ttg ctc			836
Pro Val Ala His Gly Ala Gln Tyr Ile Tyr Met Asp Lys Ser Leu Leu			
230	235	240	245
caa caa gtg cag ctt ggc cac cac aac gag atg agc ctc gtg ggg gat			884
Gln Gln Val Gln Leu Gly His His Asn Glu Met Ser Leu Val Gly Asp			
250	255	260	
gca ggg aag cac ccc tct tat agc ttt tct gac agc ccc cca gaa gtg			932
Ala Gly Lys His Pro Ser Tyr Ser Phe Ser Asp Ser Pro Pro Glu Val			

265	270	275	
tca acc acc act gct gac cca gga gct tca ttc aac atg caa aca tct			980
Ser Thr Thr Thr Ala Asp Pro Gly Ala Ser Phe Asn Met Gln Thr Ser			
280	285	290	
gag cca ggc cct cac cct gag gga gac aca gtc cag aca gtc cac atc			1028
Glu Pro Gly Pro His Pro Glu Gly Asp Thr Val Gln Thr Val His Ile			
295	300	305	
aaa tcc tgc ttt cta gag gac gcc acc att ggt aac ggc aac aag atg			1076
Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn Gly Asn Lys Met			
310	315	320	325
acc atc cac ctt agg tca aag ggt gaa gtc atg gag tct gga gac agt			1124
Thr Ile His Leu Arg Ser Lys Gly Glu Val Met Glu Ser Gly Asp Ser			
330	335	340	
gaa gag ccg aag aag gaa gac aca ggt aca agc tct gaa gcc act cca			1172
Glu Glu Pro Lys Lys Glu Asp Thr Gly Thr Ser Ser Glu Ala Thr Pro			
345	350	355	
ccc aga agc tgc cag cac acg ccc agt gac tcc atg ctg ccc acc tct			1220
Pro Arg Ser Cys Gln His Thr Pro Ser Asp Ser Met Leu Pro Thr Ser			
360	365	370	
gag ctg aga gct atg gct ctg gga gac agt agc ccc cag acc aca gaa			1268
Glu Leu Arg Ala Met Ala Leu Gly Asp Ser Ser Pro Gln Thr Thr Glu			
375	380	385	
cct gtg ctt aga gag cat gaa gtc cag gac ata gaa agc tct caa gac			1316
Pro Val Leu Arg Glu His Glu Val Gln Asp Ile Glu Ser Ser Gln Asp			
390	395	400	405
aca gga ctg agc aag caa tgaagctgtg ggaccatagg ctgaccctc			1364
Thr Gly Leu Ser Lys Gln			

410

tgccactata agtcaaatac acctttcctg cctcaagatc aatcaatcga tcaaccgcag	1424
gagccagttc taccactcct ggatgctcac ccaaaggcaa aagtcaacac agagagatct	1484
ccgcatatcc atgtagattg ggacactgtt cacagcagct aagaagtgga accgaccttg	1544
ctaccacagca gtaaaagatg ggtgaattgg agtatgcaca cagccatggg aaatactgag	1604
gctgtcattg gccagaagag gatgtgacca gaggccacca tgttgaatga atgaaagcca	1664
tcttagaaaag acaagggcca cattttctct gctgtggctc ctagacttta gatagattta	1724
taaaatcata tacacagatg tgacatgaaa gtacatgtaa caccaaccag gggatgagga	1784
tggtgcatgg ggaggagagg cgggggtcac agcctggggg ggggtcacgg tctgggaggg	1844
tgtcaccacc taaagagatc acagctgggg ggatcagggc cgggaggggg gacactgctg	1904
aatgcactgt acttttataa aaaggtgtac ctctgaaa	1942

**<210> 242**

$\langle 211 \rangle$  411

<212> PRT

<213> Mus musculus

<400> 242

Met Ala Glu Ala Pro Val Asp Leu Ser Thr Gly Asp Asn Leu Glu Gln  
1 5 10 15  
Lys Ile Leu Gln Val Leu Ser Asp Asp Gly Gly Pro Val Lys Ile Gly  
20 25 30  
Gln Leu Val Lys Lys Cys Gln Val Pro Lys Lys Thr Leu Asn Gln Val  
35 40 45  
Leu Tyr Arg Leu Lys Lys Glu Asp Arg Val Ser Ser Pro Glu Pro Ala  
50 55 60  
Thr Trp Ser Ile Gly Gly Ala Ala Ser Gly Asp Gly Ala Pro Ala Ile  
65 70 75 80



728/861

290                      295                      300  
 Gln Thr Val His Ile Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly  
 305                      310                      315                      320  
 Asn Gly Asn Lys Met Thr Ile His Leu Arg Ser Lys Gly Glu Val Met  
                     325                      330                      335  
 Glu Ser Gly Asp Ser Glu Glu Pro Lys Lys Glu Asp Thr Gly Thr Ser  
                     340                      345                      350  
 Ser Glu Ala Thr Pro Pro Arg Ser Cys Gln His Thr Pro Ser Asp Ser  
                     355                      360                      365  
 Met Leu Pro Thr Ser Glu Leu Arg Ala Met Ala Leu Gly Asp Ser Ser  
                     370                      375                      380  
 Pro Gln Thr Thr Glu Pro Val Leu Arg Glu His Glu Val Gln Asp Ile  
 385                      390                      395                      400  
 Glu Ser Ser Gln Asp Thr Gly Leu Ser Lys Gln  
                     405                      410

&lt;210&gt; 243

&lt;211&gt; 2195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (179)..(1465)

&lt;400&gt; 243

gctgacacct gccagtgga agctggcatc cctccccttg tgggttcaga gctgcaagaa 60  
 gcaccaggct cggccacttc agaagcccca gcctcgacct agcccacct ctcagggccca 120  
 cagtgcagaa gcctgcacac ctgccaagtc tctccgactc cttgcagctg ctgtcagc 178

atg gcc cag gct cct gct gac ccg ggc aga gaa ggc cac ctt gaa caa	226
Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln	
1 5 10 15	
aga atc ctg cag gtg ctg aca gag gct ggc tcc ccg gtg aaa ctt gcc	274
Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala	
20 25 30	
cag ctg gtg aag gaa tgc caa gca ccc aag agg gag ctc aac caa gtc	322
Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val	
35 40 45	
ctc tac cga atg aaa aag gag ttg aaa gtc tcc ctc aca tcc cct gcc	370
Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala	
50 55 60	
acc tgg tgc ttg ggc ggg act gat cct gaa ggc gag ggt cct gca gag	418
Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu	
65 70 75 80	
ctg gcc ttg tcc agc cct gcc gag agg ccc cag caa cat gca gct aca	466
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr	
85 90 95	
att cca gag acc cct ggc cct cag ttc agc caa caa cgg gag gaa gac	514
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp	
100 105 110	
atc tac agg ttt ctc aaa gac aat ggt ccc cag agg gcc ctg gtc atc	562
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile	
115 120 125	
gcc caa gca ctg gga atg agg aca gca aaa gat gtg aac cga gac ttg	610
Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu	
130 135 140	

tac agg atg aag agc agg cac ctt ctg gac atg gat gag cag tcc aaa	658
Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys	
145                      150                      155                      160	
gca tgg acg att tac cgc cca gaa gat tct gga aga aga gca aag tca	706
Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser	
165                      170                      175	
gcc tca att att tac cag cac aat cca atc aac atg atc tgc cag aat	754
Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn	
180                      185                      190	
gga ccc aac agc tgg att tcc att gca aac tcc gaa gcc atc cag att	802
Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile	
195                      200                      205	
gga cac ggg aac atc att aca aga cag aca gtc tcc agg gag gac ggt	850
Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly	
210                      215                      220	
tcc gcc ggt cca cgc cac ctc cct tca atg gca cca ggt gat tcc tca	898
Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser	
225                      230                      235                      240	
act tgg ggg acc cta gtt gat ccc tgg ggg ccc cag gac atc cac atg	946
Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met	
245                      250                      255	
gag cgg tcc ata ctg aga cgg gtg cag ctg gga cac agc aat gag atg	994
Glu Arg Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met	
260                      265                      270	
agg ctc cac ggc gtc ccg tcc gag ggc cct gcc cac atc ccc cct ggc	1042
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly	
275                      280                      285	

agc ccc cca gtc tct gcc act gct gcc ggc cca gaa gct tcg ttt gaa 1090  
 Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu  
 290 295 300  
 gca aga att ccc agt cca gga act cac cct gag ggg gaa gcc gcc cag 1138  
 Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln  
 305 310 315 320  
 aga atc cac atg aaa tcg tgc ttt ctc gag gac gcc acc atc ggc aac 1186  
 Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn  
 325 330 335  
 agc aac aaa atg tct atc agc cca ggg gtg gct ggc cca gga gga gtc 1234  
 Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val  
 340 345 350  
 gca ggg tct gga gag ggg gag cca ggg gag gac gca ggt cgt cgt ccc 1282  
 Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro  
 355 360 365  
 gca gac aca caa tcc aga agt cac ttt cct cga gac att ggt cag ccc 1330  
 Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro  
 370 375 380  
 atc act ccc agc cac tcg aag ctc acc ccc aag ctg gaa act atg act 1378  
 Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr  
 385 390 395 400  
 ctt gga aac agg agt cac aaa gct gca gaa ggc agc cac tat gtg gat 1426  
 Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp  
 405 410 415  
 gaa gcc tca cac gag ggg agc tgg tgg gga ggt ggg att tagtgacag 1475  
 Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile  
 420 425

cctcacgtgg ggcttggaca caggctgggg gtgggcgcat gctagggaga ctagcctgct 1535  
 gctctctgca ttccttagcg tcttgtttga cctgcttgct tccagacata acctgcatga 1595  
 atcagttttg ggggaatgga cctggcatgg ggatgggttc aggccaggtc ttttgatggc 1655  
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 cggggcatct gcctggagtt accttccatc atggctacct gctgtggttt gaatgtttga 1835  
 gtcccaacaa aattcatatc aaaacataat cccaactggg tgcagtggct cagcctgta 1895  
 atcccagcac tttgggaggc cgaggcgggc ggatcaatag gtcaggaaat ccagaccgtc 1955  
 ctggctaaca tggtgaaacc ccgtctctac taaaaaaaaa aatacaaaaa attagccggg 2015  
 cgttgtggcg ggcacctgga gtcccagcta ctccggaggc tgagggagga gaatggtgtg 2075  
 aacccgggag gtggagcttc cagtgagccg agatcgcgcc actgcactcc aggctgggcg 2135  
 acagagcgag actccgtctc aaaaaataa atacataaat aaaaaataaa ccaccataa 2195

<210> 244

<211> 429

<212> PRT

<213> Homo sapiens

<400> 244

Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln  
 1 5 10 15  
 Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala  
 20 25 30  
 Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val  
 35 40 45  
 Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala  
 50 55 60  
 Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu

65	70	75	80
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr			
	85	90	95
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp			
	100	105	110
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile			
	115	120	125
Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu			
	130	135	140
Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys			
145	150	155	160
Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser			
	165	170	175
Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn			
	180	185	190
Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile			
	195	200	205
Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly			
	210	215	220
Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser			
225	230	235	240
Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met			
	245	250	255
Glu Arg Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met			
	260	265	270
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly			
	275	280	285

Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu  
290 295 300  
Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln  
305 310 315 320  
Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn  
325 330 335  
Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val  
340 345 350  
Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro  
355 360 365  
Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro  
370 375 380  
Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr  
385 390 395 400  
Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp  
405 410 415  
Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile  
420 425

&lt;210&gt; 245

&lt;211&gt; 2195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (179)..(1465)

&lt;400&gt; 245



gctgacacct gccagtgga agctggcatc cctccccttg tgggttcaga gctgcaagaa	60
gcaccaggct cggccacttc agaagcccca gcctcgacct agcccaccct ctcagggccca	120
cagtgcagaa gcctgcacac ctgccaagtc tctccgactc cttgcagctg ctgtcagc	178
atg gcc cag gct cct gct gac ccg ggc aga gaa ggc cac ctt gaa caa	226
Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln	
1                      5                      10                      15	
aga atc ctg cag gtg ctg aca gag gct ggc tcc ccg gtg aaa ctt gcc	274
Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala	
20                      25                      30	
cag ctg gtg aag gaa tgc caa gca ccc aag agg gag ctc aac caa gtc	322
Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val	
35                      40                      45	
ctc tac cga atg aaa aag gag ttg aaa gtc tcc ctc aca tcc cct gcc	370
Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala	
50                      55                      60	
acc tgg tgc ttg ggc ggg act gat cct gaa ggc gag ggt cct gca gag	418
Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu	
65                      70                      75                      80	
ctg gcc ttg tcc agc cct gcc gag agg ccc cag caa cat gca gct aca	466
Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr	
85                      90                      95	
att cca gag acc cct ggc cct cag ttc agc caa caa cgg gag gaa gac	514
Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp	
100                      105                      110	
atc tac agg ttt ctc aaa gac aat ggt ccc cag agg gcc ctg gtc atc	562
Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile	
115                      120                      125	

gcc caa gca ctg gga atg agg aca gca aaa gat gtg aac cga gac ttg 610  
 Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu  
 130 135 140  
 tac agg atg aag agc agg cac ctt ctg gac atg gat gag cag tcc aaa 658  
 Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys  
 145 150 155 160  
 gca tgg acg att tac cgc cca gaa gat tct gga aga aga gca aag tca 706  
 Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser  
 165 170 175  
 gcc tca att att tac cag cac aat cca atc aac atg atc tgc cag aat 754  
 Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn  
 180 185 190  
 gga ccc aac agc tgg att tcc att gca aac tcc gaa gcc atc cag att 802  
 Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile  
 195 200 205  
 gga cac ggg aac atc att aca aga cag aca gtc tcc agg gag gac ggt 850  
 Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly  
 210 215 220  
 tcc gcc ggt cca cgc cac ctc cct tca atg gca cca ggt gat tcc tca 898  
 Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser  
 225 230 235 240  
 act tgg ggg acc cta gtt gat ccc tgg ggg ccc cag gac atc cac atg 946  
 Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met  
 245 250 255  
 gag cag tcc ata ctg aga cgg gtg cag ctg gga cac agc aat gag atg 994  
 Glu Gln Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met  
 260 265 270

agg ctc cac ggc gtc ccg tcc gag ggc cct gcc cac atc ccc cct ggc	1042
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly	
275 280 285	
agc ccc cca gtc tct gcc act gct gcc ggc cca gaa gct tcg ttt gaa	1090
Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu	
290 295 300	
gca aga att ccc agt cca gga act cac cct gag ggg gaa gcc gcc cag	1138
Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln	
305 310 315 320	
aga atc cac atg aaa tcg tgc ttt ctc gag gac gcc acc atc ggc aac	1186
Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn	
325 330 335	
agc aac aaa atg tct atc agc cca ggg gtg gct ggc cca gga gga gtc	1234
Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val	
340 345 350	
gca ggg tct gga gag ggg gag cca ggg gag gac gca ggt cgt cgt ccc	1282
Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro	
355 360 365	
gca gac aca caa tcc aga agt cac ttt cct cga gac att ggt cag ccc	1330
Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro	
370 375 380	
atc act ccc agc cac tcg aag ctc acc ccc aag ctg gaa act atg act	1378
Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr	
385 390 395 400	
ctt gga aac agg agt cac aaa gct gca gaa ggc agc cac tat gtg gat	1426
Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp	
405 410 415	

gaa gcc tca cac gag ggg agc tgg tgg gga ggt ggg att tagtgcacag 1475  
 Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile

420

425

cctcacgtgg ggcttgaca caggctgggg gtgggcgcat gctagggaga ctagcctgct 1535  
 gctctctgca ttccttagcg tcttgittga cctgcttgct tccagacata acctgcatga 1595  
 atcagttttg ggggaatgga cctggcatgg ggatgggttc aggccaggtc ttttgatggc 1655  
 caggagtaga tgacaggagag ttgccttggg gaacctttgg tgtgccaaga ggaggtgggt 1715  
 agatgggagt ggggctcggg cccccaggcc caggggactc tctccactct ttcctgggct 1775  
 cggggcatct gcctggagtt accttccatc atggctacct gctgtggttt gaatgtttga 1835  
 gtcccaacaa aattcatatc aaaacataat cccaactggg tgcagtggct cagccttgta 1895  
 atcccagcac tttgggaggc cgaggcgggc ggatcaatag gtcaggaaat ccagaccgctc 1955  
 ctggctaaca tgggtgaaacc ccgtctctac taaaaaaaaa aatacaaaaa attagccggg 2015  
 cgttggtggcg ggcacctgga gtcccagcta ctccggaggc tgaggaggga gaatggtgtg 2075  
 aaccggggag gtggagcttc cagtgagccg agatcgcgcc actgcactcc aggctgggcg 2135  
 acagagcgag actccgtctc aaaaaataa atacataaat aaaaaataaa ccaccataa 2195

&lt;210&gt; 246

&lt;211&gt; 429

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Gly His Leu Glu Gln

1

5

10

15

Arg Ile Leu Gln Val Leu Thr Glu Ala Gly Ser Pro Val Lys Leu Ala

20

25

30

Gln Leu Val Lys Glu Cys Gln Ala Pro Lys Arg Glu Leu Asn Gln Val

35

40

45

Leu Tyr Arg Met Lys Lys Glu Leu Lys Val Ser Leu Thr Ser Pro Ala  
 50 55 60  
 Thr Trp Cys Leu Gly Gly Thr Asp Pro Glu Gly Glu Gly Pro Ala Glu  
 65 70 75 80  
 Leu Ala Leu Ser Ser Pro Ala Glu Arg Pro Gln Gln His Ala Ala Thr  
 85 90 95  
 Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp  
 100 105 110  
 Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln Arg Ala Leu Val Ile  
 115 120 125  
 Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp Val Asn Arg Asp Leu  
 130 135 140  
 Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met Asp Glu Gln Ser Lys  
 145 150 155 160  
 Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser  
 165 170 175  
 Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn Met Ile Cys Gln Asn  
 180 185 190  
 Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile  
 195 200 205  
 Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val Ser Arg Glu Asp Gly  
 210 215 220  
 Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala Pro Gly Asp Ser Ser  
 225 230 235 240  
 Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro Gln Asp Ile His Met  
 245 250 255  
 Glu Gln Ser Ile Leu Arg Arg Val Gln Leu Gly His Ser Asn Glu Met

260	265	270
Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala His Ile Pro Pro Gly		
275	280	285
Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu		
290	295	300
Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu Gly Glu Ala Ala Gln		
305	310	315
Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn		
325	330	335
Ser Asn Lys Met Ser Ile Ser Pro Gly Val Ala Gly Pro Gly Gly Val		
340	345	350
Ala Gly Ser Gly Glu Gly Glu Pro Gly Glu Asp Ala Gly Arg Arg Pro		
355	360	365
Ala Asp Thr Gln Ser Arg Ser His Phe Pro Arg Asp Ile Gly Gln Pro		
370	375	380
Ile Thr Pro Ser His Ser Lys Leu Thr Pro Lys Leu Glu Thr Met Thr		
385	390	395
Leu Gly Asn Arg Ser His Lys Ala Ala Glu Gly Ser His Tyr Val Asp		
405	410	415
Glu Ala Ser His Glu Gly Ser Trp Trp Gly Gly Gly Ile		
420	425	

&lt;210&gt; 247

&lt;211&gt; 1926

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14).. (1513)

&lt;400&gt; 247

```

gaagcgggaag aag atg gcg ctc acc agc ttt tta cct gcg cct act cag      49
      Met Ala Leu Thr Ser Phe Leu Pro Ala Pro Thr Gln
              1              5              10
ctg tct cag gac caa ctt gaa gct gaa gaa agg gca aga tct cag aga      97
Leu Ser Gln Asp Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg
              15              20              25
tca ctg cag acc tct ctg gtc tcc tct cga agg gag cct ccc cca tac      145
Ser Leu Gln Thr Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr
              30              35              40
gga tat agg aaa ggc tgg att cca aga cta tta gag gat ttt gga gat      193
Gly Tyr Arg Lys Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp
              45              50              55              60
gga ggt gct ttc cca gaa atc cat gtg gcc cag tat cct ctg gat atg      241
Gly Gly Ala Phe Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met
              65              70              75
ggg cga aag aaa aaa atg tcg aat gct ctg gcc att cag gtg gat cct      289
Gly Arg Lys Lys Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro
              80              85              90
gaa ggg aaa att aag tat gat gca att gct cgg cag gga cag tcc aaa      337
Glu Gly Lys Ile Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys
              95              100              105
gac aag gtc att tac agc aaa tac act gac ctg gtt cct aag gag gtt      385
Asp Lys Val Ile Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val
              110              115              120

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atg aat gca gat gac cca gac ctg caa cgg ccc gat gaa gag gca att	433
Met Asn Ala Asp Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile	
125                      130                      135                      140	
aaa gag ata aca gaa aag act aga gtt gcc ttg gag aaa tct gtg tgc	481
Lys Glu Ile Thr Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser	
145                      150                      155	
cag aag gtt gct gca gcc atg cca gtt cgt gca gct gac aag ctg gct	529
Gln Lys Val Ala Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala	
160                      165                      170	
cct gct cag tat atc cgc tac aca cca tct cag caa gga gta gcg ttc	577
Pro Ala Gln Tyr Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe	
175                      180                      185	
aat tct gga gct aaa cag agg gtc att cgg atg gta gaa atg cag aaa	625
Asn Ser Gly Ala Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys	
190                      195                      200	
gac cca atg gag cct cca aga ttc aag att aat aag aaa att ccc cgg	673
Asp Pro Met Glu Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg	
205                      210                      215                      220	
gga cca ccg tct cct cct gca cct gta atg cac tct cct agt cgg aag	721
Gly Pro Pro Ser Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys	
225                      230                      235	
atg act gta aag gaa caa caa gag tgg aag atc ccg cct tgt att tcc	769
Met Thr Val Lys Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser	
240                      245                      250	
aac tgg aag aac gct aag ggg tat acg atc cca tta gat aaa cgg ctg	817
Asn Trp Lys Asn Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu	
255                      260                      265	



gct gct gat gga aga gga ctt cag act gtc cac ata aat gaa aat ttt	865
Ala Ala Asp Gly Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe	
270 275 280	
gcc aaa ctg gct gaa gcg ctc tac att gct gat cgg aag gct cgt gaa	913
Ala Lys Leu Ala Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu	
285 290 295 300	
gcg gtg gaa atg cga gcc cag gta gag aga aag atg gct caa aaa gaa	961
Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu	
305 310 315	
aag gag aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa gcc aga	1009
Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg	
320 325 330	
gaa agg aga gct gga atc aaa acc cac gtg gag aaa gag gat gga gag	1057
Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu	
335 340 345	
gcc cgt gag aga gat gaa atc cgt cat gac agg cga aaa gag agg cag	1105
Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln	
350 355 360	
cat gac cgg aac ctt tcc agg gca gct cct gat aag agg tca aaa cta	1153
His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu	
365 370 375 380	
cag aga aat gaa aat cga gac atc agt gaa gtc att gct ctt ggt gtg	1201
Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val	
385 390 395	
ccc aat cct cga act tcc aat gaa gtt cag tat gac caa agg ctc ttc	1249
Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe	
400 405 410	

aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa gat gaa 1297  
 Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu  
 415 420 425  
 att tac aat gtt tat gat caa gcc tgg aga ggt ggg aaa gat atg gcc 1345  
 Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala  
 430 435 440  
 cag agc atc tac agg ccc agt aaa aat ctg gac aag gac atg tat ggt 1393  
 Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly  
 445 450 455 460  
 gat gac ctg gaa gcc agg ata aag acc aac aga ttt gtt cct gat aag 1441  
 Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys  
 465 470 475  
 gag ttt tct gga tca gac cgc aaa cag aga ggc cga gaa gga cca gtg 1489  
 Glu Phe Ser Gly Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val  
 480 485 490  
 cag ttt gag gaa tca tca gag aga tgaccaggag ggagataaag actggactgt 1543  
 Gln Phe Glu Glu Ser Ser Glu Arg  
 495 500  
 taaaaaaaaaaaagattaa aaaatctcga tgatagatcc cagcactcct tttcattctg 1603  
 ggatgtaggg gcattgatta ttctatttcg gagtagtttt tttatatgga atggggttat 1663  
 gtttgtgctt ctccaatctt gcagcactta gaaataccac tgccccacac agaattgaga 1723  
 ttccttcctt gtgtgtgaca ctaatccagc tgtaaccttt tctgtaaacg ttatgaataa 1783  
 cctcacctca aatgggtgagt gggctaagt tcacacactg gagctctgtc aactgcattt 1843  
 gccctgtgtg cttctccacc gcgccatggg gaactaaggt cttgcttagt gcacctcatt 1903  
 tcaaataaaa acgtgtagaa aaa 1926

&lt;210&gt; 248

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 248

Met Ala Leu Thr Ser Phe Leu Pro Ala Pro Thr Gln Leu Ser Gln Asp  
1 5 10 15  
Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg Ser Leu Gln Thr  
20 25 30  
Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr Gly Tyr Arg Lys  
35 40 45  
Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe  
50 55 60  
Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys  
65 70 75 80  
Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro Glu Gly Lys Ile  
85 90 95  
Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile  
100 105 110  
Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp  
115 120 125  
Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr  
130 135 140  
Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala  
145 150 155 160  
Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr  
165 170 175  
Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala

180	185	190
Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu		
195	200	205
Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser		
210	215	220
Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys		
225	230	235
Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn		
245	250	255
Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly		
260	265	270
Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala		
275	280	285
Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met		
290	295	300
Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His		
305	310	315
Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala		
325	330	335
Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg		
340	345	350
Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn		
355	360	365
Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu		
370	375	380
Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg		
385	390	395
		400

Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys  
                     405                    410                    415  
 Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val  
                     420                    425                    430  
 Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr  
                     435                    440                    445  
 Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu  
                     450                    455                    460  
 Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly  
 465                    470                    475                    480  
 Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu  
                     485                    490                    495  
 Ser Ser Glu Arg  
                     500

<210> 249

<211> 1844

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14)..(1621)

<400> 249

gaagcggaag aag atg gcg ctc acc agc ttt tta cct gcg cct act cag 49  
                     Met Ala Leu Thr Ser Phe Leu Pro Ala Pro Thr Gln  
                     1                    5                    10  
 ctg tct cag gac caa ctt gaa gct gaa gaa agg gca aga tct cag aga 97

Leu Ser Gln Asp Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg  
 15 20 25  
 tca ctg cag acc tct ctg gtc tcc tct cga agg gag cct ccc cca tac 145  
 Ser Leu Gln Thr Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr  
 30 35 40  
 gga tat agg aaa ggc tgg att cca aga cta tta gag gat ttt gga gat 193  
 Gly Tyr Arg Lys Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp  
 45 50 55 60  
 gga ggt gct ttc cca gaa atc cat gtg gcc cag tat cct ctg gat atg 241  
 Gly Gly Ala Phe Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met  
 65 70 75  
 ggg cga aag aaa aaa atg tcg aat gct ctg gcc att cag gtg gat cct 289  
 Gly Arg Lys Lys Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro  
 80 85 90  
 gaa ggg aaa att aag tat gat gca att gct cgg cag gga cag tcc aaa 337  
 Glu Gly Lys Ile Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys  
 95 100 105  
 gac aag gtc att tac agc aaa tac act gac ctg gtt cct aag gag gtt 385  
 Asp Lys Val Ile Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val  
 110 115 120  
 atg aat gca gat gac cca gac ctg caa cgg ccc gat gaa gag gca att 433  
 Met Asn Ala Asp Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile  
 125 130 135 140  
 aaa gag ata aca gaa aag act aga gtt gcc ttg gag aaa tct gtg tcg 481  
 Lys Glu Ile Thr Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser  
 145 150 155  
 cag aag gtt gct gca gcc atg cca gtt cgt gca gct gac aag ctg gct 529

Gln Lys Val Ala Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala  
 160 165 170  
 cct gct cag tat atc cgc tac aca cca tct cag caa gga gta gcg ttc 577  
 Pro Ala Gln Tyr Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe  
 175 180 185  
 aat tct gga gct aaa cag agg gtc att cgg atg gta gaa atg cag aaa 625  
 Asn Ser Gly Ala Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys  
 190 195 200  
 gac cca atg gag cct cca aga ttc aag att aat aag aaa att ccc cgg 673  
 Asp Pro Met Glu Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg  
 205 210 215 220  
 gga cca ccg tct cct cct gca cct gta atg cac tct cct agt cgg aag 721  
 Gly Pro Pro Ser Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys  
 225 230 235  
 atg act gta aag gaa caa caa gag tgg aag atc ccg cct tgt att tcc 769  
 Met Thr Val Lys Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser  
 240 245 250  
 aac tgg aag aac gct aag ggg tat acg atc cca tta gat aaa cgg ctg 817  
 Asn Trp Lys Asn Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu  
 255 260 265  
 gct gct gat gga aga gga ctt cag act gtc cac ata aat gaa aat ttt 865  
 Ala Ala Asp Gly Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe  
 270 275 280  
 gcc aaa ctg gct gaa gcg ctc tac att gct gat cgg aag gct cgt gaa 913  
 Ala Lys Leu Ala Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu  
 285 290 295 300  
 gcg gtg gaa atg cga gcc cag gta gag aga aag atg gct caa aaa gaa 961

Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu  
305 310 315  
aag gag aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa gcc aga 1009  
Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg  
320 325 330  
gaa agg aga gct gga atc aaa acc cac gtg gag aaa gag gat gga gag 1057  
Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu  
335 340 345  
gcc cgt gag aga gat gaa atc cgt cat gac agg cga aaa gag agg cag 1105  
Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln  
350 355 360  
cat gac cgg aac ctt tcc agg gca gct cct gat aag agg tca aaa cta 1153  
His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu  
365 370 375 380  
cag aga aat gaa aat cga gac atc agt gaa gtc att gct ctt ggt gtg 1201  
Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val  
385 390 395  
ccc aat cct cga act tcc aat gaa gtt cag tat gac caa agg ctc ttc 1249  
Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe  
400 405 410  
aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa gat gaa 1297  
Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu  
415 420 425  
att tac aat gtt tat gat caa gcc tgg aga ggt ggg aaa gat atg gcc 1345  
Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala  
430 435 440  
cag agc atc tac agg ccc agt aaa aat ctg gac aag gac atg tat ggt 1393



Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly	
445	450
gat gac ctg gaa gcc agg ata aag acc aac aga ttt gtt cct gat aag	1441
Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys	
465	470
gag ttt tct gga tca gac cgc aaa cag aga ggc cga gaa gga cca gtg	1489
Glu Phe Ser Gly Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val	
480	485
cag ttt gag gag gat cct ttt ggt ttg gac aag ttt ttg gaa gaa gcc	1537
Gln Phe Glu Glu Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala	
495	500
aaa cag cac ggt ggt tct aaa aga ccc tct gat agc agt cgc ccc aag	1585
Lys Gln His Gly Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys	
510	515
gaa cat gag cat gaa ggc aag aag cgg agg aaa gag tagagggacc	1631
Glu His Glu His Glu Gly Lys Lys Arg Arg Lys Glu	
525	530
tcttaaaact aaatctgaca tatgcagcag aggactgcct ggtctggcct cattgtgaac	1691
agatgtcccc accccctcca gacacttgag actccaggga atagggcgtc ctagtgggtg	1751
ggggtgggga catcctcttg gaaatggggg aggaggaatg ggatgaggaa tcatcagaga	1811
gatgaccagg agggagataa agactggact gtt	1844

<210> 250

**<211> 536**

&lt;212&gt; PRT

<213> Mus musculus

$\langle 400 \rangle$  250

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 Gln Leu Glu Ala Glu Glu Arg Ala Arg Ser Gln Arg Ser Leu Gln Thr  
                     20                      25                      30  
 Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr Gly Tyr Arg Lys  
                     35                      40                      45  
 Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe  
                     50                      55                      60  
 Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys  
 65                      70                      75                      80  
 Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Pro Glu Gly Lys Ile  
                     85                      90                      95  
 Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile  
                     100                      105                      110  
 Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp  
                     115                      120                      125  
 Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr  
                     130                      135                      140  
 Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala  
 145                      150                      155                      160  
 Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr  
                     165                      170                      175  
 Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala  
                     180                      185                      190  
 Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu  
                     195                      200                      205  
 Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser

210	215	220	
Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys			
225	230	235	240
Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn			
	245	250	255
Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly			
	260	265	270
Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala			
	275	280	285
Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met			
	290	295	300
Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His			
305	310	315	320
Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala			
	325	330	335
Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg			
	340	345	350
Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn			
	355	360	365
Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu			
	370	375	380
Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg			
385	390	395	400
Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys			
	405	410	415
Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val			
	420	425	430

Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr  
 435 440 445

Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu  
 450 455 460

Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly  
 465 470 475 480

Ser Asp Arg Lys Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu  
 485 490 495

Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala Lys Gln His Gly  
 500 505 510

Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys Glu His Glu His  
 515 520 525

Glu Gly Lys Lys Arg Arg Lys Glu  
 530 535

<210> 251

<211> 2121

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1629)

<400> 251

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Met Ala Leu Thr Ser Phe Leu Pro Ala Pro

1 5 10

act cag cta tct cag gac cag ctt gag gct gaa gaa aag gca aga tcc 99

Thr	Gln	Leu	Ser	Gln	Asp	Gln	Leu	Glu	Ala	Glu	Glu	Lys	Ala	Arg	Ser		
				15					20						25		
cag	aga	tca	cgg	cag	acc	tca	ctg	gtc	tcc	tcc	cga	aga	gaa	cct	ccc	147	
Gln	Arg	Ser	Arg	Gln	Thr	Ser	Leu	Val	Ser	Ser	Arg	Arg	Glu	Pro	Pro		
				30					35					40			
ccg	tac	gga	tac	cgg	aaa	ggc	tgg	ata	cct	cgg	tta	tta	gag	gat	ttt	195	
Pro	Tyr	Gly	Tyr	Arg	Lys	Gly	Trp	Ile	Pro	Arg	Leu	Leu	Glu	Asp	Phe		
				45					50					55			
gga	gat	gga	ggt	gct	ttt	cca	gag	atc	cat	gtg	gcc	cag	tat	cca	ctg	243	
Gly	Asp	Gly	Gly	Ala	Phe	Pro	Glu	Ile	His	Val	Ala	Gln	Tyr	Pro	Leu		
				60					65					70			
gat	atg	gga	cga	aag	aaa	aaa	atg	tcg	aat	gcg	ctg	gcc	att	cag	gtg	291	
Asp	Met	Gly	Arg	Lys	Lys	Lys	Met	Ser	Asn	Ala	Leu	Ala	Ile	Gln	Val		
				75					80					85		90	
gat	tct	gaa	gga	aaa	att	aaa	tat	gat	gca	att	gct	cga	caa	gga	cag	339	
Asp	Ser	Glu	Gly	Lys	Ile	Lys	Tyr	Asp	Ala	Ile	Ala	Arg	Gln	Gly	Gln		
				95					100					105			
tca	aaa	gac	aag	gtc	att	tat	agc	aaa	tac	act	gac	ctg	gtt	cca	aag	387	
Ser	Lys	Asp	Lys	Val	Ile	Tyr	Ser	Lys	Tyr	Thr	Asp	Leu	Val	Pro	Lys		
				110					115					120			
gag	gtt	atg	aat	gca	gat	gat	cca	gac	ctg	caa	agg	ccc	gat	gaa	gaa	435	
Glu	Val	Met	Asn	Ala	Asp	Asp	Pro	Asp	Leu	Gln	Arg	Pro	Asp	Glu	Glu		
				125					130					135			
gct	att	aaa	gag	ata	aca	gaa	aag	aca	aga	gta	gcc	tta	gaa	aaa	tct	483	
Ala	Ile	Lys	Glu	Ile	Thr	Glu	Lys	Thr	Arg	Val	Ala	Leu	Glu	Lys	Ser		
				140					145					150			
gta	tca	cag	aag	gtc	gcc	gca	gcc	atg	cca	gtt	cga	gca	gct	gac	aaa	531	

757/861

Arg Glu Ala Val Glu Met Arg Ala Gln Val Glu Arg Lys Met Ala Gln  
 300 305 310  
 aaa gaa aag gaa aaa cat gaa gag aaa ctt aga gaa atg gcc cag aaa 1011  
 Lys Glu Lys Glu Lys His Glu Glu Lys Leu Arg Glu Met Ala Gln Lys  
 315 320 325 330  
 gcc agg gaa aga aga gct ggg atc aaa act cat gtg gaa aaa gag gat 1059  
 Ala Arg Glu Arg Arg Ala Gly Ile Lys Thr His Val Glu Lys Glu Asp  
 335 340 345  
 ggg gag gca cgt gag agg gat gaa atc cgg cat gac agg cga aaa gag 1107  
 Gly Glu Ala Arg Glu Arg Asp Glu Ile Arg His Asp Arg Arg Lys Glu  
 350 355 360  
 aga cag cat gac cgg aat ctt tcc agg gca gct cct gat aag agg tcg 1155  
 Arg Gln His Asp Arg Asn Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser  
 365 370 375  
 aaa ctt cag aga aat gaa aat cgg gat atc agt gaa gtt att gct ctc 1203  
 Lys Leu Gln Arg Asn Glu Asn Arg Asp Ile Ser Glu Val Ile Ala Leu  
 380 385 390  
 ggt gtt cct aat cct cgg act tcc aat gaa gtt cag tat gac caa agg 1251  
 Gly Val Pro Asn Pro Arg Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg  
 395 400 405 410  
 ctc ttc aac caa tcc aag ggt atg gac agt gga ttt gca ggt gga gaa 1299  
 Leu Phe Asn Gln Ser Lys Gly Met Asp Ser Gly Phe Ala Gly Gly Glu  
 415 420 425  
 gat gaa att tat aat gtt tat gat caa gcc tgg aga ggt ggt aaa gat 1347  
 Asp Glu Ile Tyr Asn Val Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp  
 430 435 440  
 atg gcc cag agt att tat agg ccc agt aaa aat ctg gac aag gac atg 1395

Met Ala Gln Ser Ile Tyr Arg Pro Ser Lys Asn Leu Asp Lys Asp Met  
445 450 455  
tat ggt gat gac cta gaa gcc aga ata aag acc aac aga ttt gtt ccc 1443  
Tyr Gly Asp Asp Leu Glu Ala Arg Ile Lys Thr Asn Arg Phe Val Pro  
460 465 470  
gac aag gag ttt tct ggt tca gac cgt aga cag aga ggc cga gaa gga 1491  
Asp Lys Glu Phe Ser Gly Ser Asp Arg Arg Gln Arg Gly Arg Glu Gly  
475 480 485 490  
cca gtt cag ttt gag gaa gat cct ttt ggt ttg gac aag ttt ttg gaa 1539  
Pro Val Gln Phe Glu Glu Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu  
495 500 505  
gaa gcc aaa cag cat ggt ggc tct aaa aga ccc tca gat agc agc cgc 1587  
Glu Ala Lys Gln His Gly Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg  
510 515 520  
ccc aag gaa cac gag cat gaa ggc aag aag agg agg aag gaa 1629  
Pro Lys Glu His Glu His Glu Gly Lys Lys Arg Arg Lys Glu  
525 530 535  
taggcacagg tctctccaaa gtgaatgaac tcttaccat aaccctaatg atgcaagtca 1689  
tatgggggaa cactttgtaa atggtcagga taaaaaccaa atctgggtgc cagatcccag 1749  
cactactttt tattactgga gaaatggggg ggatagaaaa ttctactttg aattatttag 1809  
ttttttttta agagtgggtt gtgtttgtgc ttctcccacc ttccagcatt tatagaacat 1869  
gctgccccac atacaaagtc aagaccactt acttttatgt gacactagta gtttgggggtt 1929  
aatgttttgt gtaagaacag ctgcatatga gtaaagttac cccaaccaca gtgaggagga 1989  
agatgttcac atactggaac tgtcctgcca aataaatttt gccctattg tgctctgttt 2049  
taatttgag tgggcaaagt aacctcttgc ttggtgcaac tatttgtttc aaataaaaac 2109  
atttagacaa aa 2121



&lt;210&gt; 252

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

Met Ala Leu Thr Ser Phe Leu Pro Ala Pro Thr Gln Leu Ser Gln Asp  
 1                      5                      10                      15  
 Gln Leu Glu Ala Glu Glu Lys Ala Arg Ser Gln Arg Ser Arg Gln Thr  
                     20                      25                      30  
 Ser Leu Val Ser Ser Arg Arg Glu Pro Pro Pro Tyr Gly Tyr Arg Lys  
                     35                      40                      45  
 Gly Trp Ile Pro Arg Leu Leu Glu Asp Phe Gly Asp Gly Gly Ala Phe  
                     50                      55                      60  
 Pro Glu Ile His Val Ala Gln Tyr Pro Leu Asp Met Gly Arg Lys Lys  
 65                      70                      75                      80  
 Lys Met Ser Asn Ala Leu Ala Ile Gln Val Asp Ser Glu Gly Lys Ile  
                     85                      90                      95  
 Lys Tyr Asp Ala Ile Ala Arg Gln Gly Gln Ser Lys Asp Lys Val Ile  
                     100                      105                      110  
 Tyr Ser Lys Tyr Thr Asp Leu Val Pro Lys Glu Val Met Asn Ala Asp  
                     115                      120                      125  
 Asp Pro Asp Leu Gln Arg Pro Asp Glu Glu Ala Ile Lys Glu Ile Thr  
                     130                      135                      140  
 Glu Lys Thr Arg Val Ala Leu Glu Lys Ser Val Ser Gln Lys Val Ala  
 145                      150                      155                      160  
 Ala Ala Met Pro Val Arg Ala Ala Asp Lys Leu Ala Pro Ala Gln Tyr  
                     165                      170                      175

Ile Arg Tyr Thr Pro Ser Gln Gln Gly Val Ala Phe Asn Ser Gly Ala  
180 185 190  
Lys Gln Arg Val Ile Arg Met Val Glu Met Gln Lys Asp Pro Met Glu  
195 200 205  
Pro Pro Arg Phe Lys Ile Asn Lys Lys Ile Pro Arg Gly Pro Pro Ser  
210 215 220  
Pro Pro Ala Pro Val Met His Ser Pro Ser Arg Lys Met Thr Val Lys  
225 230 235 240  
Glu Gln Gln Glu Trp Lys Ile Pro Pro Cys Ile Ser Asn Trp Lys Asn  
245 250 255  
Ala Lys Gly Tyr Thr Ile Pro Leu Asp Lys Arg Leu Ala Ala Asp Gly  
260 265 270  
Arg Gly Leu Gln Thr Val His Ile Asn Glu Asn Phe Ala Lys Leu Ala  
275 280 285  
Glu Ala Leu Tyr Ile Ala Asp Arg Lys Ala Arg Glu Ala Val Glu Met  
290 295 300  
Arg Ala Gln Val Glu Arg Lys Met Ala Gln Lys Glu Lys Glu Lys His  
305 310 315 320  
Glu Glu Lys Leu Arg Glu Met Ala Gln Lys Ala Arg Glu Arg Arg Ala  
325 330 335  
Gly Ile Lys Thr His Val Glu Lys Glu Asp Gly Glu Ala Arg Glu Arg  
340 345 350  
Asp Glu Ile Arg His Asp Arg Arg Lys Glu Arg Gln His Asp Arg Asn  
355 360 365  
Leu Ser Arg Ala Ala Pro Asp Lys Arg Ser Lys Leu Gln Arg Asn Glu  
370 375 380  
Asn Arg Asp Ile Ser Glu Val Ile Ala Leu Gly Val Pro Asn Pro Arg

385                      390                      395                      400  
Thr Ser Asn Glu Val Gln Tyr Asp Gln Arg Leu Phe Asn Gln Ser Lys  
                         405                      410                      415  
Gly Met Asp Ser Gly Phe Ala Gly Gly Glu Asp Glu Ile Tyr Asn Val  
                         420                      425                      430  
Tyr Asp Gln Ala Trp Arg Gly Gly Lys Asp Met Ala Gln Ser Ile Tyr  
                         435                      440                      445  
Arg Pro Ser Lys Asn Leu Asp Lys Asp Met Tyr Gly Asp Asp Leu Glu  
                         450                      455                      460  
Ala Arg Ile Lys Thr Asn Arg Phe Val Pro Asp Lys Glu Phe Ser Gly  
465                      470                      475                      480  
Ser Asp Arg Arg Gln Arg Gly Arg Glu Gly Pro Val Gln Phe Glu Glu  
                         485                      490                      495  
Asp Pro Phe Gly Leu Asp Lys Phe Leu Glu Glu Ala Lys Gln His Gly  
                         500                      505                      510  
Gly Ser Lys Arg Pro Ser Asp Ser Ser Arg Pro Lys Glu His Glu His  
                         515                      520                      525  
Glu Gly Lys Lys Arg Arg Lys Glu  
                         530                      535

<210> 253

<211> 2003

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (23).. (1075)

&lt;400&gt; 253

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                               Met Ala Ala Ala Val Asn Ser Gly Ser Ser
                               1           5           10

ctc ccg ctg ttc gac tgc ccg act tgg gca ggt aaa cca cca cct ggc      100
Leu Pro Leu Phe Asp Cys Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly
                               15           20           25

tta cat ctg gat gtg gtg aaa gga gac aag cta att gag aag ctg att      148
Leu His Leu Asp Val Val Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile
                               30           35           40

att gat gag aaa aag tat tac tta ttt ggg agg aac ccc gat ctg tgt      196
Ile Asp Glu Lys Lys Tyr Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys
                               45           50           55

gac ttc act atc gac cac cag tca tgc tct cga gtc cac gca gcg ctg      244
Asp Phe Thr Ile Asp His Gln Ser Cys Ser Arg Val His Ala Ala Leu
                               60           65           70

gtg tac cac aaa cac ctg aag aga gtt ttc ttg ata gac ctc aac agc      292
Val Tyr His Lys His Leu Lys Arg Val Phe Leu Ile Asp Leu Asn Ser
                               75           80           85           90

aca cat ggc act ttc ttg ggt cac att cgg ctg gaa cct cac aag cct      340
Thr His Gly Thr Phe Leu Gly His Ile Arg Leu Glu Pro His Lys Pro
                               95           100           105

caa cag att ccc atc gat tct acg gtc tca ttt ggc gcg tcc acg agg      388
Gln Gln Ile Pro Ile Asp Ser Thr Val Ser Phe Gly Ala Ser Thr Arg
                               110           115           120

gca tac act ctg cga gag aag cct cag aca ttg cca tcg gct gtg aaa      436
Ala Tyr Thr Leu Arg Glu Lys Pro Gln Thr Leu Pro Ser Ala Val Lys

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125	130	135	
gga gat gag aag atg ggc gga gag gat gat gaa ctc aag ggc ttg ttg			484
Gly Asp Glu Lys Met Gly Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu			
140	145	150	
gga ctt ccc gaa gag gag acc gag ctg gat aac ctg aca gag ttc aac			532
Gly Leu Pro Glu Glu Glu Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn			
155	160	165	170
act gcc cac aac aag cgg att tca acc ctc act att gag gag ggg aac			580
Thr Ala His Asn Lys Arg Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn			
	175	180	185
ctg gac atc cag aga cca aag agg aag agg aag aac tca agg gtg acc			628
Leu Asp Ile Gln Arg Pro Lys Arg Lys Arg Lys Asn Ser Arg Val Thr			
190	195	200	
ttc agt gag gat gac gag atc atc aac cca gag gac gtg gat ccg tct			676
Phe Ser Glu Asp Asp Glu Ile Ile Asn Pro Glu Asp Val Asp Pro Ser			
205	210	215	
gtt ggt cgg ttc cgg aac atg gtg cag aca gca gtg gtt cca gtc aag			724
Val Gly Arg Phe Arg Asn Met Val Gln Thr Ala Val Val Pro Val Lys			
220	225	230	
aag aag cgg atg gag ggc tct ggc tct ctg ggc ctg gag gag tcg ggg			772
Lys Lys Arg Met Glu Gly Ser Gly Ser Leu Gly Leu Glu Glu Ser Gly			
235	240	245	250
agc agg cgc atg cag aac ttt gcc ttc agt gga gga cta tat ggg ggc			820
Ser Arg Arg Met Gln Asn Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly			
	255	260	265
ctg ccc ccc aca cac agt gaa acg ggc tcc cag ccg cat ggc att cat			868
Leu Pro Pro Thr His Ser Glu Thr Gly Ser Gln Pro His Gly Ile His			

270	275	280	
ggg aca gcg ctc att ggt ggc ttg ccc atg cca tac ccg aac ctc gcc			916
Gly Thr Ala Leu Ile Gly Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala			
285	290	295	
cct gat gtg gac ttg act cct gtt gtg cca tca gca gtg gcc ata aat			964
Pro Asp Val Asp Leu Thr Pro Val Val Pro Ser Ala Val Ala Ile Asn			
300	305	310	
ccc aca cca aac cct gca gtc tat aac cct gag gct gtg aat gaa ccc			1012
Pro Thr Pro Asn Pro Ala Val Tyr Asn Pro Glu Ala Val Asn Glu Pro			
315	320	325	330
aag aag aag aaa tac gcg aag gag gct tgg ccg ggc aag aag ccc aca			1060
Lys Lys Lys Lys Tyr Ala Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr			
335	340	345	
cct tcc tta ctg att tgatattttg gttatggaga ggggtggggag gggggtggag			1115
Pro Ser Leu Leu Ile			
350			
ggatgacaag gggagctact gaactaggga gaaaactttc catgtgtgca gtatcgtctt			1175
tcagaaagtc tcctgaggtc ccaaccatgt aatactgaga ccaggggtgg ggctaaagta			1235
ccagtaagga ctaaagtcag gcagcttgaa gtgtagagag aggcttccca gtcccttctg			1295
agccgactgt cctggcgatg tccctgtgcc acctattagg actgttttat gtaaagtcgc			1355
tcatgggagg catctggagc aatgagaggg tagagcctca ttagttaata ttcccttccc			1415
tcgggagacc caagtaacag agcggttgca tggataccag gttggttgac actgttcatt			1475
taaaccacag taaacgagtg tcctcttgtg cctgtggttt tgaggtctaa taggccattc			1535
tgtgtcatgt ctggtggcat gaggccattt tgagttcccc tcatctgtag ccagtgtcac			1595
aggacaggct aatgggtttg tacagtattg ttggacttta cctatgtttc ttgtccacac			1655
tgaaaaactca tttagttcga gtgcagcctc ctccctgtgg cctcactgtt ggtgtgtgcc			1715
ctgaggcagt tcctggtgaa caggaagact atactgcaag gaccagggtgt gtgttaggag			1775

aacacctcag ttttggtttg gaggtcctc tcccctgacc ccccccac ccccatgag 1835  
 agttcttcag atctccagaa tagacctggc taacaggaga caaggtagga accattgtac 1895  
 gagctttgta cagatttgta catttgtgta ataggccttt tctgctttaa gtgtagcttt 1955  
 ttacctgtaa cctttattac attgtaaatt aaatgtaact tttgtcaa 2003

<210> 254

<211> 351

<212> PRT

<213> Mus musculus

<400> 254

Met Ala Ala Ala Val Asn Ser Gly Ser Ser Leu Pro Leu Phe Asp Cys  
 1 5 10 15  
 Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly Leu His Leu Asp Val Val  
 20 25 30  
 Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu Lys Lys Tyr  
 35 40 45  
 Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His  
 50 55 60  
 Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu  
 65 70 75 80  
 Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu  
 85 90 95  
 Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp  
 100 105 110  
 Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu  
 115 120 125  
 Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu Lys Met Gly

130	135	140	
Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro Glu Glu Glu			
145	150	155	160
Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His Asn Lys Arg			
	165	170	175
Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile Gln Arg Pro			
	180	185	190
Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu Asp Asp Glu			
	195	200	205
Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg Phe Arg Asn			
	210	215	220
Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg Met Glu Gly			
225	230	235	240
Ser Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg Met Gln Asn			
	245	250	255
Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro Thr His Ser			
	260	265	270
Glu Thr Gly Ser Gln Pro His Gly Ile His Gly Thr Ala Leu Ile Gly			
	275	280	285
Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val Asp Leu Thr			
	290	295	300
Pro Val Val Pro Ser Ala Val Ala Ile Asn Pro Thr Pro Asn Pro Ala			
305	310	315	320
Val Tyr Asn Pro Glu Ala Val Asn Glu Pro Lys Lys Lys Lys Tyr Ala			
	325	330	335
Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr Pro Ser Leu Leu Ile			
	340	345	350



&lt;210&gt; 255

&lt;211&gt; 2148

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (12).. (1064)

&lt;400&gt; 255

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ggagacgcaa g atg gcg gca gcc gcg aac tcc ggc tct agc ctc ccg ctg      50
      Met Ala Ala Ala Ala Asn Ser Gly Ser Ser Leu Pro Leu
              1              5              10

ttc gac tgc cca acc tgg gca ggt aag ccc cct ccc ggt tta cat ctg      98
Phe Asp Cys Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly Leu His Leu
      15              20              25

gat gta gtc aaa gga gac aaa cta att gag aaa ctg att att gat gag      146
Asp Val Val Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu
      30              35              40              45

aag aag tat tac tta ttt ggg aga aac cct gat ttg tgt gac ttt acc      194
Lys Lys Tyr Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr
              50              55              60

att gac cac cag tct tgc tct cgg gtc cat gct gca ctt gtc tac cac      242
Ile Asp His Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His
              65              70              75

aag cat ctg aag aga gtt ttc ctg ata gat ctc aac agt aca cac ggc      290
Lys His Leu Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly
              80              85              90

```

act ttc ttg ggt cac att cgg ttg gaa cct cac aag cct cag caa att	338
Thr Phe Leu Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile	
95 100 105	
ccc atc gat tcc acg gtc tca ttt ggc gca tcc aca agg gca tac act	386
Pro Ile Asp Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr	
110 115 120 125	
ctg cgc gag aag cct cag aca ttg cca tcg gct gtg aaa gga gat gag	434
Leu Arg Glu Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu	
130 135 140	
aag atg ggt gga gag gat gat gaa ctc aag ggc tta ctg ggg ctt cca	482
Lys Met Gly Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro	
145 150 155	
gag gag gaa act gag ctt gat aac ctg aca gag ttc aac act gcc cac	530
Glu Glu Glu Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His	
160 165 170	
aac aag cgg att tct acc ctt acc att gag gag gga aat ctg gac att	578
Asn Lys Arg Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile	
175 180 185	
caa aga cca aag agg aag agg aag aac tca cgg gtg aca ttc agt gag	626
Gln Arg Pro Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu	
190 195 200 205	
gat gat gag atc atc aac cca gag gat gtg gat ccc tca gtt ggt cga	674
Asp Asp Glu Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg	
210 215 220	
ttc agg aac atg gtg caa act gca gtg gtc cca gtc aag aag aag cgt	722
Phe Arg Asn Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg	
225 230 235	

gtg gag ggc cct ggc tcc ctg ggc ctg gag gaa tca ggg agc agg cgc 770  
 Val Glu Gly Pro Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg  
 240 245 250  
 atg cag aac ttt gcc ttc agc gga gga ctc tac ggg ggc ctg ccc ccc 818  
 Met Gln Asn Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro  
 255 260 265  
 aca cac agt gaa gca ggc tcc cag cca cat ggc atc cat ggg aca gca 866  
 Thr His Ser Glu Ala Gly Ser Gln Pro His Gly Ile His Gly Thr Ala  
 270 275 280 285  
 ctc atc ggt ggc ttg ccc atg cca tac cca aac ctt gcc cct gat gtg 914  
 Leu Ile Gly Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val  
 290 295 300  
 gac ttg act cct gtt gtg ccg tca gca gtg aac atg aac cct gca cca 962  
 Asp Leu Thr Pro Val Val Pro Ser Ala Val Asn Met Asn Pro Ala Pro  
 305 310 315  
 aac cct gca gtc tat aac cct gaa gct gta aat gaa ccc aag aag aag 1010  
 Asn Pro Ala Val Tyr Asn Pro Glu Ala Val Asn Glu Pro Lys Lys Lys  
 320 325 330  
 aaa tat gca aaa gag gct tgg cca ggc aag aag ccc aca cct tcc ttg 1058  
 Lys Tyr Ala Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr Pro Ser Leu  
 335 340 345  
 ctg att tgatattttt ggcatggag aagggtggga ttgggtggga atggggtgga 1114  
 Leu Ile  
 350  
 agggatgatgg ggagctaattg aactagggag aaaaactttc catgtgtgcg gatatgtctt 1174  
 tcagaatgtc tcctggcatc ctaaccatgt aatatgacaa ttgggggtgg ggttgaaata 1234  
 gcccataaag acctgtcttc acaacacttg cattgtagag aaaggcttct tatatccttt 1294

tcaatagact gccctggctc tttcctagge cttccactac ctcctttctt tctcccactt 1354  
 tctaggatca tttttatgta aagtcacata tcccaggccc tcaggttgaa tccagagctg 1414  
 tagaggttac agtagcatca ccagccttgg gggctccagag cctaatttat attcactatc 1474  
 cttccaagtc ccgggtagca gaagggttgc catagatctc agtttgatca aaaagaaggc 1534  
 ttagaattct gcagttaagc tgaggtttaa actaaaaaat gtttccttgg gtcagtgggtt 1594  
 ttgaggcca gtagctagge ttttctcttt tgtccttcct gttggaatga aaacatttcg 1654  
 attttccttc atctgtgact ggtgccatag acacagggtt atagttttaa cttacagtat 1714  
 tgtttgaaat ttacctgttt ttcttgtcaa acctgagcac tcctcctgct gaagtttctt 1774  
 atttaattcc agagtactgt cctctactct aaggcattac ttttaagtgt attatgaagg 1834  
 cagttttcaa aggatatgac cagttggggg aattcaaatt aaaaaggaaa agatttgttt 1894  
 ggaagtaact ggtgtctcta agaggaattt ttagatgtca gtttgagggc tctttccccc 1954  
 ctcaattgag agctcttggt attcagagct ccaagactag acctggctaa caaacatagg 2014  
 agacaaagtt aggaaacatt gatacaagct ttgtacagag atttgtagat ttgtgtaata 2074  
 ggccttttca tgctttatgt gtagcttttt acctgtaacc tttattacat tgtaaattaa 2134  
 acgtaacttt tgtc 2148

<210> 256

<211> 351

<212> PRT

<213> Homo sapiens

<400> 256

Met Ala Ala Ala Ala Asn Ser Gly Ser Ser Leu Pro Leu Phe Asp Cys

1 5 10 15

Pro Thr Trp Ala Gly Lys Pro Pro Pro Gly Leu His Leu Asp Val Val

20 25 30

Lys Gly Asp Lys Leu Ile Glu Lys Leu Ile Ile Asp Glu Lys Lys Tyr

35

40

45

Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His  
 50 55 60  
 Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu  
 65 70 75 80  
 Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu  
 85 90 95  
 Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp  
 100 105 110  
 Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu  
 115 120 125  
 Lys Pro Gln Thr Leu Pro Ser Ala Val Lys Gly Asp Glu Lys Met Gly  
 130 135 140  
 Gly Glu Asp Asp Glu Leu Lys Gly Leu Leu Gly Leu Pro Glu Glu Glu  
 145 150 155 160  
 Thr Glu Leu Asp Asn Leu Thr Glu Phe Asn Thr Ala His Asn Lys Arg  
 165 170 175  
 Ile Ser Thr Leu Thr Ile Glu Glu Gly Asn Leu Asp Ile Gln Arg Pro  
 180 185 190  
 Lys Arg Lys Arg Lys Asn Ser Arg Val Thr Phe Ser Glu Asp Asp Glu  
 195 200 205  
 Ile Ile Asn Pro Glu Asp Val Asp Pro Ser Val Gly Arg Phe Arg Asn  
 210 215 220  
 Met Val Gln Thr Ala Val Val Pro Val Lys Lys Lys Arg Val Glu Gly  
 225 230 235 240  
 Pro Gly Ser Leu Gly Leu Glu Glu Ser Gly Ser Arg Arg Met Gln Asn  
 245 250 255  
 Phe Ala Phe Ser Gly Gly Leu Tyr Gly Gly Leu Pro Pro Thr His Ser

260 265 270  
 Glu Ala Gly Ser Gln Pro His Gly Ile His Gly Thr Ala Leu Ile Gly  
 275 280 285  
 Gly Leu Pro Met Pro Tyr Pro Asn Leu Ala Pro Asp Val Asp Leu Thr  
 290 295 300  
 Pro Val Val Pro Ser Ala Val Asn Met Asn Pro Ala Pro Asn Pro Ala  
 305 310 315 320  
 Val Tyr Asn Pro Glu Ala Val Asn Glu Pro Lys Lys Lys Lys Tyr Ala  
 325 330 335  
 Lys Glu Ala Trp Pro Gly Lys Lys Pro Thr Pro Ser Leu Leu Ile  
 340 345 350

&lt;210&gt; 257

&lt;211&gt; 1088

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15).. (965)

&lt;400&gt; 257

agagagcgta caag atg gcg gcg ccc atg gag ctg ttc tgc tgg tca ggg 50  
 Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly  
 1 5 10  
 ggc tgg gga ttg ccg tcg gtg gac ctg gat agt ctg gcc gtg ctg acc 98  
 Gly Trp Gly Leu Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr  
 15 20 25  
 tat acc aga ttt aca ggc gcc cca ctg aag ata cac aag acc agc aat 146

Tyr Thr Arg Phe Thr Gly Ala Pro Leu Lys Ile His Lys Thr Ser Asn	
30 35 40	
cct tgg cag agc cct tca gga act ctg cct gct ctt cga acc agt gat	194
Pro Trp Gln Ser Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser Asp	
45 50 55 60	
ggg aaa gtc att aca gtg cca cac aag atc atc acc cat ctt cgt aaa	242
Gly Lys Val Ile Thr Val Pro His Lys Ile Ile Thr His Leu Arg Lys	
65 70 75	
gag aag tat aat gcc gac tac gat ctg tca gct cgc caa gga gca gat	290
Glu Lys Tyr Asn Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp	
80 85 90	
acc cta gcc ttc atg tct ctg ctg gag gag aaa cta ctg cct gtg tta	338
Thr Leu Ala Phe Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu	
95 100 105	
atc cat act ttt tgg ata gac gcc aag aac tat gtg gaa gtg acc cga	386
Ile His Thr Phe Trp Ile Asp Ala Lys Asn Tyr Val Glu Val Thr Arg	
110 115 120	
aag tgg tat gca gag gct atg ccc ttt ccc ctc aac ttc ttc ctg ccc	434
Lys Trp Tyr Ala Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro	
125 130 135 140	
ggc cgc atg cag cgc cag tac atg gag cgg cta cag ctg ctg tgt ggc	482
Gly Arg Met Gln Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Cys Gly	
145 150 155	
gag cac aaa tca gag aac gag gag gaa cta gaa aaa gag cta tac caa	530
Glu His Lys Ser Glu Asn Glu Glu Glu Leu Glu Lys Glu Leu Tyr Gln	
160 165 170	
gag gct cgg gag tgc cta acc ctt ctc tct cag cgt ctg ggc tct cag	578

Glu Ala Arg Glu Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln	
175	180
aag ttc ttc ttt ggg gat gcc cct gcc tcc ctg gac gcc ttt gtt ttt	626
Lys Phe Phe Phe Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe	
190	195
agc cat ttg gcc ctg ctg ctg cag gcc aag ctg ccc agt ggg aag ctg	674
Ser His Leu Ala Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu	
205	210
cag gcc cac ctt cgg ggg ctg cac aac ctc tgc gcc tac tgc acc cac	722
Gln Ala His Leu Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His	
225	230
atc ctc aac ctc tac ttt ccc cgg gat gga gat gag gtg cca ctt cca	770
Ile Leu Asn Leu Tyr Phe Pro Arg Asp Gly Asp Glu Val Pro Leu Pro	
240	245
cgc cag aca cca gca gcc cct gag acc gag gag gag cca tac cgg cgc	818
Arg Gln Thr Pro Ala Ala Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg	
255	260
cgg acc cag att ctc tct gtg ctg gca ggg ctg gca gcc atg gtg ggc	866
Arg Thr Gln Ile Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly	
270	275
tat gcc ctg ctc agt ggc atc gtt tct atc cag cgg aca agc cct gct	914
Tyr Ala Leu Leu Ser Gly Ile Val Ser Ile Gln Arg Thr Ser Pro Ala	
285	290
cgg gcc cca ggc acc cgg gcc ttg ggc ctg gct gag gag gat gaa gag	962
Arg Ala Pro Gly Thr Arg Ala Leu Gly Leu Ala Glu Glu Asp Glu Glu	
305	310
gac tgatggcggtt cctgttccca ggactgactt ttctactcgt gcattccagc	1015



Asp

tgtccctcgt ctcccatgg ttggagcagc caaaaatggg gcgctgtcct cagaataaac 1075  
 ctgtttacac taa 1088

&lt;210&gt; 258

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 258

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu  
 1 5 10 15  
 Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Thr Arg Phe  
 20 25 30  
 Thr Gly Ala Pro Leu Lys Ile His Lys Thr Ser Asn Pro Trp Gln Ser  
 35 40 45  
 Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser Asp Gly Lys Val Ile  
 50 55 60  
 Thr Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn  
 65 70 75 80  
 Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe  
 85 90 95  
 Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Ile His Thr Phe  
 100 105 110  
 Trp Ile Asp Ala Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala  
 115 120 125  
 Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln  
 130 135 140

Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Cys Gly Glu His Lys Ser  
 145                      150                      155                      160  
 Glu Asn Glu Glu Glu Leu Glu Lys Glu Leu Tyr Gln Glu Ala Arg Glu  
                          165                      170                      175  
 Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe  
                          180                      185                      190  
 Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser His Leu Ala  
                          195                      200                      205  
 Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Ala His Leu  
                          210                      215                      220  
 Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Asn Leu  
 225                      230                      235                      240  
 Tyr Phe Pro Arg Asp Gly Asp Glu Val Pro Leu Pro Arg Gln Thr Pro  
                          245                      250                      255  
 Ala Ala Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Thr Gln Ile  
                          260                      265                      270  
 Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu  
                          275                      280                      285  
 Ser Gly Ile Val Ser Ile Gln Arg Thr Ser Pro Ala Arg Ala Pro Gly  
                          290                      295                      300  
 Thr Arg Ala Leu Gly Leu Ala Glu Glu Asp Glu Glu Asp  
 305                      310                      315

<210> 259

<211> 1065

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (951)

&lt;400&gt; 259

atg gcg gcg ccc atg gag ctg ttc tgc tgg tca ggg ggc tgg ggg ctg 48

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu

1 5 10 15

ccg tca gtg gac ctg gac agc ctg gcc gtg ctg acc tat gcc aga ttt 96

Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Ala Arg Phe

20 25 30

act ggt gct cca ctg aag gta cac aag atc agc aac ccc tgg cag agc 144

Thr Gly Ala Pro Leu Lys Val His Lys Ile Ser Asn Pro Trp Gln Ser

35 40 45

cct tca gga act ctg cct gcc ctt cgg acc agt cat gga gag gtc atc 192

Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser His Gly Glu Val Ile

50 55 60

tca gtt cca cac aag atc atc acc cac ctt cga aaa gag aag tac aat 240

Ser Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn

65 70 75 80

gct gat tat gat ctg tca gct cgg caa ggg gca gac acc ctg gcc ttc 288

Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe

85 90 95

atg tct ctc ctg gag gag aag ttg ctc ccg gtg ctg gta cat act ttt 336

Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Val His Thr Phe

100 105 110

tgg ata gac acc aag aac tac gtg gaa gtg acc cgg aag tgg tat gca 384

Trp Ile Asp Thr Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala

115	120	125	
gag gct atg ccc ttt ccc ctc aac ttc ttc ctg cct ggc cgc atg cag			432
Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln			
130	135	140	
cgg cag tac atg gaa cgg cta cag ctg ctg act ggg gag cac agg cct			480
Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Thr Gly Glu His Arg Pro			
145	150	155	160
gag gac gag gaa gag ctg gag aag gag ctg tac cga gag gct cgg gag			528
Glu Asp Glu Glu Glu Leu Glu Lys Glu Leu Tyr Arg Glu Ala Arg Glu			
165	170	175	
tgt ctg acc ctg ctc tct cag cgc ctg ggc tct caa aag ttc ttc ttt			576
Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe			
180	185	190	
gga gat gcc cct gcc tcc ttg gac gcc ttc gtc ttc agc tac ttg gcc			624
Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser Tyr Leu Ala			
195	200	205	
ctg ctg ctg cag gca aag ctg ccc agt ggg aag ctg cag gtc cac ctg			672
Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Val His Leu			
210	215	220	
cgt ggg ctg cac aac ctc tgt gcc tat tgt acc cac att ctc agt ctc			720
Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Ser Leu			
225	230	235	240
tac ttc ccc tgg gat gga gct gag gta cca ccg caa cgc cag aca cca			768
Tyr Phe Pro Trp Asp Gly Ala Glu Val Pro Pro Gln Arg Gln Thr Pro			
245	250	255	
gca ggc cca gag act gag gag gag cca tac cgg cgc cgg aac cag atc			816
Ala Gly Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Asn Gln Ile			

260	265	270	
cta tct gtg ctg gca gga ctg gca gcc atg gtg ggc tac gcc ttg ctc			864
Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu			
275	280	285	
agc ggc att gtc tcc atc cag cgg gca acg cct gct cgg gcc cca ggc			912
Ser Gly Ile Val Ser Ile Gln Arg Ala Thr Pro Ala Arg Ala Pro Gly			
290	295	300	
acc cgg acc ctg ggc atg gct gag gag gat gaa gag gaa tgatttgtcc			961
Thr Arg Thr Leu Gly Met Ala Glu Glu Asp Glu Glu Glu			
305	310	315	
tcacgtcccc aagactggtt tttctactct catgcattcc agaggccccc gtgcctcctc			1021
gttggttgta cagccggaca cggggtgctg ccaccagaa taaa			1065

&lt;210&gt; 260

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 260

Met Ala Ala Pro Met Glu Leu Phe Cys Trp Ser Gly Gly Trp Gly Leu

1 5 10 15

Pro Ser Val Asp Leu Asp Ser Leu Ala Val Leu Thr Tyr Ala Arg Phe

20 25 30

Thr Gly Ala Pro Leu Lys Val His Lys Ile Ser Asn Pro Trp Gln Ser

35 40 45

Pro Ser Gly Thr Leu Pro Ala Leu Arg Thr Ser His Gly Glu Val Ile

50 55 60

Ser Val Pro His Lys Ile Ile Thr His Leu Arg Lys Glu Lys Tyr Asn

65	70	75	80
Ala Asp Tyr Asp Leu Ser Ala Arg Gln Gly Ala Asp Thr Leu Ala Phe			
	85	90	95
Met Ser Leu Leu Glu Glu Lys Leu Leu Pro Val Leu Val His Thr Phe			
	100	105	110
Trp Ile Asp Thr Lys Asn Tyr Val Glu Val Thr Arg Lys Trp Tyr Ala			
	115	120	125
Glu Ala Met Pro Phe Pro Leu Asn Phe Phe Leu Pro Gly Arg Met Gln			
	130	135	140
Arg Gln Tyr Met Glu Arg Leu Gln Leu Leu Thr Gly Glu His Arg Pro			
145	150	155	160
Glu Asp Glu Glu Glu Leu Glu Lys Glu Leu Tyr Arg Glu Ala Arg Glu			
	165	170	175
Cys Leu Thr Leu Leu Ser Gln Arg Leu Gly Ser Gln Lys Phe Phe Phe			
	180	185	190
Gly Asp Ala Pro Ala Ser Leu Asp Ala Phe Val Phe Ser Tyr Leu Ala			
	195	200	205
Leu Leu Leu Gln Ala Lys Leu Pro Ser Gly Lys Leu Gln Val His Leu			
	210	215	220
Arg Gly Leu His Asn Leu Cys Ala Tyr Cys Thr His Ile Leu Ser Leu			
225	230	235	240
Tyr Phe Pro Trp Asp Gly Ala Glu Val Pro Pro Gln Arg Gln Thr Pro			
	245	250	255
Ala Gly Pro Glu Thr Glu Glu Glu Pro Tyr Arg Arg Arg Asn Gln Ile			
	260	265	270
Leu Ser Val Leu Ala Gly Leu Ala Ala Met Val Gly Tyr Ala Leu Leu			
	275	280	285

Ser Gly Ile Val Ser Ile Gln Arg Ala Thr Pro Ala Arg Ala Pro Gly

290

295

300

Thr Arg Thr Leu Gly Met Ala Glu Glu Asp Glu Glu Glu

305

310

315

<210> 261

<211> 1580

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (29).. (223)

<400> 261

agagcctccg aagaggggac tgcgcacc atg gcc tcc cgt gca gcg ccg gtc 52

Met Ala Ser Arg Ala Ala Pro Val

1

5

aga cag aca tgc tgt tgt ttc aac atc cga gtc gcc acc ata gcc ctg 100

Arg Gln Thr Cys Cys Cys Phe Asn Ile Arg Val Ala Thr Ile Ala Leu

10

15

20

gcc att tac cac ata gtc atg agt gtc ctg ctg ttc att gag cat gtg 148

Ala Ile Tyr His Ile Val Met Ser Val Leu Leu Phe Ile Glu His Val

25

30

35

40

gtg gag gtg gcc cgc ggt aaa gtg tcc tgt agg ttc ttc aag atg ccg 196

Val Glu Val Ala Arg Gly Lys Val Ser Cys Arg Phe Phe Lys Met Pro

45

50

55

agc gat acg acg aaa tgg tgg aat caa tgaagaaagt agcagggatg 243

Ser Asp Thr Thr Lys Trp Trp Asn Gln

60

65

gacgtggagc tgacagttga agaacgaaac cttttatctg ttgcatataa aaatgtgatt 303  
 ggagccagaa gagcatcctg gagaataatc agcagcattg aacagaagga agaaaacaag 363  
 ggaggagagg acaaattaaa gatgattcgg gagtaccggc aaatggttga aactgagctc 423  
 aagttaatct gttgtgacat tctggatgta ctggacaaac acctcattcc agcagctaac 483  
 actggttggc aaaagcagct tttgatgacg cgattgcaga actggacacg ctgagtgaag 543  
 aaagttataa ggactctacg ctcatcatgc agctgctacg tgataacctg acgctgtgga 603  
 cctcagacat gcagggcgat ggtgaagagc agaataaaga agcgctgcag gatgtggaag 663  
 atgagaatca gtgagacgta ataaaagcca acaagagaaa ccatctctga ctacccttc 723  
 cccccctccc cttggaagtt ccccatgtgc actgagaacc accaaatttg actttcacat 783  
 ttggtctcag aatttaggtt cctgccctgt tgttttcttt ctttttcttt ttttttctc 843  
 ccctcccctt ttttaaaaca aacaaacaaa caaacagttt tcagaagttc ttaaggcaag 903  
 agtgaatttc tgtggatttt actggtccca gctttaggtt ctttacgaca ctaacaggac 963  
 tgcatagagg ctttttcagc attactgtat tgtctccggc cacactggca agatcatcat 1023  
 tagaaatgga aatgacattt gaaagccatt agacttctag gtgatgcac taagaaagat 1083  
 taatcacaca atagaggcat atgcgctgtc atttttcctt ttttaattg ttaaattgaa 1143  
 tttataacca atgtttaaac ttaaattggg tgtagcttg aggtgttttg ggggagtttg 1203  
 ttgtaatggt tttgctgtaa actgtgtttg gaactctgct gaagtgttgc tgaaaagcat 1263  
 ggtgctggta acagttcaac aatccgtggc tgctcattct tgccgactcc tccccctctg 1323  
 aagcaggtta gcattgaagg tggatatgaa gcctgcatgc gtgttcaact ctgttctcc 1383  
 tccctcctcc tcggcctccc tcctcccctc cttcgctcgc tcaacctctt ttgttcagta 1443  
 cgtgtaactt gaagctaatt tgtactactg gatctctgac tggagccgca ggtacagatc 1503  
 tgtattgttc ttactgaaac acagcatgga attaacatta aacttaaata aaacaaacct 1563  
 aaattaaaaa tgccaaa 1580

&lt;210&gt; 262

&lt;211&gt; 65



&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 262

Met Ala Ser Arg Ala Ala Pro Val Arg Gln Thr Cys Cys Cys Phe Asn

1 5 10 15

Ile Arg Val Ala Thr Ile Ala Leu Ala Ile Tyr His Ile Val Met Ser

20 25 30

Val Leu Leu Phe Ile Glu His Val Val Glu Val Ala Arg Gly Lys Val

35 40 45

Ser Cys Arg Phe Phe Lys Met Pro Ser Asp Thr Thr Lys Trp Trp Asn

50 55 60

Gln

65

&lt;210&gt; 263

&lt;211&gt; 1373

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(327)

&lt;400&gt; 263

gaa atg gtg gaa tca atg aag aaa gta gca ggg atg gac gtg gag ctg 48

Met Val Glu Ser Met Lys Lys Val Ala Gly Met Asp Val Glu Leu

1 5 10 15

aca gtt gaa gaa cga aac ctt tta tct gtt gca tat aaa aat gtg att 96

Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile

20	25	30	
gga gcc aga aga gca tcc tgg aga ata atc agc agc att gaa cag aag			144
Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys			
35	40	45	
gaa gaa aac aag gga gga gag gac aaa tta aag atg att cgg gag tac			192
Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys Met Ile Arg Glu Tyr			
50	55	60	
cgg caa atg gtt gaa act gag ctc aag tta atc tgt tgt gac att ctg			240
Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile Cys Cys Asp Ile Leu			
65	70	75	
gat gta ctg gac aaa cac ctc att cca gca gct aac act ggt tgg caa			288
Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala Asn Thr Gly Trp Gln			
80	85	90	95
aag cag ctt ttg atg acg caa ttg cag aac tgg aca cgc tgagtgaaga			337
Lys Gln Leu Leu Met Thr Gln Leu Gln Asn Trp Thr Arg			
100	105		
aagttataag gactctacgc tcatcatgca gctgctacgt gataacctga cgctgtggac			397
ctcagacatg cagggcgatg gtgaagagca gaataaagaa gcgctgcagg atgtggaaga			457
tgagaatcag tgagacgtaa taaaagccaa caagagaaac catctctgac tacccttcc			517
ccccctcccc ttggaagtgc ccattgtca ctgagaacca ccaaatttga ctttcacatt			577
tggtctcaga atttaggttc ctgcctgtt gttttctttc tttttctttt tttttctcc			637
cctcccccttt tttaaaacaa acaaacaac aaacagtttt cagaagttct taaggcaaga			697
gtgaatttct gtggatttta ctggtcccag ctttaggttc tttacgacac taacaggact			757
gcatagaggc tttttcagca ttactgtatt gtctccggcc aactggcaa gatcatcatt			817
agaaatggaa atgacatttg aaagccatta gacttctagg tgatgcatct aagaaagatt			877
aatcacacaa tagaggcata tgcgctgtca tttttctttt ttttaattgt taaattgaat			937
tttataccaa tgtttaaact taaattgggt gttagcttga ggtgttttgg gggagtttgt			997

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tgtaatgggtt ttgctgtaaa ctgtgttttg aactctgctg aagtgttgct gaaaagcatg 1057
gtgctggtaa cagttcaaca atccgtggct gtcattctt gccgactcct cccctctga 1117
agcaggtag cattgaaggt ggtatggaag cctgcatgcg tgttcaactc tgttcctcct 1177
ccctcctcct cggcctccct cctccctcc ttcgctcgct caacctcttt tgttcagtag 1237
gtgtaacttg aagctaattt gtactactgg atatctgact ggagccgcag gtacagatct 1297
gtattgttct tactgaaaca cagcatggaa ttaacattaa acttaaataa aacaaaccta 1357
aattaaaaat gccaaa 1373

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<210> 264

<211> 108

<212> PRT

<213> Mus musculus

<400> 264

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Met Val Glu Ser Met Lys Lys Val Ala Gly Met Asp Val Glu Leu Thr
1           5           10           15
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
           20           25           30
Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln Lys Glu
           35           40           45
Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys Met Ile Arg Glu Tyr Arg
           50           55           60
Gln Met Val Glu Thr Glu Leu Lys Leu Ile Cys Cys Asp Ile Leu Asp
65           70           75           80
Val Leu Asp Lys His Leu Ile Pro Ala Ala Asn Thr Gly Trp Gln Lys
           85           90           95
Gln Leu Leu Met Thr Gln Leu Gln Asn Trp Thr Arg
           100          105

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&lt;210&gt; 265

&lt;211&gt; 1704

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (61)..(825)

&lt;400&gt; 265

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gagtcggaga cactatccgc ttccatccgt cgcgcagacc ctgccggagc cgctgccgct      60
atg gat gat cga gag gat ctg gtg tac cag gcg aag ctg gcc gag cag      108
Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln
1           5           10           15
gct gag cga tac gac gaa atg gtg gag tca atg aag aaa gta gca ggg      156
Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
           20           25           30
atg gat gtg gag ctg aca gtt gaa gaa aga aac ctc cta tct gtt gca      204
Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
           35           40           45
tat aag aat gtg att gga gct aga aga gcc tcc tgg aga ata atc agc      252
Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
           50           55           60
agc att gaa cag aaa gaa gaa aac aag gga gga gaa gac aag cta aaa      300
Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
           65           70           75           80
atg att cgg gaa tat cgg caa atg gtt gag act gag cta aag tta atc      348
Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile

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85	90	95	
tgt tgt gac att ctg gat gta ctg gac aaa cac ctc att cca gca gct			396
Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala			
100	105	110	
aac act ggc gag tcc aag gtt ttc tat tat aaa atg aaa ggg gac tac			444
Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr			
115	120	125	
cac agg tat ctg gca gaa ttt gcc aca gga aac gac agg aag gag gct			492
His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala			
130	135	140	
gcg gag aac agc cta gtg gct tat aaa gct gct agt gat att gca atg			540
Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met			
145	150	155	160
aca gaa ctt cca cca acg cat cct att cgc tta ggt ctt gct ctc aat			588
Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn			
165	170	175	
ttt tcc gta ttc tac tac gaa att ctt aat tcc cct gac cgt gcc tgc			636
Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys			
180	185	190	
agg ttg gca aaa gca gct ttt gat gat gca att gca gaa ctg gat acg			684
Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr			
195	200	205	
ctg agt gaa gaa agc tat aag gac tct aca ctt atc atg cag ttg tta			732
Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu			
210	215	220	
cgt gat aat ctg aca cta tgg act tca gac atg cag ggt gac ggt gaa			780
Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu			

225	230	235	240	
gag cag aat aaa gaa gcg ctg cag gac gtg gaa gac gaa aat cag				825
Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln				
	245	250	255	
tgagacataa gccacaaga gaaaccatct ctgaccaccc cctcctcccc atcccaccct				885
ttggaaactc ccatttgtca ctgagaacca ccaaactctga cttttacatt tgggtctcaga				945
atttaggttc ctgccctgtt ggtttttttt tttttttttt ttaaacagtt ttcaaaagtt				1005
cttaaaggca agagtgaatt tctgttgatt ttactgggtcc cagcttttag gttctttaag				1065
acactaacag gactacatag aggctttttc agcattactg tgtcgtctcc gtgccagatg				1125
tggcaagatc accattagca aatggaaatt acatttgaaa gccattagac ttataggtga				1185
tgcaagcatc taagagagag gttaatcaca ctatagaggc aataagtggc atcagttttc				1245
atTTTTtctaa ttgtttaaac tgtgttttat accagtgttt gcaagtaatt ggggtgttagc				1305
ttgagatggc taaaggtggc ttggggaggg acttcgttgt aatggtttg ctgttgctga				1365
aaagcatggc gctggttaaca gttcaacaat ccgtggctgc tcattcttgc ctactttact				1425
ctccactga agcaggttag ctgttgaagg tggatatgaa aagcctgcat gcctgttcaa				1485
ttcttttggt tcttctcctt cccctcctcc ctacctcctt cccctcactc ctccctcct				1545
tcgctcgtc aacctctttt gttcagtatg tgtaacttga agctaatttg tactactgga				1605
tatctgactg gagccacaga tacagaatct gtattgttct tactgaaaca cagcatggaa				1665
ttaacattaa acttaaataa aacaaaccta aattaaana				1704

&lt;210&gt; 266

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 266

Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln

1

5

10

15

Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly  
                   20                                  25                                  30  
 Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala  
                   35                                  40                                  45  
 Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser  
                   50                                  55                                  60  
 Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys  
                   65                                  70                                  75                                  80  
 Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile  
                                   85                                  90                                  95  
 Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala  
                                   100                                  105                                  110  
 Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr  
                                   115                                  120                                  125  
 His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala  
                                   130                                  135                                  140  
 Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met  
                                   145                                  150                                  155                                  160  
 Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn  
                                   165                                  170                                  175  
 Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys  
                                   180                                  185                                  190  
 Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr  
                                   195                                  200                                  205  
 Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu  
                                   210                                  215                                  220  
 Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu

225	230	235	240
Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln			
245	250	255	
<p>&lt;210&gt; 267</p> <p>&lt;211&gt; 2162</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Homo sapiens</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (104).. (1546)</p> <p>&lt;400&gt; 267</p>			
gggctgcgct gtccagctgt ggctatggcc ccagccccga gatgaggagg gagagaacta			60
ggggccccgca ggcctgggaa tttccgtccc ccaccaagtc cgg atg ctc act cca			115
Met Leu Thr Pro			
1			
aag tct cag cag gcc cct gag gga ggg agc tgt cag cca ggg aaa acc			163
Lys Ser Gln Gln Ala Pro Glu Gly Gly Ser Cys Gln Pro Gly Lys Thr			
5	10	15	20
gag aac acc atc acc atg aca acc agt cac cag cct cag gac aga tac			211
Glu Asn Thr Ile Thr Met Thr Thr Ser His Gln Pro Gln Asp Arg Tyr			
25	30	35	
aaa gct gtc tgg ctt atc ttc ttc atg ctg ggt ctg gga acg ctg ctc			259
Lys Ala Val Trp Leu Ile Phe Phe Met Leu Gly Leu Gly Thr Leu Leu			
40	45	50	
ccg tgg aat ttt ttc atg acg gcc act cag tat ttc aca aac cgc ctg			307
Pro Trp Asn Phe Phe Met Thr Ala Thr Gln Tyr Phe Thr Asn Arg Leu			
55	60	65	



gac atg tcc cag aat gtg tcc ttg gtc act gct gaa ctg agc aag gac 355  
 Asp Met Ser Gln Asn Val Ser Leu Val Thr Ala Glu Leu Ser Lys Asp  
 70 75 80  
 gcc cag gcg tca gcc gcc cct gca gca ccc ttg cct gag cgg aac tct 403  
 Ala Gln Ala Ser Ala Ala Pro Ala Ala Pro Leu Pro Glu Arg Asn Ser  
 85 90 95 100  
 ctc agt gcc atc ttc aac aat gtc atg acc cta tgt gcc atg ctg ccc 451  
 Leu Ser Ala Ile Phe Asn Asn Val Met Thr Leu Cys Ala Met Leu Pro  
 105 110 115  
 ctg ctg tta ttc acc tac ctc aac tcc ttc ctg cat cag agg atc ccc 499  
 Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His Gln Arg Ile Pro  
 120 125 130  
 cag tcc gta cgg atc ctg ggc agc ctg gtg gcc atc ctg ctg gtg ttt 547  
 Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile Leu Leu Val Phe  
 135 140 145  
 ctg atc act gcc atc ctg gtg aag gtg cag ctg gat gct ctg ccc ttc 595  
 Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp Ala Leu Pro Phe  
 150 155 160  
 ttt gtc atc acc atg atc aag atc gtg ctc att aat tca ttt ggt gcc 643  
 Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn Ser Phe Gly Ala  
 165 170 175 180  
 atc ctg cag ggc agc ctg ttt ggt ctg gct ggc ctt ctg cct gcc agc 691  
 Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu Leu Pro Ala Ser  
 185 190 195  
 tac acg gcc ccc atc atg agt ggc cag ggc cta gca ggc ttc ttt gcc 739  
 Tyr Thr Ala Pro Ile Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala  
 200 205 210

tcc gtg gcc atg atc tgc gct att gcc agt ggc tcg gag cta tca gaa	787
Ser Val Ala Met Ile Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu	
215 220 225	
agt gcc ttc ggc tac ttt atc aca gcc tgt gct gtt atc att ttg acc	835
Ser Ala Phe Gly Tyr Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr	
230 235 240	
atc atc tgt tac ctg ggc ctg ccc cgc ctg gaa ttc tac cgc tac tac	883
Ile Ile Cys Tyr Leu Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr	
245 250 255 260	
cag cag ctc aag ctt gaa gga ccc ggg gag cag gag acc aag ttg gac	931
Gln Gln Leu Lys Leu Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp	
265 270 275	
ctc att agc aaa gga gag gag cca aga gca ggc aaa gag gaa tct gga	979
Leu Ile Ser Lys Gly Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly	
280 285 290	
gtt tca gtc tcc aac tct cag ccc acc aat gaa agc cac tct atc aaa	1027
Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser His Ser Ile Lys	
295 300 305	
gcc atc ctg aaa aat atc tca gtc ctg gct ttc tct gtc tgc ttc atc	1075
Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser Val Cys Phe Ile	
310 315 320	
ttc act atc acc att ggg atg ttt cca gcc gtg act gtt gag gtc aag	1123
Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu Val Lys	
325 330 335 340	
tcc agc atc gca ggc agc agc acc tgg gaa cgt tac ttc att cct gtg	1171
Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val	
345 350 355	

tcc tgt ttc ttg act ttc aat atc ttt gac tgg ttg ggc cgg agc ctc 1219  
 Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu  
 360 365 370  
 aca gct gta ttc atg tgg cct ggg aag gac agc cgc tgg ctg cca agc 1267  
 Thr Ala Val Phe Met Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser  
 375 380 385  
 ctg gtg ctg gcc cgg ctg gtg ttt gtg cca ctg ctg ctg ctg tgc aac 1315  
 Leu Val Leu Ala Arg Leu Val Phe Val Pro Leu Leu Leu Leu Cys Asn  
 390 395 400  
 att aag ccc cgc cgc tac ctg act gtg gtc ttc gag cac gat gcc tgg 1363  
 Ile Lys Pro Arg Arg Tyr Leu Thr Val Val Phe Glu His Asp Ala Trp  
 405 410 415 420  
 ttc atc ttc ttc atg gct gcc ttt gcc ttc tcc aac ggc tac ctc gcc 1411  
 Phe Ile Phe Phe Met Ala Ala Phe Ala Phe Ser Asn Gly Tyr Leu Ala  
 425 430 435  
 agc ctc tgc atg tgc ttc ggg ccc aag aaa gtg aag cca gct gag gca 1459  
 Ser Leu Cys Met Cys Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala  
 440 445 450  
 gag acc gca gga gcc atc atg gcc ttc ttc ctg tgt ctg ggt ctg gca 1507  
 Glu Thr Ala Gly Ala Ile Met Ala Phe Phe Leu Cys Leu Gly Leu Ala  
 455 460 465  
 ctg ggg gct gtt ttc tcc ttc ctg ttc cgg gca att gtg tgacaaagga 1556  
 Leu Gly Ala Val Phe Ser Phe Leu Phe Arg Ala Ile Val  
 470 475 480  
 tggacagaag gactgctgc ctccctccct gtctgctcc tgccccttcc ttctgccagg 1616  
 ggtgatcctg agtggctctgg cggttttttc ttctaactga cttctgcttt ccacggcgtg 1676  
 tgctggggccc ggatctccag gccctgggga gggagcctct ggacggacag tggggacatt 1736

gtgggttttg ggctcagagt cgagggacgg ggtgtagcct cggcatttgc ttgagtttct 1796  
 ccactcttgg ctctgactga tccctgcttg tgcaggccag tggaggctct tgggcttgga 1856  
 gaacacgtgt gtctctgtgt atgtgtctgt gtgtctgcgt ccgtgtctgt cagactgtct 1916  
 gcctgtcctg gggtagctag gagctgggtc tgaccgttgt atggtttgac ctgatatact 1976  
 ccattctccc ctgcgcctcc tcctctgtgt ttttccatg tccccctccc aactccccat 2036  
 gccagtttt taccatcat gcaccctgta cagttgccac gttactgcct tttttaaaaa 2096  
 tatatttgac agaaaccagg tgccttcaga ggctctctga tttaaataaa ctttcttgt 2156  
 tttttt 2162

<210> 268

<211> 481

<212> PRT

<213> Homo sapiens

<400> 268

Met Leu Thr Pro Lys Ser Gln Gln Ala Pro Glu Gly Gly Ser Cys Gln  
 1 5 10 15  
 Pro Gly Lys Thr Glu Asn Thr Ile Thr Met Thr Thr Ser His Gln Pro  
 20 25 30  
 Gln Asp Arg Tyr Lys Ala Val Trp Leu Ile Phe Phe Met Leu Gly Leu  
 35 40 45  
 Gly Thr Leu Leu Pro Trp Asn Phe Phe Met Thr Ala Thr Gln Tyr Phe  
 50 55 60  
 Thr Asn Arg Leu Asp Met Ser Gln Asn Val Ser Leu Val Thr Ala Glu  
 65 70 75 80  
 Leu Ser Lys Asp Ala Gln Ala Ser Ala Ala Pro Ala Ala Pro Leu Pro  
 85 90 95  
 Glu Arg Asn Ser Leu Ser Ala Ile Phe Asn Asn Val Met Thr Leu Cys

100	105	110
Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His		
115	120	125
Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile		
130	135	140
Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp		
145	150	155
Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn		
165	170	175
Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu		
180	185	190
Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly Gln Gly Leu Ala		
195	200	205
Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile Ala Ser Gly Ser		
210	215	220
Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr Ala Cys Ala Val		
225	230	235
Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro Arg Leu Glu Phe		
245	250	255
Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro Gly Glu Gln Glu		
260	265	270
Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro Arg Ala Gly Lys		
275	280	285
Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser		
290	295	300
His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser		
305	310	315
		320

Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr  
                             325                            330                            335  
 Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr  
                             340                            345                            350  
 Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu  
                             355                            360                            365  
 Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly Lys Asp Ser Arg  
                             370                            375                            380  
 Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe Val Pro Leu Leu  
 385                            390                            395                            400  
 Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr Val Val Phe Glu  
                             405                            410                            415  
 His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe Ala Phe Ser Asn  
                             420                            425                            430  
 Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro Lys Lys Val Lys  
                             435                            440                            445  
 Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala Phe Phe Leu Cys  
                             450                            455                            460  
 Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu Phe Arg Ala Ile  
 465                            470                            475                            480  
 Val

<210> 269

<211> 1373

<212> DNA

<213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; (105).. (656)

&lt;400&gt; 269

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ggagcatcgc ggctcaggct gcgggaaagc ggtgcgcgtg cagcgggggtg ggtgccctgg      60
tccgcggggcg agctcgagca gccaaaccccg ggcgcgctcg ggcc atg gac ggc ctg      116
                                     Met Asp Gly Leu
                                     1
agg cag cgc gtg gag cac ttc ctg gag caa agg aac ctg gtc acc gaa      164
Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu
5              10              15              20
gtg ctg ggg gcg ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg      212
Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu
              25              30              35
gct gca gga gcc gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac      260
Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr
              40              45              50
gga gcg tct ctg ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat      308
Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr
              55              60              65
gcc tca atc aaa gct atc gag agc cca agc aag gac gac gac act gtg      356
Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val
              70              75              80
tgg ctc acc tac tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc      404
Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe
85              90              95              100
ttc agc gat cta ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag      452
Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys

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105	110	115	
tgc gcc ttc ctg ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct			500
Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala			
120	125	130	
ctc atg ctg tat cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac			548
Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His			
135	140	145	
ggg gcc gta gac aga atc atg aac gac ctc agc ggg cga gcc ctg gac			596
Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp			
150	155	160	
gcg gcg gcc gga ata acc agg aac gtc aag cca agc cag acc ccg cag			644
Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln			
165	170	175	180
ccg aag gac aag tgaagcagcc ccctgagcct cacaaggacc tcctggetgg			696
Pro Lys Asp Lys			
tgaggagggg gccgcgccag gctcccaggc ctccacagag tcttcagcgc atcccccaac			756
agcagccccct gccagtcctt cgggtccagg caaggccctg ggggtctcct taaatgccac			816
ctcgggcaag tcccagtcct agtcctcggc cccccccagc tctggatccc agggccagct			876
gccctctggc tctggctgtg gctcccgcct gtccggcagg gccaggggc agcgtcgggc			936
acagggcagc tcccactggt ctcggaaca caccagccg cctggtactt cctccagccc			996
ctcccagtcg gccctcccgt cctcgggggc cctgcagcca cccaacgtca cctccagccc			1056
ggtctcacc cttggtccagt ctcccagcag cagcaacatc cccacgcagc cccccagcaa			1116
gtcctctggc aagccggagg acgcagcccc caagaccagc ggacagcgcc agaaggaatc			1176
gtcgaacacag cctgccagca gcgcctcagt gcccgagctg gtcccctgcc attccgggac			1236
ctctctggag tacacttcgg agtccaccac cgagatcacc tgcagctggc cacaccacag			1296
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<210> 270

<211> 184

<212> PRT

<213> Homo sapiens

<400> 270

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn

1 5 10 15

Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu

20 25 30

Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu

35 40 45

Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val

50 55 60

Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp

65 70 75 80

Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly

85 90 95

Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr

100 105 110

Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro

115 120 125

Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

130 135 140

Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly

145 150 155 160

Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser

	165	170	175	
Gln Thr Pro Gln Pro Lys Asp Lys				
	180			
<210>	271			
<211>	885			
<212>	DNA			
<213>	Homo sapiens			
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<221>	CDS			
<222>	(15).. (785)			
<400>	271			
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Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile				
	1	5	10	
gcc ttc ggg cct gcg ctc gcc ctt tat gtc ttc acc atc gcc acc gag				98
Ala Phe Gly Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Thr Glu				
	15	20	25	
ccg ttg cgt atc atc ttc ctc atc gcc gga gct ttc ttc tgg ttg gtg				146
Pro Leu Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val				
	30	35	40	
tct cta ctg att tcg tcc ctt gtt tgg ttc atg gca aga gtc att att				194
Ser Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile				
	45	50	55	60
gac aac aaa gat gga cca aca cag aaa tat ctg ctg atc ttt gga gcg				242
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly Ala				
	65	70	75	

ttt gtc tct gtc tat atc caa gaa atg ttc cga ttt gca tat tat aaa	290
Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr Tyr Lys	
80 85 90	
ctc tta aaa aaa gcc agt gaa ggt ttg aag agt ata aac cca ggt gag	338
Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Gly Glu	
95 100 105	
aca gca ccc tct atg cga ctg ctg gcc tat gtt tct ggc ttg ggc ttt	386
Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe	
110 115 120	
gga atc atg agt gga gta ttt tcc ttt gtg aat acc cta tct gac tcc	434
Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asp Ser	
125 130 135 140	
ttg ggg cca ggc aca gtg ggc att cat gga gat tct cct caa ttc ttc	482
Leu Gly Pro Gly Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe	
145 150 155	
ctt tat tca gct ttc atg acg ctg gtc att atc ttg ctg cat gta ttc	530
Leu Tyr Ser Ala Phe Met Thr Leu Val Ile Ile Leu Leu His Val Phe	
160 165 170	
tgg ggc att gta ttt ttt gat ggc tgt gag aag aaa aag tgg ggc atc	578
Trp Gly Ile Val Phe Phe Asp Gly Cys Glu Lys Lys Lys Trp Gly Ile	
175 180 185	
ctc ctt atc gtt ctc ctg acc cac ctg ctg gtg tca gcc cag acc ttc	626
Leu Leu Ile Val Leu Leu Thr His Leu Leu Val Ser Ala Gln Thr Phe	
190 195 200	
ata agt tct tat tat gga ata aac ctg gcg tca gca ttt ata atc ctg	674
Ile Ser Ser Tyr Tyr Gly Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu	
205 210 215 220	

gtg ctc atg ggc acc tgg gca ttc tta gct gcg gga ggc agc tgc cga 722  
 Val Leu Met Gly Thr Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg  
                   225                  230                  235  
 agc ctg aaa ctc tgc ctg ctc tgc caa gac aag aac ttt ctt ctt tac 770  
 Ser Leu Lys Leu Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr  
                   240                  245                  250  
 aac cag cgc tcc aga taacctcagg gaaccagcac ttcccaaacc gcagactaca 825  
 Asn Gln Arg Ser Arg  
                   255  
 tcttttagagg aagcacaact gtgccttttt ctgaaaatcc ctttttctgg tggaaaaaaa 885

&lt;210&gt; 272

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly Pro  
   1                  5                  10                  15  
 Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Thr Glu Pro Leu Arg Ile  
                   20                  25                  30  
 Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Ile  
                   35                  40                  45  
 Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile Asp Asn Lys Asp  
                   50                  55                  60  
 Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly Ala Phe Val Ser Val  
   65                  70                  75                  80  
 Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys

85	90	95
Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Gly Glu Thr Ala Pro Ser		
100	105	110
Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe Gly Ile Met Ser		
115	120	125
Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asp Ser Leu Gly Pro Gly		
130	135	140
Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala		
145	150	155
Phe Met Thr Leu Val Ile Ile Leu Leu His Val Phe Trp Gly Ile Val		
165	170	175
Phe Phe Asp Gly Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val		
180	185	190
Leu Leu Thr His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr		
195	200	205
Tyr Gly Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly		
210	215	220
Thr Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu		
225	230	235
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg Ser		
245	250	255
Arg		

&lt;210&gt; 273

&lt;211&gt; 2670

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (9)..(1664)

&lt;400&gt; 273

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gaacaaac atg gcc gct ctg gcg ccc gtc ggc tcc ccc gcc tcc cgc ggt      50
      Met Ala Ala Leu Ala Pro Val Gly Ser Pro Ala Ser Arg Gly
          1              5              10

cct agg ctg gcc gcg ggc ctc cgg ctg ctc cca atg ctg ggt ttg ctg      98
Pro Arg Leu Ala Ala Gly Leu Arg Leu Leu Pro Met Leu Gly Leu Leu
15              20              25              30

cag ttg ctg gcc gag cct ggc ctg ggc cgc gtc cat cac ctg gca ctc      146
Gln Leu Leu Ala Glu Pro Gly Leu Gly Arg Val His His Leu Ala Leu
          35              40              45

aag gat gat gtg agg cat aaa gtt cat ctg aac acc ttt ggc ttc ttc      194
Lys Asp Asp Val Arg His Lys Val His Leu Asn Thr Phe Gly Phe Phe
          50              55              60

aag gat ggg tac atg gtg gtg aat gtc agt agc ctc tca ctg aat gag      242
Lys Asp Gly Tyr Met Val Val Asn Val Ser Ser Leu Ser Leu Asn Glu
          65              70              75

cct gaa gac aag gat gtg act att gga ttt agc cta gac cgt aca aag      290
Pro Glu Asp Lys Asp Val Thr Ile Gly Phe Ser Leu Asp Arg Thr Lys
          80              85              90

aat gat ggc ttt tct tct tac ctg gat gaa gat gtg aat tac tgt att      338
Asn Asp Gly Phe Ser Ser Tyr Leu Asp Glu Asp Val Asn Tyr Cys Ile
          95              100             105             110

tta aag aaa cag tct gtc tct gtc acc ctt tta atc cta gac atc tcc      386
Leu Lys Lys Gln Ser Val Ser Val Thr Leu Leu Ile Leu Asp Ile Ser

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115	120	125	
aga agt gag gta aga gta aag tct cca cca gaa gct ggt acc cag tta			434
Arg Ser Glu Val Arg Val Lys Ser Pro Pro Glu Ala Gly Thr Gln Leu			
130	135	140	
cca aag atc atc ttc agc agg gat gag aaa gtc ctt ggt cag agc cag			482
Pro Lys Ile Ile Phe Ser Arg Asp Glu Lys Val Leu Gly Gln Ser Gln			
145	150	155	
gag cct aat gtt aac cct gct tca gca ggc aac cag acc cag aag aca			530
Glu Pro Asn Val Asn Pro Ala Ser Ala Gly Asn Gln Thr Gln Lys Thr			
160	165	170	
caa gat ggt gga aag tct aaa aga agt aca gtg gat tca aag gcc atg			578
Gln Asp Gly Gly Lys Ser Lys Arg Ser Thr Val Asp Ser Lys Ala Met			
175	180	185	190
gga gag aaa tcc ttt tct gtt cat aat aat ggt ggg gca gtg tca ttt			626
Gly Glu Lys Ser Phe Ser Val His Asn Asn Gly Gly Ala Val Ser Phe			
195	200	205	
cag ttt ttc ttt aac atc agc act gat gac caa gaa ggc ctt tac agt			674
Gln Phe Phe Phe Asn Ile Ser Thr Asp Asp Gln Glu Gly Leu Tyr Ser			
210	215	220	
ctt tat ttt cat aaa tgc ctt gga aaa gaa ttg cca agt gac aag ttt			722
Leu Tyr Phe His Lys Cys Leu Gly Lys Glu Leu Pro Ser Asp Lys Phe			
225	230	235	
aca ttc agc ctt gat att gag atc aca gag aag aat cct gac agc tac			770
Thr Phe Ser Leu Asp Ile Glu Ile Thr Glu Lys Asn Pro Asp Ser Tyr			
240	245	250	
ctc tca gca gga gaa att cct ctc ccc aaa tta tac atc tca atg gcc			818
Leu Ser Ala Gly Glu Ile Pro Leu Pro Lys Leu Tyr Ile Ser Met Ala			

255	260	265	270	
ttt ttc ttc ttt ctt tct ggg acc atc tgg att cat atc ctt cga aaa				866
Phe Phe Phe Phe Leu Ser Gly Thr Ile Trp Ile His Ile Leu Arg Lys				
	275	280	285	
cga cgg aat gat gta ttt aaa atc cac tgg ctg atg gcg gcc ctt cct				914
Arg Arg Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Pro				
	290	295	300	
ttc acc aag tct ctt tcc ttg gtg ttc cat gca att gac tac cac tac				962
Phe Thr Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His Tyr				
	305	310	315	
atc tcc tcc cag ggc ttc cct atc gaa ggc tgg gct gtt gtg tac tac				1010
Ile Ser Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr Tyr				
	320	325	330	
ata act cac ctt ttg aaa ggg gcg cta ctc ttc atc acc att gca ctc				1058
Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu				
335	340	345	350	
att ggc act ggc tgg gct ttc att aag cac atc ctt tct gat aaa gac				1106
Ile Gly Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys Asp				
	355	360	365	
aaa aag atc ttc atg att gtc att cca ctc cag gtc ctg gca aat gta				1154
Lys Lys Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val				
	370	375	380	
gcc tac atc atc ata gag tcc acc gag gag ggc acg act gaa tat ggc				1202
Ala Tyr Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr Gly				
	385	390	395	
ttg tgg aag gac tct cta ttt ctg gtc gac ctg ttg tgt tgt ggt gcc				1250
Leu Trp Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly Ala				



400	405	410	
atc ctc ttc cca gtg gtg tgg tca atc aga cat tta caa gaa gca tca			1298
Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala Ser			
415	420	425	430
gca aca gat gga aaa gct gct att aac tta gca aag ctg aaa ctt ttc			1346
Ala Thr Asp Gly Lys Ala Ala Ile Asn Leu Ala Lys Leu Lys Leu Phe			
	435	440	445
aga cat tat tac gtc ttg att gtg tgt tac ata tac ttc act agg atc			1394
Arg His Tyr Tyr Val Leu Ile Val Cys Tyr Ile Tyr Phe Thr Arg Ile			
	450	455	460
att gca ttt ctc ctc aaa ctc gct gtt cca ttc cag tgg aag tgg ctc			1442
Ile Ala Phe Leu Leu Lys Leu Ala Val Pro Phe Gln Trp Lys Trp Leu			
	465	470	475
tac cag ctc ctg gat gaa acg gcc aca ctg gtc ttc ttt gtt cta acg			1490
Tyr Gln Leu Leu Asp Glu Thr Ala Thr Leu Val Phe Phe Val Leu Thr			
	480	485	490
ggg tat aaa ttc cgt ccg gct tca gat aac ccc tac cta caa ctt tct			1538
Gly Tyr Lys Phe Arg Pro Ala Ser Asp Asn Pro Tyr Leu Gln Leu Ser			
495	500	505	510
cag gaa gaa gaa gac ttg gaa atg gag tcc gtt gtg aca aca tct ggg			1586
Gln Glu Glu Glu Asp Leu Glu Met Glu Ser Val Val Thr Thr Ser Gly			
	515	520	525
gtg atg gaa agt atg aag aaa gtc aag aag gtg acc aac ggc tcc gtg			1634
Val Met Glu Ser Met Lys Lys Val Lys Lys Val Thr Asn Gly Ser Val			
	530	535	540
gag ccc cag ggc gag tgg gaa ggc gcc gtg tgacagagcc gaccctgagg			1684
Glu Pro Gln Gly Glu Trp Glu Gly Ala Val			

545

550

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tcctacagtg aactattggc accaccgaca gtgacaccag ggcacatggc tggagcacag 1804
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gcctgatgga tggaagaaa tgtattttta agttcaaaaa gcattatcct gtggcggttg 2464
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gctttgttgt gtttgatcag aattttgggg gaaatggaaa gttttcctca aggagcagct 2584
gggggcagaa taggtagtat ttaagcaaat acttaagtcc aagcaaatca tccccattaa 2644
aaagcttttc ctgtaggcta gtagga 2670

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&lt;210&gt; 274

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

Met Ala Ala Leu Ala Pro Val Gly Ser Pro Ala Ser Arg Gly Pro Arg

1

5

10

15

Leu Ala Ala Gly Leu Arg Leu Leu Pro Met Leu Gly Leu Leu Gln Leu

	20		25		30										
Leu	Ala	Glu	Pro	Gly	Leu	Gly	Arg	Val	His	His	Leu	Ala	Leu	Lys	Asp
	35					40						45			
Asp	Val	Arg	His	Lys	Val	His	Leu	Asn	Thr	Phe	Gly	Phe	Phe	Lys	Asp
	50					55						60			
Gly	Tyr	Met	Val	Val	Asn	Val	Ser	Ser	Leu	Ser	Leu	Asn	Glu	Pro	Glu
65					70					75				80	
Asp	Lys	Asp	Val	Thr	Ile	Gly	Phe	Ser	Leu	Asp	Arg	Thr	Lys	Asn	Asp
			85						90				95		
Gly	Phe	Ser	Ser	Tyr	Leu	Asp	Glu	Asp	Val	Asn	Tyr	Cys	Ile	Leu	Lys
			100						105				110		
Lys	Gln	Ser	Val	Ser	Val	Thr	Leu	Leu	Ile	Leu	Asp	Ile	Ser	Arg	Ser
		115							120				125		
Glu	Val	Arg	Val	Lys	Ser	Pro	Pro	Glu	Ala	Gly	Thr	Gln	Leu	Pro	Lys
		130							135				140		
Ile	Ile	Phe	Ser	Arg	Asp	Glu	Lys	Val	Leu	Gly	Gln	Ser	Gln	Glu	Pro
145					150					155				160	
Asn	Val	Asn	Pro	Ala	Ser	Ala	Gly	Asn	Gln	Thr	Gln	Lys	Thr	Gln	Asp
				165						170				175	
Gly	Gly	Lys	Ser	Lys	Arg	Ser	Thr	Val	Asp	Ser	Lys	Ala	Met	Gly	Glu
			180							185				190	
Lys	Ser	Phe	Ser	Val	His	Asn	Asn	Gly	Gly	Ala	Val	Ser	Phe	Gln	Phe
		195							200				205		
Phe	Phe	Asn	Ile	Ser	Thr	Asp	Asp	Gln	Glu	Gly	Leu	Tyr	Ser	Leu	Tyr
		210							215				220		
Phe	His	Lys	Cys	Leu	Gly	Lys	Glu	Leu	Pro	Ser	Asp	Lys	Phe	Thr	Phe
225						230						235			240

Ser Leu Asp Ile Glu Ile Thr Glu Lys Asn Pro Asp Ser Tyr Leu Ser  
245 250 255

Ala Gly Glu Ile Pro Leu Pro Lys Leu Tyr Ile Ser Met Ala Phe Phe  
260 265 270

Phe Phe Leu Ser Gly Thr Ile Trp Ile His Ile Leu Arg Lys Arg Arg  
275 280 285

Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Pro Phe Thr  
290 295 300

Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His Tyr Ile Ser  
305 310 315 320

Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr Tyr Ile Thr  
325 330 335

His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile Gly  
340 345 350

Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys Asp Lys Lys  
355 360 365

Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val Ala Tyr  
370 375 380

Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr Gly Leu Trp  
385 390 395 400

Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly Ala Ile Leu  
405 410 415

Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala Ser Ala Thr  
420 425 430

Asp Gly Lys Ala Ala Ile Asn Leu Ala Lys Leu Lys Leu Phe Arg His  
435 440 445

Tyr Tyr Val Leu Ile Val Cys Tyr Ile Tyr Phe Thr Arg Ile Ile Ala

450                      455                      460  
 Phe Leu Leu Lys Leu Ala Val Pro Phe Gln Trp Lys Trp Leu Tyr Gln  
 465                      470                      475                      480  
 Leu Leu Asp Glu Thr Ala Thr Leu Val Phe Phe Val Leu Thr Gly Tyr  
                     485                      490                      495  
 Lys Phe Arg Pro Ala Ser Asp Asn Pro Tyr Leu Gln Leu Ser Gln Glu  
                     500                      505                      510  
 Glu Glu Asp Leu Glu Met Glu Ser Val Val Thr Thr Ser Gly Val Met  
                     515                      520                      525  
 Glu Ser Met Lys Lys Val Lys Lys Val Thr Asn Gly Ser Val Glu Pro  
                     530                      535                      540  
 Gln Gly Glu Trp Glu Gly Ala Val  
 545                      550

<210> 275

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)..(1593)

<400> 275

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 Met Ala Ala Val Gly Pro Arg Thr Gly Pro Gly Thr Gly Ala Glu Ala  
 1                      5                      10                      15  
 cta gcg ctg gcg gca gag ctg cag ggc gag gcg acg tgc tcc atc tgc 156



His Ala Val Leu Pro Leu Asp Glu Ala Val Gln Glu Ala Lys Glu Leu

165

170

175

ttg gag tcc agg ctg agg gtc ttg aag aag gaa ctg gag gac tgt gag 636

Leu Glu Ser Arg Leu Arg Val Leu Lys Lys Glu Leu Glu Asp Cys Glu

180

185

190

gtg ttc cgg tcc acg gaa aag aag gag agc aag gag ctg ctg aaa cag 684

Val Phe Arg Ser Thr Glu Lys Lys Glu Ser Lys Glu Leu Leu Lys Gln

195

200

205

atg gca gcg gag cag gag aag gtg ggg gca gag ttc cag gca ctg agg 732

Met Ala Ala Glu Gln Glu Lys Val Gly Ala Glu Phe Gln Ala Leu Arg

210

215

220

gct ttc ctg gtg gag cag gag ggt cgg ctg cta ggc cgc ctg gag gaa 780

Ala Phe Leu Val Glu Gln Glu Gly Arg Leu Leu Gly Arg Leu Glu Glu

225

230

235

240

ctg tcc cgg gag gtg gca cag aag cag aat gag aac ctg gcc cag ctc 828

Leu Ser Arg Glu Val Ala Gln Lys Gln Asn Glu Asn Leu Ala Gln Leu

245

250

255

ggg gtt gag atc acc cag ctg tcc aag ctc agc agc cag atc cag gag 876

Gly Val Glu Ile Thr Gln Leu Ser Lys Leu Ser Ser Gln Ile Gln Glu

260

265

270

aca gct caa aag cct gac ctt gac ttt ctc cag gaa ttc aaa agc acg 924

Thr Ala Gln Lys Pro Asp Leu Asp Phe Leu Gln Glu Phe Lys Ser Thr

275

280

285

ctg agc agg tgt agc aat gtg cct ggc ccc aag cca acc aca gtc tct 972

Leu Ser Arg Cys Ser Asn Val Pro Gly Pro Lys Pro Thr Thr Val Ser

290

295

300

tct gag atg aag aat aaa gtc tgg aat gtt tct ctc aag acc ttt gtc 1020

Ser Glu Met Lys Asn Lys Val Trp Asn Val Ser Leu Lys Thr Phe Val  
 305 310 315 320  
 tta aaa ggg atg ctg aag aag ttc aaa gag gac ctt cgg gga gag ctg 1068  
 Leu Lys Gly Met Leu Lys Lys Phe Lys Glu Asp Leu Arg Gly Glu Leu  
 325 330 335  
 gag aaa gag gag aaa gtg gag ctc acc ttg gat ccc gac acg gcc aac 1116  
 Glu Lys Glu Glu Lys Val Glu Leu Thr Leu Asp Pro Asp Thr Ala Asn  
 340 345 350  
 ccg cgc ctc atc ctc tct ctg gat ctt aag ggc gtg cgc ctc ggc gag 1164  
 Pro Arg Leu Ile Leu Ser Leu Asp Leu Lys Gly Val Arg Leu Gly Glu  
 355 360 365  
 cgg gcc cag gac ctg ccc aac cac ccc tgc cgc ttc gac acc aac acc 1212  
 Arg Ala Gln Asp Leu Pro Asn His Pro Cys Arg Phe Asp Thr Asn Thr  
 370 375 380  
 cgc gtc ctg gcg tcc tgc ggc ttc tcc tcg ggc cgg cat cac tgg gag 1260  
 Arg Val Leu Ala Ser Cys Gly Phe Ser Ser Gly Arg His His Trp Glu  
 385 390 395 400  
 gtg gag gtg ggc tct aag gac ggc tgg gcc ttt ggc gtg gcc cgc gag 1308  
 Val Glu Val Gly Ser Lys Asp Gly Trp Ala Phe Gly Val Ala Arg Glu  
 405 410 415  
 agc gtg cgc cga aag ggc ctg acg ccc ttc act ccc gag gag ggc gtc 1356  
 Ser Val Arg Arg Lys Gly Leu Thr Pro Phe Thr Pro Glu Glu Gly Val  
 420 425 430  
 tgg gcc ctg cag ctc aac ggc ggc cag tac tgg gcc gtg acc agc ccc 1404  
 Trp Ala Leu Gln Leu Asn Gly Gly Gln Tyr Trp Ala Val Thr Ser Pro  
 435 440 445  
 gag cgg tcg ccc ctc agc tgc ggg cac ctg tcg cgc gtg cgg gtg gcc 1452



Glu Arg Ser Pro Leu Ser Cys Gly His Leu Ser Arg Val Arg Val Ala  
 450 455 460  
 ctg gac ctg gag gtg gga gcc gtg tcc ttc tac gct gtg gag gac atg 1500  
 Leu Asp Leu Glu Val Gly Ala Val Ser Phe Tyr Ala Val Glu Asp Met  
 465 470 475 480  
 cgc cac ctc tac acc ttc cgc gtc aac ttc cag gag cgc gtg ttc ccg 1548  
 Arg His Leu Tyr Thr Phe Arg Val Asn Phe Gln Glu Arg Val Phe Pro  
 485 490 495  
 ctt ttc tct gtt tgc tcc acg ggc acc tac ttg cga atc tgg cct 1593  
 Leu Phe Ser Val Cys Ser Thr Gly Thr Tyr Leu Arg Ile Trp Pro  
 500 505 510  
 tgaggggcac tgctggggag ctctgtctc tgggctgccg gtgggagggg atgtcgcctc 1653  
 cccagagatg cctgggtccgt cttgggtctg ccctccgtgc tctgacccc tgctgccc aa 1713  
 gagagcctgc tacagacaca accccgaggc aggagagtga ctgtggccaa ccgagcaggg 1773  
 gaacaggggc tttggactcc tgagggtgtt cccttcctga ggtcacatgt ggatttggcc 1833  
 agagccttca ggaggtggag gccggtgagg tcaggagccc agctctccag ggggcttctg 1893  
 ccctgactgg gaagggtgcc tggctcccta aaacaatgtc aaagccagtc ctgctgttct 1953  
 ctgttgccag ggggcaggtc tgggcctggg ccaaccacgt ttgttatcat ggctgtgccc 2013  
 ttctggacag ctgccagctc tgccttgaga ggttgtggga cctctggatc cagctgacct 2073  
 gacaggtcat ctactcaggg aggagccctg tgctcccagc tcagaggaca gtctgggcca 2133  
 gaactggaag gagaca 2149

<210> 276

<211> 511

<212> PRT

<213> Homo sapiens

<400> 276

Met Ala Ala Val Gly Pro Arg Thr Gly Pro Gly Thr Gly Ala Glu Ala  
 1 5 10 15  
 Leu Ala Leu Ala Ala Glu Leu Gln Gly Glu Ala Thr Cys Ser Ile Cys  
 20 25 30  
 Leu Glu Leu Phe Arg Glu Pro Val Ser Val Glu Cys Gly His Ser Phe  
 35 40 45  
 Cys Arg Ala Cys Ile Gly Arg Cys Trp Glu Arg Pro Gly Ala Gly Ser  
 50 55 60  
 Val Gly Ala Ala Thr Arg Ala Pro Pro Phe Pro Leu Pro Cys Pro Gln  
 65 70 75 80  
 Cys Arg Glu Pro Ala Arg Pro Ser Gln Leu Arg Pro Asn Arg Gln Leu  
 85 90 95  
 Ala Ala Val Ala Thr Leu Leu Arg Arg Phe Ser Leu Pro Ala Ala Ala  
 100 105 110  
 Pro Gly Glu His Gly Ser Gln Ala Ala Ala Arg Ala Ala Ala Ala  
 115 120 125  
 Arg Cys Gly Gln His Gly Glu Pro Phe Lys Leu Tyr Cys Gln Asp Asp  
 130 135 140  
 Gly Arg Ala Ile Cys Val Val Cys Asp Arg Ala Arg Glu His Arg Glu  
 145 150 155 160  
 His Ala Val Leu Pro Leu Asp Glu Ala Val Gln Glu Ala Lys Glu Leu  
 165 170 175  
 Leu Glu Ser Arg Leu Arg Val Leu Lys Lys Glu Leu Glu Asp Cys Glu  
 180 185 190  
 Val Phe Arg Ser Thr Glu Lys Lys Glu Ser Lys Glu Leu Leu Lys Gln  
 195 200 205  
 Met Ala Ala Glu Gln Glu Lys Val Gly Ala Glu Phe Gln Ala Leu Arg

210 215 220  
Ala Phe Leu Val Glu Gln Glu Gly Arg Leu Leu Gly Arg Leu Glu Glu  
225 230 235 240  
Leu Ser Arg Glu Val Ala Gln Lys Gln Asn Glu Asn Leu Ala Gln Leu  
245 250 255  
Gly Val Glu Ile Thr Gln Leu Ser Lys Leu Ser Ser Gln Ile Gln Glu  
260 265 270  
Thr Ala Gln Lys Pro Asp Leu Asp Phe Leu Gln Glu Phe Lys Ser Thr  
275 280 285  
Leu Ser Arg Cys Ser Asn Val Pro Gly Pro Lys Pro Thr Thr Val Ser  
290 295 300  
Ser Glu Met Lys Asn Lys Val Trp Asn Val Ser Leu Lys Thr Phe Val  
305 310 315 320  
Leu Lys Gly Met Leu Lys Lys Phe Lys Glu Asp Leu Arg Gly Glu Leu  
325 330 335  
Glu Lys Glu Glu Lys Val Glu Leu Thr Leu Asp Pro Asp Thr Ala Asn  
340 345 350  
Pro Arg Leu Ile Leu Ser Leu Asp Leu Lys Gly Val Arg Leu Gly Glu  
355 360 365  
Arg Ala Gln Asp Leu Pro Asn His Pro Cys Arg Phe Asp Thr Asn Thr  
370 375 380  
Arg Val Leu Ala Ser Cys Gly Phe Ser Ser Gly Arg His His Trp Glu  
385 390 395 400  
Val Glu Val Gly Ser Lys Asp Gly Trp Ala Phe Gly Val Ala Arg Glu  
405 410 415  
Ser Val Arg Arg Lys Gly Leu Thr Pro Phe Thr Pro Glu Glu Gly Val  
420 425 430

Trp Ala Leu Gln Leu Asn Gly Gly Gln Tyr Trp Ala Val Thr Ser Pro

435

440

445

Glu Arg Ser Pro Leu Ser Cys Gly His Leu Ser Arg Val Arg Val Ala

450

455

460

Leu Asp Leu Glu Val Gly Ala Val Ser Phe Tyr Ala Val Glu Asp Met

465

470

475

480

Arg His Leu Tyr Thr Phe Arg Val Asn Phe Gln Glu Arg Val Phe Pro

485

490

495

Leu Phe Ser Val Cys Ser Thr Gly Thr Tyr Leu Arg Ile Trp Pro

500

505

510

<210> 277

<211> 3113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (193).. (1656)

<400> 277

ggcacgaggc cgtcctgggtg ccttactgtg catacagttc tactcgtctc agaaacgtat 60

gtcaaacgag gatacagtgt ctggaactat tggttctaag atataagtgg aatgagcctg 120

gatcaggaga agtatgctga gctagagttg aaggaagctt ctctttctaa caagagaaag 180

cagagttaaa tt atg gca gag aca agt ctg tta gag gct ggg gcc tct gca 231

Met Ala Glu Thr Ser Leu Leu Glu Ala Gly Ala Ser Ala

1

5

10

gcc tct aca gct gcg gct ttg gag aac tta cag gtg gag gcg agc tgc 279

Ala Ser Thr Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser Cys

15	20	25	
tct gtg tgc ctg gag tat ctg aag gaa cct gtc atc att gag tgt ggg			327
Ser Val Cys Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys Gly			
30	35	40	45
cac aac ttc tgc aaa gct tgc atc acc cgc tgg tgg gag gac cta gag			375
His Asn Phe Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu Glu			
	50	55	60
agg gac ttc cct tgt cct gtc tgt cga aag aca tcc cgc tac cgc agt			423
Arg Asp Phe Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg Ser			
	65	70	75
ctc cga cct aat cgg caa cta ggc agt atg gtg gaa att gcc aag cag			471
Leu Arg Pro Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys Gln			
	80	85	90
ctc cag gcc gtc aag cgg aag atc cgg gat gag agc ctc tgc ccc caa			519
Leu Gln Ala Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro Gln			
	95	100	105
cac cat gag gcc ctc agc ctt ttc tgt tat gag gac cag gag gct gta			567
His His Glu Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala Val			
110	115	120	125
tgc ttg ata tgt gca att tcc cac acc cac cgg gcc cac acc gtt gtg			615
Cys Leu Ile Cys Ala Ile Ser His Thr His Arg Ala His Thr Val Val			
	130	135	140
cca ctg gac gac gct aca cag gag tac aag gaa aaa ctg cag aag tgt			663
Pro Leu Asp Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys Cys			
	145	150	155
ctg gag ccc ctg gaa cag aag ctg cag gag atc act cgc tgc aag tcc			711
Leu Glu Pro Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys Ser			

160	165	170	
tct gag gag aag aag cct ggt gag ctc aag aga cta gtg gaa agt cgc			759
Ser Glu Glu Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser Arg			
175	180	185	
cga cag cag atc ttg agg gag ttt gaa gag ctt cat agg cgg ctg gat			807
Arg Gln Gln Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu Asp			
190	195	200	205
gaa gag cag cag gtg ttg ctt tca cga ctg gaa gaa gag gaa cag gac			855
Glu Glu Gln Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln Asp			
210	215	220	
att ctg cag cga ctc cga gaa aat gct gct cac ctt ggg gac aag cgc			903
Ile Leu Gln Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys Arg			
225	230	235	
cgg gac ctg gcc cac ttg gct gcc gag gtg gag ggc aag tgc tta cag			951
Arg Asp Leu Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu Gln			
240	245	250	
tca ggc ttc gag atg ctt aag gat gtc aaa agt acc ctg gaa aaa tgt			999
Ser Gly Phe Glu Met Leu Lys Asp Val Lys Ser Thr Leu Glu Lys Cys			
255	260	265	
gaa aag gtg aag acc atg gag gtg act tca gta tcc ata gag ctg gaa			1047
Glu Lys Val Lys Thr Met Glu Val Thr Ser Val Ser Ile Glu Leu Glu			
270	275	280	285
aag aac ttc agc aat ttt ccc cga cag tac ttt gcc cta agg aaa atc			1095
Lys Asn Phe Ser Asn Phe Pro Arg Gln Tyr Phe Ala Leu Arg Lys Ile			
290	295	300	
ctt aaa cag cta att gcg gat gtg acc ctg gac cct gag aca gct cat			1143
Leu Lys Gln Leu Ile Ala Asp Val Thr Leu Asp Pro Glu Thr Ala His			

305	310	315	
cct aac cta gtc ctg tca gag gat cgt aag agc gtc aag ttc gtg gag			1191
Pro Asn Leu Val Leu Ser Glu Asp Arg Lys Ser Val Lys Phe Val Glu			
320	325	330	
aca aga ctc cgg gat ctc cct gac aca cca agg cgt ttc acc ttc tac			1239
Thr Arg Leu Arg Asp Leu Pro Asp Thr Pro Arg Arg Phe Thr Phe Tyr			
335	340	345	
cct tgc gtc ctg gct act gag ggt ttc acc tca ggt cga cac tac tgg			1287
Pro Cys Val Leu Ala Thr Glu Gly Phe Thr Ser Gly Arg His Tyr Trp			
350	355	360	365
gag gtg gag gtg ggc gac aag acc cac tgg gca gtg ggt gta tgc cgg			1335
Glu Val Glu Val Gly Asp Lys Thr His Trp Ala Val Gly Val Cys Arg			
370	375	380	
gac tcc gtg agc cga aag ggc gag ttg act cca ctc cct gag act ggc			1383
Asp Ser Val Ser Arg Lys Gly Glu Leu Thr Pro Leu Pro Glu Thr Gly			
385	390	395	
tac tgg cgg gtg cgg cta tgg aat ggg gac aaa tat gca gcc acc acc			1431
Tyr Trp Arg Val Arg Leu Trp Asn Gly Asp Lys Tyr Ala Ala Thr Thr			
400	405	410	
aca cct ttt acc cct ttg cac atc aag gtg aaa ccc aag cgg gta ggc			1479
Thr Pro Phe Thr Pro Leu His Ile Lys Val Lys Pro Lys Arg Val Gly			
415	420	425	
ata ttc cta gac tat gag gcc ggc aca ctg tct ttc tac aat gtc aca			1527
Ile Phe Leu Asp Tyr Glu Ala Gly Thr Leu Ser Phe Tyr Asn Val Thr			
430	435	440	445
gac cgc tct cat atc tac acc ttc act gat act ttt act gag aaa ctt			1575
Asp Arg Ser His Ile Tyr Thr Phe Thr Asp Thr Phe Thr Glu Lys Leu			

450	455	460	
tgg ccc ctc ttc tac cca ggc atc cgg gct gga cgg aag aat gct gca			1623
Trp Pro Leu Phe Tyr Pro Gly Ile Arg Ala Gly Arg Lys Asn Ala Ala			
465	470	475	
cca ctt acc atc agg ccc cca aca gat tgg gag tgacaggttg ggatgtggga			1676
Pro Leu Thr Ile Arg Pro Pro Thr Asp Trp Glu			
480	485		
atgactgggg tgaggcaggg tcaagtgcta cgggcctcct tcccgtgtcc tgctggaacg			1736
tcttcgtgtc cacctgggtc cagtcctgaa tcatcttgga gaaacacctt ggtttctagg			1796
atggttttgt gtggaggggg aggtaggact gggctggatg agagagcaca gctgtgactt			1856
cctcctaact gtcagggtgg ggagctggtt cccagaggat tgtctaccct gaagtccatc			1916
aggtttttctg ttgcacaagg acgggtcagg aaggaaggag aggcttttcc agaaacaaaa			1976
aatctgtgag ggtctgactt gctcaaacca gaggaggaaa cagaaacccc tgcacatctt			2036
tttagggggt tctttgacct aggatagtct tgcttcttga ggtagatcac aggggtctgt			2096
gtacctctga attcatgaga gatgaacgac agatgctctc atgggtctag atattgagga			2156
gtttttctga gggcagagat tggacatcaa caaggctaga agggtcaggg aagtgggcta			2216
aaggaacaga ttcctagaga ttaatgaaga ggaggagggt ttctttggtc ttctattcca			2276
agggtaaagg tgcgattatg ggtaagattg gccagaggta ggaatgtggg gagaaggaga			2336
ggctgaaaag aaagcagagg agaaccagg tccctgcctc agccttcagc agagttggct			2396
tattgcctgc ctctatacca ataagtcagt caccttgctc ctctccagag gcaaagtgga			2456
agagatcctg caagacacat ctatcctttc acagtgttcc caagggaact tggaaaggag			2516
agtcaggtat tagaggaaag agaagggtat ttgtatacaa agccctggcc ttaaagaatg			2576
ttacttagta gctactccca aattgtcagc cttcttacct ggccaagggtg tccaagccag			2636
aaaggaaaaa aggttatgga gtctttctca ccctaaggac aggggtggaag aggggtggtat			2696
atagggaagg gccagatagg caacttcatt tggcttgtgt gcatctggcc tggaactggt			2756
gttaagccag gcttttgctt gtttgttgcc atccctcacc ctttgccatt tcccttttca			2816
gagaatgtaa atgattttca tgtaggcca aaataaacia cttatagggt atatatgttg			2876



tcataaaagg taaaagtgat gcatgccaaa ccaaactaaa ccaatttgga ttatctgcta 2936  
 ttcgggtaat cttcacagaa atgactgaga gaagaatctg cagtttactg agggcatttc 2996  
 agttcctcct accacctcaa caggactttg tccagactct cctcctctta cctttgtgcc 3056  
 ttgactgtgg ttctttgtgg caagatactt tggttggta aaataatatg gaacaaa 3113

<210> 278

<211> 488

<212> PRT

<213> Homo sapiens

<400> 278

Met Ala Glu Thr Ser Leu Leu Glu Ala Gly Ala Ser Ala Ala Ser Thr  
 1 5 10 15  
 Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser Cys Ser Val Cys  
 20 25 30  
 Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys Gly His Asn Phe  
 35 40 45  
 Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu Glu Arg Asp Phe  
 50 55 60  
 Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg Ser Leu Arg Pro  
 65 70 75 80  
 Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys Gln Leu Gln Ala  
 85 90 95  
 Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro Gln His His Glu  
 100 105 110  
 Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala Val Cys Leu Ile  
 115 120 125  
 Cys Ala Ile Ser His Thr His Arg Ala His Thr Val Val Pro Leu Asp

130	135	140	
Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys Cys Leu Glu Pro			
145	150	155	160
Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys Ser Ser Glu Glu			
165	170	175	
Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser Arg Arg Gln Gln			
180	185	190	
Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu Asp Glu Glu Gln			
195	200	205	
Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln Asp Ile Leu Gln			
210	215	220	
Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys Arg Arg Asp Leu			
225	230	235	240
Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu Gln Ser Gly Phe			
245	250	255	
Glu Met Leu Lys Asp Val Lys Ser Thr Leu Glu Lys Cys Glu Lys Val			
260	265	270	
Lys Thr Met Glu Val Thr Ser Val Ser Ile Glu Leu Glu Lys Asn Phe			
275	280	285	
Ser Asn Phe Pro Arg Gln Tyr Phe Ala Leu Arg Lys Ile Leu Lys Gln			
290	295	300	
Leu Ile Ala Asp Val Thr Leu Asp Pro Glu Thr Ala His Pro Asn Leu			
305	310	315	320
Val Leu Ser Glu Asp Arg Lys Ser Val Lys Phe Val Glu Thr Arg Leu			
325	330	335	
Arg Asp Leu Pro Asp Thr Pro Arg Arg Phe Thr Phe Tyr Pro Cys Val			
340	345	350	

Leu Ala Thr Glu Gly Phe Thr Ser Gly Arg His Tyr Trp Glu Val Glu  
                   355                                  360                                  365  
 Val Gly Asp Lys Thr His Trp Ala Val Gly Val Cys Arg Asp Ser Val  
                   370                                  375                                  380  
 Ser Arg Lys Gly Glu Leu Thr Pro Leu Pro Glu Thr Gly Tyr Trp Arg  
 385                                  390                                  395                                  400  
 Val Arg Leu Trp Asn Gly Asp Lys Tyr Ala Ala Thr Thr Thr Pro Phe  
                                   405                                  410                                  415  
 Thr Pro Leu His Ile Lys Val Lys Pro Lys Arg Val Gly Ile Phe Leu  
                                   420                                  425                                  430  
 Asp Tyr Glu Ala Gly Thr Leu Ser Phe Tyr Asn Val Thr Asp Arg Ser  
                                   435                                  440                                  445  
 His Ile Tyr Thr Phe Thr Asp Thr Phe Thr Glu Lys Leu Trp Pro Leu  
                                   450                                  455                                  460  
 Phe Tyr Pro Gly Ile Arg Ala Gly Arg Lys Asn Ala Ala Pro Leu Thr  
 465                                  470                                  475                                  480  
 Ile Arg Pro Pro Thr Asp Trp Glu  
                                   485

<210> 279

<211> 2967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (359).. (1897)

<400> 279

827/861

ccc atc tgc gtg gtg tgc gac cgc tcc cgc gag cac cgc ggc cac agc	742
Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser	
115 120 125	
gtg ctg ccg ctc gag gag gcg gtg gag ggc ttc aag gag caa atc cag	790
Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln	
130 135 140	
aac cag ctc gac cat tta aaa aga gtg aaa gat tta aag aag aga cgt	838
Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg	
145 150 155 160	
cgg gcc cag ggg gaa cag gca cga gct gaa ctc ttg agc cta acc cag	886
Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln	
165 170 175	
atg gag agg gag aag att gtt tgg gag ttt gag cag ctg tat cac tcc	934
Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser	
180 185 190	
tta aag gag cat gag tat cgc ctc ctg gcc cgc ctt gag gag cta gac	982
Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp	
195 200 205	
ttg gcc atc tac aat agc atc aat ggt gcc atc acc cag ttc tct tgc	1030
Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys	
210 215 220	
aac atc tcc cac ctc agc agc ctg atc gct cag cta gaa gag aag cag	1078
Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln	
225 230 235 240	
cag cag ccc acc agg gag ctc ctg cag gac att ggg gac aca ttg agc	1126
Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser	
245 250 255	

agg gct gaa aga atc agg att cct gaa cct tgg atc aca cct cca gat	1174
Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp	
260 265 270	
ttg caa gag aaa atc cac att ttt gcc caa aaa tgt cta ttc ttg acg	1222
Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr	
275 280 285	
gag agt cta aag cag ttc aca gaa aaa atg cag tca gat atg gag aaa	1270
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys	
290 295 300	
atc caa gaa tta aga gag gct cag tta tac tca gtg gac gtg act ctg	1318
Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu	
305 310 315 320	
gac cca gac acg gcc tac ccc agc ctg atc ctc tct gat aat ctg cgg	1366
Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg	
325 330 335	
caa gtg cgg tac agt tac ctc caa cag gac ctg cct gac aac ccc gag	1414
Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu	
340 345 350	
agg ttc aat ctg ttt ccc tgt gtc ttg ggc tct cca tgc ttc atc gcc	1462
Arg Phe Asn Leu Phe Pro Cys Val Leu Gly Ser Pro Cys Phe Ile Ala	
355 360 365	
ggg aga cat tat tgg gag gta gag gtg gga gat aaa gcc aag tgg acc	1510
Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Lys Ala Lys Trp Thr	
370 375 380	
ata ggt gtc tgt gaa gac tca gtg tgc aga aaa ggt gga gta acc tca	1558
Ile Gly Val Cys Glu Asp Ser Val Cys Arg Lys Gly Gly Val Thr Ser	
385 390 395 400	

gcc ccc cag aat gga ttc tgg gca gtg tct ttg tgg tat ggg aaa gaa 1606  
 Ala Pro Gln Asn Gly Phe Trp Ala Val Ser Leu Trp Tyr Gly Lys Glu  
 405 410 415  
 tat tgg gct ctt acc tcc cca atg act gcc cta ccc ctg cgg acc ccg 1654  
 Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu Arg Thr Pro  
 420 425 430  
 ctc cag cgg gtg ggg att ttc ttg gac tat gat gct ggt gag gtc tcc 1702  
 Leu Gln Arg Val Gly Ile Phe Leu Asp Tyr Asp Ala Gly Glu Val Ser  
 435 440 445  
 ttc tac aac gtg aca gag agg tgt cac acc ttc act ttc tct cat gct 1750  
 Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe Ser His Ala  
 450 455 460  
 acc ttt tgt ggg cct gtc cgg ccc tac ttc agt ctg agt tac tcg gga 1798  
 Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser Tyr Ser Gly  
 465 470 475 480  
 ggg aaa agt gca gct cct ctg atc atc tgc ccc atg agt ggg ata gat 1846  
 Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser Gly Ile Asp  
 485 490 495  
 ggg ttt tct ggc cat gtt ggg aat cat ggt cat tcc atg gag acc tcc 1894  
 Gly Phe Ser Gly His Val Gly Asn His Gly His Ser Met Glu Thr Ser  
 500 505 510  
 cct tgaggaggtg aattcaggcc aaaagggtg ttggctgtaa tcctacgcca 1947  
 Pro  
 ggcacaaggc atcttgttgc cttgccacgt cctgtcacag ctgggtatcc ttaccatgtt 2007  
 ccacgccctt gcagtgggag acaggatgtc catgttctct accatccttt tccttcccat 2067  
 gcagattgtg aaatgtaatg agatgtatca agacatccta gaaataaaaa ccagatgtcc 2127  
 acctccagt tttcatactt tctggtttta cacatcgctg gagggataaa gagtatggat 2187

aatcttttga tttggagagc cgttcaagat acttccagct tcttggctca gcctggcttc 2247  
ctctgggttca gccccacata atgattatgg ctatttgctg tcatttctgg gctagggctc 2307  
ctttctaaca acctagactg gaataaggcc ctgtcagcat ggctcccttt atcccagttt 2367  
tccgtctggg aacagtacct ctgcccctga ttcccaatgt gccatagttt tattaactcc 2427  
attaaagaag cctgtatgtg ttttggttag ttacagttat ttacaataa tgggtgggtaa 2487  
tggccccacc tctgttatga gataatgttc taatcaatgt ctctgccttt gtatcttttc 2547  
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tcatccagga taatattctg cccaactcca tcctctgtta ctagatccct taccagtcac 2667  
atttgtggac tgggtggccag tcgtatacca tccctggaag gattctggga caatattcca 2727  
gggattcatt gacttcttgg ctctttttct ccatttcctt tgggggaagg gggaattgac 2787  
catgettaag tgcatectat caaggggcag ctccgtcccc atggccattg gatcatgaga 2847  
cactcgaagt cagaaggctg gggcagatca cttcaagcaa gccccatga tggttctcag 2907  
tcctgcttct ctgtgggtac gtgcccctct gtttaaaaat aaactgaata tggatgttta 2967

<210> 280

<211> 513

<212> PRT

<213> Homo sapiens

<400> 280

Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys

1 5 10 15

Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly

20 25 30

His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu

35 40 45

Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His

50 55 60



Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln  
 65                                70                                75                                80  
 Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys  
                                  85                                90                                95  
 Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met  
                                  100                                105                                110  
 Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser  
                                  115                                120                                125  
 Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln  
                                  130                                135                                140  
 Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg  
 145                                150                                155                                160  
 Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln  
                                  165                                170                                175  
 Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser  
                                  180                                185                                190  
 Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp  
                                  195                                200                                205  
 Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys  
                                  210                                215                                220  
 Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln  
 225                                230                                235                                240  
 Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser  
                                  245                                250                                255  
 Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp  
                                  260                                265                                270  
 Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr

275 280 285  
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys  
290 295 300  
Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu  
305 310 315 320  
Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg  
325 330 335  
Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu  
340 345 350  
Arg Phe Asn Leu Phe Pro Cys Val Leu Gly Ser Pro Cys Phe Ile Ala  
355 360 365  
Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Lys Ala Lys Trp Thr  
370 375 380  
Ile Gly Val Cys Glu Asp Ser Val Cys Arg Lys Gly Gly Val Thr Ser  
385 390 395 400  
Ala Pro Gln Asn Gly Phe Trp Ala Val Ser Leu Trp Tyr Gly Lys Glu  
405 410 415  
Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu Arg Thr Pro  
420 425 430  
Leu Gln Arg Val Gly Ile Phe Leu Asp Tyr Asp Ala Gly Glu Val Ser  
435 440 445  
Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe Ser His Ala  
450 455 460  
Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser Tyr Ser Gly  
465 470 475 480  
Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser Gly Ile Asp  
485 490 495

Gly Phe Ser Gly His Val Gly Asn His Gly His Ser Met Glu Thr Ser

500

505

510

Pro

&lt;210&gt; 281

&lt;211&gt; 2687

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (359).. (1432)

&lt;400&gt; 281

gttttacgct gccgccggca tccgctcgga cgcgccacg ttgtcttgcg cgctttgccc 60

gcctggccct gggactctga ccctcggtta ccctttcctg cccactagc gtggccgcga 120

gcctcggtga gccggccgta ttcccgtctt cgcttagggg gcacaggcgc aggcacgcgc 180

ccggccactc caagccttcg gtgcgcgggc gcgtctggga tacgggcccg ggaggcgccg 240

ccctccgtcc gcccggtgcc tctcaggaac agcgaaccgg agagagcgcc ggagagtggg 300

gctcagtgcg gagctcggcg ccggggccca tgcccgtgcg ccccgccagg ccggcgcc 358

atg gcc tcc ggg agt gtg gcc gag tgc ctg cag cag gag acc acc tgc 406

Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys

1 5 10 15

ccc gtg tgc ctg cag tac ttc gca gag ccc atg atg ctc gac tgc ggc 454

Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly

20

25

30

cat aac atc tgt tgc gcg tgc ctc gcc cgc tgc tgg ggc acg gca gag 502

His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu

35

40

45

act aac gtg tgc tgc ccg cag tgc cgg gag acc ttc ccg cag agg cac	550
Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His	
50 55 60	
atg cgg ccc aac cgg cac ctg gcc aac gtg acc caa ctg gta aag cag	598
Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln	
65 70 75 80	
ctg cgc acc gag cgg ccg tgc ggg ccc ggc ggc gag atg ggc gtg tgc	646
Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys	
85 90 95	
gag aag cac cgc gag ccc ctg aag ctg tac tgc gag gag gac cag atg	694
Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met	
100 105 110	
ccc atc tgc gtg gtg tgc gac cgc tcc cgc gag cac cgc ggc cac agc	742
Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser	
115 120 125	
gtg ctg ccg ctc gag gag gcg gtg gag ggc ttc aag gag caa atc cag	790
Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln	
130 135 140	
aac cag ctc gac cat tta aaa aga gtg aaa gat tta aag aag aga cgt	838
Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg	
145 150 155 160	
cgg gcc cag ggg gaa cag gca cga gct gaa ctc ttg agc cta acc cag	886
Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln	
165 170 175	
atg gag agg gag aag att gtt tgg gag ttt gag cag ctg tat cac tcc	934
Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser	
180 185 190	

tta aag gag cat gag tat cgc ctc ctg gcc cgc ctt gag gag cta gac	982
Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp	
195 200 205	
ttg gcc atc tac aat agc atc aat ggt gcc atc acc cag ttc tct tgc	1030
Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys	
210 215 220	
aac atc tcc cac ctc agc agc ctg atc gct cag cta gaa gag aag cag	1078
Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln	
225 230 235 240	
cag cag ccc acc agg gag ctc ctg cag gac att ggg gac aca ttg agc	1126
Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser	
245 250 255	
agg gct gaa aga atc agg att cct gaa cct tgg atc aca cct cca gat	1174
Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp	
260 265 270	
ttg caa gag aaa atc cac att ttt gcc caa aaa tgt cta ttc ttg acg	1222
Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr	
275 280 285	
gag agt cta aag cag ttc aca gaa aaa atg cag tca gat atg gag aaa	1270
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys	
290 295 300	
atc caa gaa tta aga gag gct cag tta tac tca gtg gac gtg act ctg	1318
Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu	
305 310 315 320	
gac cca gac acg gcc tac ccc agc ctg atc ctc tct gat aat ctg cgg	1366
Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg	
325 330 335	

caa gtg cgg tac agt tac ctc caa cag gac ctg cct gac aac ccc gag 1414  
 Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu  
 340 345 350  
 agg tct cct tct aca acg tgacagagag gtgtcacacc ttcactttct 1462  
 Arg Ser Pro Ser Thr Thr  
 355  
 ctcatgtctac cttttgtggg cctgtccggc cctacttcag tctgagttac tcgggaggga 1522  
 aaagtgcagc tcctctgac atctgcccc tgagtgggat agatgggttt tctggccatg 1582  
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 ggctgttggc tgtaatccta cgccaggcac aaggcatctt gttgccttgc cacgtcctgt 1702  
 cacagctggg tatccttacc atgttccacg cccttgcagt gggagacagg atgtccatgt 1762  
 tctctaccat ccttttcctt cccatgcaga ttgtgaaatg taatgagatg tatcaagaca 1822  
 tcctagaaat aaaaaccaga tgtccacctc cagtgtttca tactttcttg ttttacacat 1882  
 cgctggaggg ataaagagta tggataatct ttggatttgg agagccgttc aagatacttc 1942  
 cagcttcttg gctcagcctg gcttcctctg gttcagcccc acataatgat tatggctatt 2002  
 tgctgtcatt tctgggctag ggctccttcc taacaaccta gactggaata aggccctgtc 2062  
 agcatggctc cctttatccc agttttccgt ctgggaacag tacctctgcc cctgattccc 2122  
 aatgtgccat agttttatta actccattaa agaagcctgt atgtgttttg gttagttaca 2182  
 gttattttac aataatgggt ggtaatggcc ccacctctgt tatgagataa tgttctaata 2242  
 aatgtctctg cctttgtatc ttttctgagg gctttgtctg ttctcttcat tctaatgaaa 2302  
 ggtgtattct agtgctgggt gcataatcag caggataata ttctgcccga ctccatcctc 2362  
 tgttactaga tcccttacca gtcacatttg tggactgggt gccagtcgta taccatccct 2422  
 ggaaggattc tgggacaata ttccagggat tcattgactt cttggctcct tttctccatt 2482  
 tcctttgggg gaagggggaa ttgacctgc ttaagtgcac cctatcaagg ggcagctccg 2542  
 tccccatggc cattggatca tgagacactc gaagtcagaa ggctggggca gatcattca 2602  
 agcaagcccc catgatggtt ctcatcctg cttctctgtg ggtacgtgcc cctctgttta 2662  
 aaaataaact gaatatggat gtta 2687

&lt;210&gt; 282

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys  
 1                      5                      10                      15  
 Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly  
                     20                      25                      30  
 His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu  
                     35                      40                      45  
 Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His  
                     50                      55                      60  
 Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu Val Lys Gln  
 65                      70                      75                      80  
 Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys  
                     85                      90                      95  
 Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met  
                     100                      105                      110  
 Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser  
                     115                      120                      125  
 Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln  
                     130                      135                      140  
 Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg  
 145                      150                      155                      160  
 Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln

165 170 175  
Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser  
180 185 190  
Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp  
195 200 205  
Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys  
210 215 220  
Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln  
225 230 235 240  
Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser  
245 250 255  
Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp  
260 265 270  
Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr  
275 280 285  
Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys  
290 295 300  
Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu  
305 310 315 320  
Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg  
325 330 335  
Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu  
340 345 350  
Arg Ser Pro Ser Thr Thr  
355

&lt;210&gt; 283



&lt;211&gt; 4777

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (548).. (2704)

&lt;400&gt; 283

cgaaaacccg gagcagctgc gtacgctcat ggacagtcct ccgaggggcg aagccgggca 60

gctgggcatg ctacagtagct gggggaggtt tgggtggaga gtagaaagct gtggctctgc 120

ctctcatccc ctcccgctgg ccccgcccc ccttgcccct accagccag tagtagttcc 180

ccagcgtgcg cccggggaga ccgggaacat ggcgctggga gcgctgtagc agctgagaag 240

gggctgaggc accgccgctt cgctgacagc cggccaccag atgttcatgc attctagaga 300

aagtggaaaa cttagaagcc taattaatga ctgtcttctg gacctctgag accatgtttc 360

tagtgttttc cgtggaatat tatcagaaat aactgttgtt gaaatgcttc cacctcttgc 420

taaaatgaac actgaggaaa aatgaagaag actgacaagc accagcgaaa agttgcagaa 480

tagaaatagc cacactcctc tggagtcttt aattcatcca cagccatcat ataaaggttt 540

tggcatc atg ttt ggg aag aaa aag aaa aag att gaa ata tct ggc ccg 589

Met Phe Gly Lys Lys Lys Lys Lys Ile Glu Ile Ser Gly Pro

1

5

10

tcc aac ttt gaa cac agg gtt cat act ggg ttt gat cca caa gag cag 637

Ser Asn Phe Glu His Arg Val His Thr Gly Phe Asp Pro Gln Glu Gln

15

20

25

30

aag ttt acc ggc ctt ccc cag cag tgg cac agc ctg tta gca gat acg 685

Lys Phe Thr Gly Leu Pro Gln Gln Trp His Ser Leu Leu Ala Asp Thr

35

40

45

gcc aac agg cca aag cct atg gtg gac cct tca tgc atc aca ccc atc 733

Ala Asn Arg Pro Lys Pro Met Val Asp Pro Ser Cys Ile Thr Pro Ile

50	55	60	
cag ctg gct cct atg aag aca atc gtt aga gga aac aaa ccc tgc aag			781
Gln Leu Ala Pro Met Lys Thr Ile Val Arg Gly Asn Lys Pro Cys Lys			
65	70	75	
gaa acc tcc atc aac ggc ctg cta gag gat ttt gac aac atc tcg gtg			829
Glu Thr Ser Ile Asn Gly Leu Leu Glu Asp Phe Asp Asn Ile Ser Val			
80	85	90	
act cgc tcc aac tcc cta agg aaa gaa agc cca ccc acc cca gat cag			877
Thr Arg Ser Asn Ser Leu Arg Lys Glu Ser Pro Pro Thr Pro Asp Gln			
95	100	105	110
gga gcc tcc agc cac ggt cca ggc cac gcg gaa gaa aat ggc ttc atc			925
Gly Ala Ser Ser His Gly Pro Gly His Ala Glu Glu Asn Gly Phe Ile			
115	120	125	
acc ttc tcc cag tat tcc agc gaa tcc gat act act gct gac tac acg			973
Thr Phe Ser Gln Tyr Ser Ser Glu Ser Asp Thr Thr Ala Asp Tyr Thr			
130	135	140	
acc gaa aag tac agg gag aag agt ctc tat gga gat gat ctg gat ccg			1021
Thr Glu Lys Tyr Arg Glu Lys Ser Leu Tyr Gly Asp Asp Leu Asp Pro			
145	150	155	
tat tat aga ggc agc cac gca gcc aag caa aat ggg cac gta atg aaa			1069
Tyr Tyr Arg Gly Ser His Ala Ala Lys Gln Asn Gly His Val Met Lys			
160	165	170	
atg aag cac ggg gag gcc tac tat tct gag gtg aag cct ttg aaa tcc			1117
Met Lys His Gly Glu Ala Tyr Tyr Ser Glu Val Lys Pro Leu Lys Ser			
175	180	185	190
gat ttt gcc aga ttt tct gcc gat tat cac tca cat ttg gac tca ctg			1165
Asp Phe Ala Arg Phe Ser Ala Asp Tyr His Ser His Leu Asp Ser Leu			

195	200	205	
agc aaa cca agt gaa tac agt gac ctc aag tgg gag tat cag aga gcc			1213
Ser Lys Pro Ser Glu Tyr Ser Asp Leu Lys Trp Glu Tyr Gln Arg Ala			
210	215	220	
tcg agt agc tcc cct ctg gat tat tca ttc caa ttc aca cct tct aga			1261
Ser Ser Ser Ser Pro Leu Asp Tyr Ser Phe Gln Phe Thr Pro Ser Arg			
225	230	235	
act gca ggg acc agc ggg tgc tcc aag gag agc ctg gcg tac agt gaa			1309
Thr Ala Gly Thr Ser Gly Cys Ser Lys Glu Ser Leu Ala Tyr Ser Glu			
240	245	250	
agt gaa tgg gga ccc agc ctg gat gac tat gac agg agg cca aag tct			1357
Ser Glu Trp Gly Pro Ser Leu Asp Asp Tyr Asp Arg Arg Pro Lys Ser			
255	260	265	270
tcg tac ctg aat cag aca agc cct cag ccc acc atg cgg cag agg tcc			1405
Ser Tyr Leu Asn Gln Thr Ser Pro Gln Pro Thr Met Arg Gln Arg Ser			
275	280	285	
agg tca ggc tcg gga ctc cag gaa ccg atg atg cca ttt gga gca agt			1453
Arg Ser Gly Ser Gly Leu Gln Glu Pro Met Met Pro Phe Gly Ala Ser			
290	295	300	
gca ttt aaa acc cat ccc caa gga cac tcc tac aac tcc tac acc tac			1501
Ala Phe Lys Thr His Pro Gln Gly His Ser Tyr Asn Ser Tyr Thr Tyr			
305	310	315	
cct cgc ttg tcc gag ccc aca atg tgc att cca aag gtg gat tac gat			1549
Pro Arg Leu Ser Glu Pro Thr Met Cys Ile Pro Lys Val Asp Tyr Asp			
320	325	330	
cga gca cag atg gtc ctc agc cct cca ctg tca ggg tct gac acc tac			1597
Arg Ala Gln Met Val Leu Ser Pro Pro Leu Ser Gly Ser Asp Thr Tyr			

335	340	345	350	
ccc agg ggc cct gcc aaa cta cct caa agt caa agc aaa tcg ggc tat				1645
Pro Arg Gly Pro Ala Lys Leu Pro Gln Ser Gln Ser Lys Ser Gly Tyr				
	355	360	365	
tcc tca agc agt cac cag tac ccg tct ggg tac cac aaa gcc acc ttg				1693
Ser Ser Ser Ser His Gln Tyr Pro Ser Gly Tyr His Lys Ala Thr Leu				
	370	375	380	
tac cat cac ccc tcc ctg cag agc agt tcg cag tac atc tcc acg gct				1741
Tyr His His Pro Ser Leu Gln Ser Ser Ser Gln Tyr Ile Ser Thr Ala				
	385	390	395	
tcc tac ctg agc tcc ctc agc ctc tca tcc agc acc tac ccg ccg ccc				1789
Ser Tyr Leu Ser Ser Leu Ser Leu Ser Ser Ser Thr Tyr Pro Pro Pro				
	400	405	410	
agc tgg ggc tcc tcc tcc gac cag cag ccc tcc agg gtg tcc cat gaa				1837
Ser Trp Gly Ser Ser Ser Asp Gln Gln Pro Ser Arg Val Ser His Glu				
415	420	425	430	
cag ttt cgg gcg gcc ctg cag ctg gtg gtc agc cca gga gac ccc agg				1885
Gln Phe Arg Ala Ala Leu Gln Leu Val Val Ser Pro Gly Asp Pro Arg				
	435	440	445	
gaa tac ttg gcc aac ttt atc aaa atc ggg gaa ggc tca acc ggc atc				1933
Glu Tyr Leu Ala Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile				
	450	455	460	
gta tgc atc gcc acc gag aaa cac aca ggg aaa caa gtt gca gtg aag				1981
Val Cys Ile Ala Thr Glu Lys His Thr Gly Lys Gln Val Ala Val Lys				
	465	470	475	
aaa atg gac ctc cgg aag caa cag aga cga gaa ctg ctt ttc aat gag				2029
Lys Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu				

480	485	490	
gtc gtg atc atg cgg gat tac cac cat gac aat gtg gtt gac atg tac			2077
Val Val Ile Met Arg Asp Tyr His His Asp Asn Val Val Asp Met Tyr			
495	500	505	510
agc agc tac ctt gtc ggc gat gag ctc tgg gtg gtc atg gag ttt cta			2125
Ser Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu			
	515	520	525
gaa ggt ggt gcc ttg aca gac att gtg act cac acc aga atg aat gaa			2173
Glu Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu			
	530	535	540
gaa cag ata gct act gtc tgc ctg tca gtt ctg aga gct ctc tcc tac			2221
Glu Gln Ile Ala Thr Val Cys Leu Ser Val Leu Arg Ala Leu Ser Tyr			
	545	550	555
ctt cat aac caa gga gtg att cac agg gac ata aaa agt gac tcc atc			2269
Leu His Asn Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile			
	560	565	570
ctc ctg aca agc gat ggc cgg ata aag ttg tct gat ttt ggt ttc tgt			2317
Leu Leu Thr Ser Asp Gly Arg Ile Lys Leu Ser Asp Phe Gly Phe Cys			
575	580	585	590
gct caa gtt tcc aaa gag gtg ccg aag agg aaa tca ttg gtt ggc act			2365
Ala Gln Val Ser Lys Glu Val Pro Lys Arg Lys Ser Leu Val Gly Thr			
	595	600	605
ccc tac tgg atg gcc cct gag gtg att tct agg cta cct tat ggg aca			2413
Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Leu Pro Tyr Gly Thr			
	610	615	620
gag gtg gac atc tgg tcc ctc ggg atc atg gtg ata gaa atg att gat			2461
Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Ile Asp			

625	630	635	
ggc gag ccc ccc tac ttc aat gag cct ccc ctc cag gcg atg cgg agg			2509
Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Gln Ala Met Arg Arg			
640	645	650	
atc cgg gac agt tta cct cca aga gtg aag gac cta cac aag gtt tct			2557
Ile Arg Asp Ser Leu Pro Pro Arg Val Lys Asp Leu His Lys Val Ser			
655	660	665	670
tca gtg ctc cgg gga ttc cta gac ttg atg ttg gtg agg gag ccc tct			2605
Ser Val Leu Arg Gly Phe Leu Asp Leu Met Leu Val Arg Glu Pro Ser			
675	680	685	
cag aga gca aca gcc cag gaa ctc ctc gga cat cca ttc tta aaa cta			2653
Gln Arg Ala Thr Ala Gln Glu Leu Leu Gly His Pro Phe Leu Lys Leu			
690	695	700	
gca ggt cca ccg tct tgc atc gtc ccc ctc atg aga caa tac agg cat			2701
Ala Gly Pro Pro Ser Cys Ile Val Pro Leu Met Arg Gln Tyr Arg His			
705	710	715	
cac tgagcagagg attcgtgtag gtggcaaagc tagatgagga catgagaata			2754
His			
attcaggaga acaaaaggaa acacagaaca tgcaaaaggc ctgtgcattc tagaccagcc			2814
aattggtggg acagcgtgat gaccggcagg gttcaacaga ccagggcattc ttcttgtgtc			2874
ttaaacaggc atctctccac tgacagccgg tgtggtcact tggagcacgg ctttaataag			2934
tcattattat atttttcagc ctttcatcca gcaaatcaga aggactcagt acaaactccg			2994
ttatgatata tcctagccac atgcagggta acatgtagga ttttctatat tgaaagaata			3054
cttttctggc aaaaaaaaaa aaaaagaaag aaaggaaaac aaaaagcact tttttcttaa			3114
tggtagcagt ataatgtatt ttgcaacgaa tttgtaattt ttctgtacga tagttttgat			3174
aatttatagt actttgatgt catgtagcca ttgtatcagt tgaagtaata cttgtttact			3234
agaggagttt gaacaaagcc tttcctactt ttttatccct ttaagagaac caatgattct			3294

ttaggaactt tgaatactga atgactctca atcacccgtca gctttagtaa aatctctttc 3354  
 ttatcctaac aagtgtctta tttggtggaa gaagaattaa gagtgatggg gatgggtgtgc 3414  
 acgtttcatt aatccaacca aaaataatga aataaaattt gagccacagt ataccactcc 3474  
 ttgggataaa gttaaataatt tttaaagatc acattttcca tgaacgcctc tagtagcaaa 3534  
 ccattctttt gcacaccaca atgtttccct cagtggccctt tctcaaattg gtacaatgtt 3594  
 cccttggtggc caaattttccc tcccagggag caatttcagt gctaggatca ttggattcag 3654  
 ttcccaaaat agaatgtttc agtgagacca tgagaattcc aggctcaca aggagagga 3714  
 gagaacaggg caagacgttt ggtttcattt gtcaccattt ttaaaactct gtatgctagc 3774  
 acaccaaaact ctgtcttata tttaccttg taccacagta ttaatcgcta ttgttcattg 3834  
 atcgtgctgg aagtctgaac tgactctaga ggatgaatta gcaagagggt attttaccag 3894  
 gtatgatctg acttcagttg tgcccatgtt ataatgtgtt tccgacatag gagagtcgtg 3954  
 ctgctgtcta gatcttcttg aatgttgata aaaatgaatg actactacaa tacattttgt 4014  
 gttgcttggt ggatgaattt gcatgttaac tgtaggcaa tatagatttg cctttaaaac 4074  
 tctggaagag ctacatagtc atcattagtt tctattaatt atgcatcaga caaaagccat 4134  
 ttgttaccaa actgggaaaa cagaggcttt tcttaactat ttcacatact gtaacaaata 4194  
 tgaatttaaa tttgtgatag cgctctgggt gctctaagca taattaagaa tttttgtaat 4254  
 taatagggtg ctaattattt atcactgcta aaaaggaaaa aaggcataaa atgaccttct 4314  
 actgattaga ttttcagttt tctttcaaac tggaaatgcc tccataaata tgatctatga 4374  
 ttttgcttca taaaacagca aatcaatgtt ttatgtaaaa tattaaagca ttaatatata 4434  
 tatgtgagaa taaaaacaat ctaaattccag aaaatggcag tcctaaatgt tcatgagaca 4494  
 gattgtatta atttaaccag gactatgtag aagtagaaag aaaagaaaaa gaaaatcttt 4554  
 tttaaaccag aataaacatt aaaaactatt gcagaaaata gtggattttg gattccaaac 4614  
 attttcgaca gtgtaatgga aatttttctg taattttctt accatcggtt attttttaaa 4674  
 gtattcattg agtttaccaa aagttactgt agcttaaaag gttttgtgag cactaactat 4734  
 tggcagaaac tgcatattgca aataaaaata aatgtttgcc ttt 4777

&lt;211&gt; 719

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 284

Met Phe Gly Lys Lys Lys Lys Lys Ile Glu Ile Ser Gly Pro Ser Asn  
1 5 10 15  
Phe Glu His Arg Val His Thr Gly Phe Asp Pro Gln Glu Gln Lys Phe  
20 25 30  
Thr Gly Leu Pro Gln Gln Trp His Ser Leu Leu Ala Asp Thr Ala Asn  
35 40 45  
Arg Pro Lys Pro Met Val Asp Pro Ser Cys Ile Thr Pro Ile Gln Leu  
50 55 60  
Ala Pro Met Lys Thr Ile Val Arg Gly Asn Lys Pro Cys Lys Glu Thr  
65 70 75 80  
Ser Ile Asn Gly Leu Leu Glu Asp Phe Asp Asn Ile Ser Val Thr Arg  
85 90 95  
Ser Asn Ser Leu Arg Lys Glu Ser Pro Pro Thr Pro Asp Gln Gly Ala  
100 105 110  
Ser Ser His Gly Pro Gly His Ala Glu Glu Asn Gly Phe Ile Thr Phe  
115 120 125  
Ser Gln Tyr Ser Ser Glu Ser Asp Thr Thr Ala Asp Tyr Thr Thr Glu  
130 135 140  
Lys Tyr Arg Glu Lys Ser Leu Tyr Gly Asp Asp Leu Asp Pro Tyr Tyr  
145 150 155 160  
Arg Gly Ser His Ala Ala Lys Gln Asn Gly His Val Met Lys Met Lys  
165 170 175  
His Gly Glu Ala Tyr Tyr Ser Glu Val Lys Pro Leu Lys Ser Asp Phe



180	185	190
Ala Arg Phe Ser Ala Asp Tyr His Ser His Leu Asp Ser Leu Ser Lys		
195	200	205
Pro Ser Glu Tyr Ser Asp Leu Lys Trp Glu Tyr Gln Arg Ala Ser Ser		
210	215	220
Ser Ser Pro Leu Asp Tyr Ser Phe Gln Phe Thr Pro Ser Arg Thr Ala		
225	230	235
Gly Thr Ser Gly Cys Ser Lys Glu Ser Leu Ala Tyr Ser Glu Ser Glu		
245	250	255
Trp Gly Pro Ser Leu Asp Asp Tyr Asp Arg Arg Pro Lys Ser Ser Tyr		
260	265	270
Leu Asn Gln Thr Ser Pro Gln Pro Thr Met Arg Gln Arg Ser Arg Ser		
275	280	285
Gly Ser Gly Leu Gln Glu Pro Met Met Pro Phe Gly Ala Ser Ala Phe		
290	295	300
Lys Thr His Pro Gln Gly His Ser Tyr Asn Ser Tyr Thr Tyr Pro Arg		
305	310	315
Leu Ser Glu Pro Thr Met Cys Ile Pro Lys Val Asp Tyr Asp Arg Ala		
325	330	335
Gln Met Val Leu Ser Pro Pro Leu Ser Gly Ser Asp Thr Tyr Pro Arg		
340	345	350
Gly Pro Ala Lys Leu Pro Gln Ser Gln Ser Lys Ser Gly Tyr Ser Ser		
355	360	365
Ser Ser His Gln Tyr Pro Ser Gly Tyr His Lys Ala Thr Leu Tyr His		
370	375	380
His Pro Ser Leu Gln Ser Ser Ser Gln Tyr Ile Ser Thr Ala Ser Tyr		
385	390	395
		400

Leu Ser Ser Leu Ser Leu Ser Ser Ser Thr Tyr Pro Pro Pro Ser Trp  
405 410 415  
Gly Ser Ser Ser Asp Gln Gln Pro Ser Arg Val Ser His Glu Gln Phe  
420 425 430  
Arg Ala Ala Leu Gln Leu Val Val Ser Pro Gly Asp Pro Arg Glu Tyr  
435 440 445  
Leu Ala Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val Cys  
450 455 460  
Ile Ala Thr Glu Lys His Thr Gly Lys Gln Val Ala Val Lys Lys Met  
465 470 475 480  
Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val Val  
485 490 495  
Ile Met Arg Asp Tyr His His Asp Asn Val Val Asp Met Tyr Ser Ser  
500 505 510  
Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly  
515 520 525  
Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu Gln  
530 535 540  
Ile Ala Thr Val Cys Leu Ser Val Leu Arg Ala Leu Ser Tyr Leu His  
545 550 555 560  
Asn Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu  
565 570 575  
Thr Ser Asp Gly Arg Ile Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln  
580 585 590  
Val Ser Lys Glu Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr  
595 600 605  
Trp Met Ala Pro Glu Val Ile Ser Arg Leu Pro Tyr Gly Thr Glu Val

610	615	620	
Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Ile Asp Gly Glu			
625	630	635	640
Pro Pro Tyr Phe Asn Glu Pro Pro Leu Gln Ala Met Arg Arg Ile Arg			
	645	650	655
Asp Ser Leu Pro Pro Arg Val Lys Asp Leu His Lys Val Ser Ser Val			
	660	665	670
Leu Arg Gly Phe Leu Asp Leu Met Leu Val Arg Glu Pro Ser Gln Arg			
	675	680	685
Ala Thr Ala Gln Glu Leu Leu Gly His Pro Phe Leu Lys Leu Ala Gly			
	690	695	700
Pro Pro Ser Cys Ile Val Pro Leu Met Arg Gln Tyr Arg His His			
705	710	715	

&lt;210&gt; 285

&lt;211&gt; 1496

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (108).. (971)

&lt;400&gt; 285

agc gat ggc	ttg cac agc	taaga tgg aa	gtg acct gag	cct cgc ccg	cg gct ttc	ctc	60
gac ggg acag	cg caa gatt	ggag cac agc	ctt gtc cgg	gag cag t	atg ccg	gaa	116
					Met	Pro Glu	
					1		
gct ggt	ttt cag	gcc aca	aat gct	ttc aca	gag tgc	aaa ttc	acc tgc 164

Ala Gly Phe Gln Ala Thr Asn Ala Phe Thr Glu Cys Lys Phe Thr Cys  
           5                          10                          15  
 acc agt ggt aaa tgc ttg tat ctt ggt tgc ctg gtc tgt aac caa cag 212  
 Thr Ser Gly Lys Cys Leu Tyr Leu Gly Ser Leu Val Cys Asn Gln Gln  
 20                          25                          30                          35  
 aac gac tgt ggg gac aac agt gac gaa gag aac tgt ctc ctg gtg acc 260  
 Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Asn Cys Leu Leu Val Thr  
                           40                          45                          50  
 gag cac ccg cct ccg ggc atc ttc aac tgc gag ctg gag ttc gcc caa 308  
 Glu His Pro Pro Pro Gly Ile Phe Asn Ser Glu Leu Glu Phe Ala Gln  
                           55                          60                          65  
 atc atc atc atc gtc gtg gtg gtc acg gtg atg gtg gtg gtc atc gtc 356  
 Ile Ile Ile Ile Val Val Val Val Thr Val Met Val Val Val Ile Val  
                           70                          75                          80  
 tgc ctg ctg aac cac tac aaa gtc tcc acg cgg tcc ttc atc aac cgc 404  
 Cys Leu Leu Asn His Tyr Lys Val Ser Thr Arg Ser Phe Ile Asn Arg  
                           85                          90                          95  
 ccg aac cag agc cgg agg cgg gag gac ggg ctg ccg cag atc atg cat 452  
 Pro Asn Gln Ser Arg Arg Arg Glu Asp Gly Leu Pro Gln Ile Met His  
 100                          105                          110                          115  
 gcc ccg cgg tcc agg gac agg ttc aca gcg ccg tcc ttc atc cag agg 500  
 Ala Pro Arg Ser Arg Asp Arg Phe Thr Ala Pro Ser Phe Ile Gln Arg  
                           120                          125                          130  
 gat cgc ttc agc cgc ttc cag ccc acc tac ccc tat gtg cag cac gag 548  
 Asp Arg Phe Ser Arg Phe Gln Pro Thr Tyr Pro Tyr Val Gln His Glu  
                           135                          140                          145  
 att gat ctt cct ccc acc atc tcc ctg tcc gac ggt gaa gag cca cct 596

Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro  
 150 155 160  
 cct tac cag ggg ccc tgc acc ctg cag ctc cgg gac cct gaa cag cag 644  
 Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln  
 165 170 175  
 atg gaa ctc aac cga gag tcc gtg agg gcc cca ccc aac cga acc ata 692  
 Met Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile  
 180 185 190 195  
 ttt gac agt gat tta ata gac att gct atg tat agc ggg ggt cca tgc 740  
 Phe Asp Ser Asp Leu Ile Asp Ile Ala Met Tyr Ser Gly Gly Pro Cys  
 200 205 210  
 cca ccc agc agc aac tcg ggc atc agt gca agc acc tgc agc agt aac 788  
 Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Ser Thr Cys Ser Ser Asn  
 215 220 225  
 ggg agg atg gag ggg cca ccc ccc aca tac agc gag gtg atg ggc cac 836  
 Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Met Gly His  
 230 235 240  
 cac cca ggc gcc tct ttc ctc cat cac cag cgc agc aac gca cac agg 884  
 His Pro Gly Ala Ser Phe Leu His His Gln Arg Ser Asn Ala His Arg  
 245 250 255  
 ggc agc aga ctg cag ttt cag cag aac aat gca gag agc aca ata gta 932  
 Gly Ser Arg Leu Gln Phe Gln Gln Asn Asn Ala Glu Ser Thr Ile Val  
 260 265 270 275  
 ccc atc aaa ggc aaa gat agg aag cct ggg aac ctg gtc tgattccttc 981  
 Pro Ile Lys Gly Lys Asp Arg Lys Pro Gly Asn Leu Val  
 280 285  
 caacgtgcac ttcagctgga gaaagaaacc aagaaggga gcgccgctg ggcccctcct 1041

gcgcacagtg ttgttcagtt tcacatggta caaataagta aaaccaaagt agcaaacacg 1101  
 gtctttgttt ctgattcctt ttaggggaat tgcattgcaa ctagactgaa atgatacaaa 1161  
 cttccatctg gtctgaccgc aaacagtgtt tatttgggga caggggttgg gatgggggtg 1221  
 tgggcagggg aaaacagaga acgggatgct ttgaagatac catgaaataa aaccacaga 1281  
 ggtatttgat gtatttaatt gtgaaaggag actttgcaga taaatgaggc cagaatggca 1341  
 tgttttataa ttaactgaat aaagaaggaa gcattattat atattattgt ggggaagaac 1401  
 cagccagttc gctttttctc ctaaggtgtg gaacttttat tttgttttaa aaatatgaat 1461  
 caaaattcct gtgttggtg ccaaggtata aagtg 1496

<210> 286

<211> 288

<212> PRT

<213> Homo sapiens

<400> 286

Met Pro Glu Ala Gly Phe Gln Ala Thr Asn Ala Phe Thr Glu Cys Lys

1 5 10 15

Phe Thr Cys Thr Ser Gly Lys Cys Leu Tyr Leu Gly Ser Leu Val Cys

20 25 30

Asn Gln Gln Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Asn Cys Leu

35 40 45

Leu Val Thr Glu His Pro Pro Pro Gly Ile Phe Asn Ser Glu Leu Glu

50 55 60

Phe Ala Gln Ile Ile Ile Ile Val Val Val Val Thr Val Met Val Val

65 70 75 80

Val Ile Val Cys Leu Leu Asn His Tyr Lys Val Ser Thr Arg Ser Phe

85 90 95

Ile Asn Arg Pro Asn Gln Ser Arg Arg Arg Glu Asp Gly Leu Pro Gln

100	105	110
Ile Met His Ala Pro Arg Ser Arg Asp Arg Phe Thr Ala Pro Ser Phe		
115	120	125
Ile Gln Arg Asp Arg Phe Ser Arg Phe Gln Pro Thr Tyr Pro Tyr Val		
130	135	140
Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu		
145	150	155
Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro		
165	170	175
Glu Gln Gln Met Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn		
180	185	190
Arg Thr Ile Phe Asp Ser Asp Leu Ile Asp Ile Ala Met Tyr Ser Gly		
195	200	205
Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Ser Thr Cys		
210	215	220
Ser Ser Asn Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val		
225	230	235
Met Gly His His Pro Gly Ala Ser Phe Leu His His Gln Arg Ser Asn		
245	250	255
Ala His Arg Gly Ser Arg Leu Gln Phe Gln Gln Asn Asn Ala Glu Ser		
260	265	270
Thr Ile Val Pro Ile Lys Gly Lys Asp Arg Lys Pro Gly Asn Leu Val		
275	280	285

&lt;210&gt; 287

&lt;211&gt; 2207

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (571).. (1752)

&lt;400&gt; 287

gttgagaggc tgcgctggac cgaagcgggtg gctgctaagc tcgcgggggt aaggggtcgc 60  
gctggggccag gggttggggc cgggatccgg cagctgagcg ggccggcacc cctcctcttc 120  
tctgccggtc acagccaatg tacggctcgg cctggctgcc ccctcccca ggattcccca 180  
tccccagctt ctgcctctcc ccgcaccgcc cccaccccg gatttcgacc cccttaaggg 240  
ctccaccccg ctccgggata cccttctccc agctcctata ccttaggact gccccgcccc 300  
ctagaacctc cccgtcagga tctccgtccc tcagccgctc acagcctcct ccagcgccc 360  
atgccttga gctgcccact acctctagac tgccctcccg ggctggcgtc ccacggagtc 420  
tcagccgcgc accccttctc cggtagctcc taccctgcc tgtgcgggcc tcgtccccgc 480  
gcccagccct cgggtgtgcc tccgacagcg ccgcgtctc tcagccgccc ccctgcccct 540  
cgggcccccc tctctgtgc ccctggcgcc atg gcg tgc agc ctc aag gac gag 594

Met Ala Cys Ser Leu Lys Asp Glu

1

5

ctg ctg tgc tcc atc tgc ctg agc atc tac cag gac ccg gtg agc ctg 642  
Leu Leu Cys Ser Ile Cys Leu Ser Ile Tyr Gln Asp Pro Val Ser Leu

10

15

20

ggc tgc gag cat tac ttc tgc cgc cgc tgc atc acg gag cac tgg gtg 690  
Gly Cys Glu His Tyr Phe Cys Arg Arg Cys Ile Thr Glu His Trp Val

25

30

35

40

cgg cag gag gcg cag ggc gcc cgc gac tgc ccc gag tgc cgg cgc acg 738  
Arg Gln Glu Ala Gln Gly Ala Arg Asp Cys Pro Glu Cys Arg Arg Thr

45

50

55

ttc gcc gag ccc gcg ctg gcg ccc agc ctc aag ctg gcc aac atc gtg 786





Glu Ala Asp Thr Ala Arg Thr Leu Thr Asp Ile Glu Gln Lys Val Gln	
205	210
cgc tac agc cag cag ctg cgc aag gtc cag gag gga gcc cag atc ctg	1266
Arg Tyr Ser Gln Gln Leu Arg Lys Val Gln Glu Gly Ala Gln Ile Leu	
220	225
cag gag cgg ctg gct gaa acc gac cgg cac acc ttc ctg gct ggg gtg	1314
Gln Glu Arg Leu Ala Glu Thr Asp Arg His Thr Phe Leu Ala Gly Val	
235	240
gcc tca ctg tcc gag cgg ctc aag gga aaa atc cat gag acc aac ctc	1362
Ala Ser Leu Ser Glu Arg Leu Lys Gly Lys Ile His Glu Thr Asn Leu	
250	255
aca tat gaa gac ttc ccg acc tcc aag tac aca ggc ccc ctg cag tac	1410
Thr Tyr Glu Asp Phe Pro Thr Ser Lys Tyr Thr Gly Pro Leu Gln Tyr	
265	270
acc atc tgg aag tcc ctg ttc cag gac atc cac cca gtg cca gcc gcc	1458
Thr Ile Trp Lys Ser Leu Phe Gln Asp Ile His Pro Val Pro Ala Ala	
285	290
cta acc ctg gac ccg ggc aca gcc cac cag cgc ctg atc ctg tcg gac	1506
Leu Thr Leu Asp Pro Gly Thr Ala His Gln Arg Leu Ile Leu Ser Asp	
300	305
gac tgc acc att gtg gct tac ggc aac ttg cac cca cag cca ctg cag	1554
Asp Cys Thr Ile Val Ala Tyr Gly Asn Leu His Pro Gln Pro Leu Gln	
315	320
gac tcg cca aag cgc ttc gat gtg gag gtg tcg gtg ctg ggt tct gaa	1602
Asp Ser Pro Lys Arg Phe Asp Val Glu Val Ser Val Leu Gly Ser Glu	
330	335
gcc ttc agt agt ggc gtc cac tac tgg gag gtg gtg gtg gcg gag aag	1650

Ala Phe Ser Ser Gly Val His Tyr Trp Glu Val Val Val Ala Glu Lys  
 345 350 355 360  
 acc cag tgg gtg atc ggg ctg gca cac gaa gcc gca agc cgc aag ggc 1698  
 Thr Gln Trp Val Ile Gly Leu Ala His Glu Ala Ala Ser Arg Lys Gly  
 365 370 375  
 agc atc cag atc cag aac ctt ggc tgc aag gga gtc tgg gaa atg tca 1746  
 Ser Ile Gln Ile Gln Asn Leu Gly Cys Lys Gly Val Trp Glu Met Ser  
 380 385 390  
 ttt ccc tagaaggaag ttaggggtggg tggagcaagc cccacctgcg ttcttctgcc 1802  
 Phe Pro  
 acagcatcca atcgtgaaga actcgggaga ggggtggagtc cacatctagg gttgtcctgc 1862  
 cccttggtc tatccctgcc cagaggtggg aactggagga gtgggctgca agactgagcc 1922  
 taaatgtctc cccggccttg acttttcttt ctagtcctgg ggcctagatt ctgcacttgg 1982  
 ggtctctgac acaacacacc atcccaaagt agccggaaga gctaaacaca gggggttctt 2042  
 aaaatggctg ccccgccac ccgggcctcc cttgggcaaa aggaattgtc agccctaccc 2102  
 caacccttca actaccagaa tctgggccac cccagcagta tttttattta aaatgttgcc 2162  
 cattttatga gttatgatca atttgtatta aattaaagtt acaga 2207

<210> 288

<211> 394

<212> PRT

<213> Homo sapiens

<400> 288

Met Ala Cys Ser Leu Lys Asp Glu Leu Leu Cys Ser Ile Cys Leu Ser  
 1 5 10 15  
 Ile Tyr Gln Asp Pro Val Ser Leu Gly Cys Glu His Tyr Phe Cys Arg  
 20 25 30

Arg Cys Ile Thr Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg  
 35 40 45  
 Asp Cys Pro Glu Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro  
 50 55 60  
 Ser Leu Lys Leu Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu  
 65 70 75 80  
 Asp Ala Ile Leu Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His  
 85 90 95  
 Asp Lys Val Lys Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe  
 100 105 110  
 Phe Cys Asp Glu Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile  
 115 120 125  
 Asp Asp Ala Phe Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln  
 130 135 140  
 Ala Leu Gln Asp Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu  
 145 150 155 160  
 Lys Arg Gln Leu Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr  
 165 170 175  
 Thr Ile Gly Glu Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg  
 180 185 190  
 Gln Lys Ala Met Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu  
 195 200 205  
 Thr Asp Ile Glu Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys  
 210 215 220  
 Val Gln Glu Gly Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp  
 225 230 235 240  
 Arg His Thr Phe Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys

	245	250	255
Gly Lys Ile His Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser			
260	265	270	
Lys Tyr Thr Gly Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln			
275	280	285	
Asp Ile His Pro Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala			
290	295	300	
His Gln Arg Leu Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly			
305	310	315	320
Asn Leu His Pro Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val			
325	330	335	
Glu Val Ser Val Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr			
340	345	350	
Trp Glu Val Val Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala			
355	360	365	
His Glu Ala Ala Ser Arg Lys Gly Ser Ile Gln Ile Gln Asn Leu Gly			
370	375	380	
Cys Lys Gly Val Trp Glu Met Ser Phe Pro			
385	390		

<210> 289

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 289

cttctgctct aaaagctgcg

20

<210> 290

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 290

cgacctgcag ctcgagcaca

20

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Organization  
International Bureau



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PCT

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G01N 33/50, A61K 48/00

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wara, Fuji-shi, Shizuoka 416-0931 (JP).

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(54) Title: NF-KAPPAB ACTIVATING GENES

(57) Abstract: Provided are proteins capable of activating NF- $\kappa$ B, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of NF- $\kappa$ B. Using plasmid pNF $\kappa$ B-Luc, cDNA encoding a protein capable of activating NF- $\kappa$ B has been cloned from a cDNA library constructed from human lung fibroblasts and the like, and the DNA sequence and the deduced amino acid sequence determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting NF- $\kappa$ B activation.

WO 2003/048202 A3

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/47 C12N15/12 C12N15/63 C12N15/11 C12N5/10  
C12Q1/68 A61K38/17 G01N33/50 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, SEQUENCE SEARCH, PAJ, WPI Data, MEDLINE, BIOSIS, EMBASE, EMBL

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! Homo sapiens, TTK protein kinase, retrieved from EBI Database accession no. BC000633 XP002233369 abstract</p> <p>---</p> <p>-/--</p>	1-13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

5 March 2003

Date of mailing of the international search report

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Mossier, B



# INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>MILLS G B ET AL: "EXPRESSION OF TTK A NOVEL HUMAN PROTEIN KINASE IS ASSOCIATED WITH CELL PROLIFERATION" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 22, 1992, pages 16000-16006, XP002233366 ISSN: 0021-9258 page 16001, column 1, paragraph 5 -column 2, paragraph 2; figure 1 &amp; DATABASE EMBL 'Online! 27 February 1992 (1992-02-27) retrieved from EBI Database accession no. M86699 abstract</p>	1-13
X	<p>DOUVILLE E M J ET AL: "MULTIPLE CDNAS ENCODING THE ESK KINASE PREDICT TRANSMEMBRANE AND INTRACELLULAR ENZYME ISOFORMS" MOLECULAR AND CELLULAR BIOLOGY, vol. 12, no. 6, 1992, pages 2681-2689, XP009006945 ISSN: 0270-7306 figure 3 &amp; DATABASE EMBL 'Online! 1 April 1992 (1992-04-01) retrieved from EBI Database accession no. M86377 abstract</p>	1-13
Y	<p>US 5 932 425 A (CIECHANOVER AARON ET AL) 3 August 1999 (1999-08-03)</p> <p>abstract column 1, line 16 - line 42 column 2, line 47 -column 3, line 15; examples 1-3</p>	1-16, 18-26, 30-33, 36,37
Y	<p>EP 0 955 372 A (SUNTORY LTD) 10 November 1999 (1999-11-10)</p> <p>page 2, line 5 - line 10 page 3, line 2 - line 17; claims 1-13; examples 1-10; table 1</p>	1-16, 18-26, 30-33, 36,37
Y	<p>WO 96 17927 A (KAROBIO AB ;NILSSON STEFAN (SE)) 13 June 1996 (1996-06-13)</p> <p>abstract page 10, line 21 -page 11, line 11 page 13, line 14 - line 16; claims 1-3,15; figures 2B,3B</p>	1-16, 18-26, 30-33, 36,37
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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>KWON BYUNGSUK ET AL: "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand"</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY, THE AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, INC.,, US, vol. 274, no. 10, 5 March 1999 (1999-03-05), pages 6056-6061, XP002147323 ISSN: 0021-9258 abstract page 6056, column 2, paragraph 2 page 6057, column 1, paragraph 1 -column 2, paragraph 2 page 6060, column 1, paragraph 2; figure 2 page 6060, column 2, paragraph 4</p>	1-16, 18-26, 30-33, 36,37
Y	<p>WANG CUN-YU ET AL: "NK-kappaB antiapoptosis: Induction of TRAF1 and TRAF2 and c-IAP1 and c-IAP2 to suppress caspase-8 activation."</p> <p>SCIENCE (WASHINGTON D C), vol. 281, no. 5383, pages 1680-1683, XP002233368 ISSN: 0036-8075 abstract</p>	1-16, 18-26, 30-33, 36,37
A	<p>WO 94 23045 A (BAEUEERLE PATRICK ;BOEHRINGER INGELHEIM INT (DE); HENKEL THOMAS (US) 13 October 1994 (1994-10-13)</p> <p>abstract column 2, line 4 - line 37 column 6, line 49 -column 9, line 36</p>	1-16, 18-26, 30-33, 36,37
A	<p>WO 01 72296 A (ANDERSSON TOVE ;ASTACAROTENE AB (SE); PETTERSSON SVEN (SE)) 4 October 2001 (2001-10-04)</p> <p>the whole document</p>	1-16, 18-26, 30-33, 36,37

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/JP 02/12644

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 34 and 35  
because they relate to subject matter not required to be searched by this Authority, namely:  
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.: 17, 27-29  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-16, 18-26, 30-33, 36, 37 (all partial)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-16, 18-26, 30-33, 36,  
37 (all partially)

A purified protein comprising the amino acid sequence as depicted in SEQ ID NO:2 and the subject matter relating to said protein, respectively an isolated polynucleotide comprising the polynucleotide sequence as depicted in SEQ ID NO:1 and the subject matter relating to said sequence.

Invention 2-144: Claims 1-16, 18-26, 30-33, 36,  
37 (all partially)

As for subject 1, but respectively relating to SEQ ID NOs: 3 - 288 (i.e. subject 2, corresponding to amino acid sequence SEQ ID NO:4 and polynucleotide sequence SEQ ID NO:3; subject 3, corresponding to SEQ IDs NO:6 and 5;.....; subject 144, corresponding to SEQ IDs NO:288 and 287).

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## Continuation of Box I.1

Although claim 14 is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Although claims 14, 23, 26, 29 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

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## Continuation of Box I.1

Claims Nos.: 34 and 35

With regard to claim 34:

Claim 34 relates to subject matter for which no search is required according to Rule 39.1(v)PCT.

Given that the claim is formulated in terms of such subject matter or merely specifies features relating to presentation of information.

With regard to claim 35:

Claim 35 relates to subject matter for which no search is required according to Rule 39.1(vi) PCT.

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## Continuation of Box I.2

Claims Nos.: 17, 27-29

Present claims 17, 27-29 relate to an extremely large number of possible compounds. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is not to be found. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search is impossible. Consequently, no search has been carried out for those claims.

Present claim 26 relates to an extremely large number of possible compounds. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the compounds claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely those parts relating to monoclonal or polyclonal antibodies according to claim 21 or 22, antisense oligonucleotides according to claim 24 and/or ribozymes or desoxyribozymes according to claim 25.

The applicant's attention is drawn to the fact that claims, or parts of

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 02/12644

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
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